



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 124765

To: Elizabeth McElwain  
Location: REM-2A11/2C18  
Art Unit: 1638  
Thursday, June 24, 2004

Case Serial Number: 10/069772

From: Beverly Shears  
Location: Remsen Bldg.  
RM 1A54  
Phone: 571-272-2528

[beverly.shears@uspto.gov](mailto:beverly.shears@uspto.gov)

### Search Notes

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 18, 2004, 17:33:47 ; Search time 46 Seconds  
(without alignments)  
2585.877 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGGRMSDPSEGNILERV.....IYIEPDESEHKGVFWYHKM 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	377	10	Q9SCG2
2	1922	93.9	377	10	Q7XA13
3	1644	80.3	326	10	Q7XA10
4	1607	78.5	326	10	Q7XA08
5	1596	78.0	326	10	Q7XA09
6	1589.5	77.7	374	10	Q65771
7	1396.5	68.2	383	10	Q82729
8	1387.5	67.8	383	10	Q8G2C3
9	1374.5	67.1	383	10	Q9LL17
10	1366.5	66.8	383	10	Q8W2F0
11	1360	66.4	383	10	Q8H2C3
12	1359.5	66.4	383	10	Q9SP28
13	1357	66.3	382	10	Q8W2E9
14	1350.5	66.0	383	10	Q9SP29
15	1348.5	65.9	383	10	Q41305
16	1347.5	65.8	387	10	Q84UB7

17	1337.5	65.3	387	10	Q84VT2	Q84vt2 punica gran
18	1336	65.3	382	10	Q24471	Q24471 petroselinu
19	1336	65.3	382	10	Q8H943	Q8H943 spinacia ol
20	1336	65.3	384	10	Q8W2B9	Q8W2B9 gosypium h
21	1335	65.2	379	10	Q65772	Q65772 crepis pala
22	1332.5	65.1	383	10	Q23956	Q23956 gosypium h
23	1323.5	64.7	383	10	Q9AT72	Q9AT72 calendula o
24	1323.5	64.6	383	10	Q8GVC9	Q8GVC9 olea europa
25	1317	64.3	384	10	Q8LPE8	Q8LPE8 brassica ca
26	1312	64.1	384	10	Q9L138	Q9L138 brassica na
27	1311	64.0	384	10	Q9ZPI2	Q9ZPI2 brassica ca
28	1296.5	63.3	385	10	Q23955	Q23955 gosypium h
29	1293.5	63.2	383	10	Q8LPE8	Q8LPE8 arabidopsis
30	1287.5	62.9	379	10	Q9LKK6	Q9LKK6 arachis hyp
31	1286.5	62.8	379	10	Q9LKK5	Q9LKK5 arachis dur
32	1282	62.6	369	10	Q84UB9	Q84UB9 trichosanthe
33	1281.5	62.6	379	10	Q22628	Q22628 arachis hyp
34	1279.5	62.5	379	10	Q94G88	Q94G88 arachis hyp
35	1277.5	62.4	379	10	Q9LKK4	Q9LKK4 arachis ipa
36	1273.5	62.2	387	10	Q41131	Q41131 ricinus com
37	1270.5	62.1	346	10	Q81364	Q81364 prunus arme
38	1260	61.6	382	10	Q7XA14	Q7XA14 hedera heli
39	1245	60.8	384	10	Q81094	Q81094 lesquerella
40	1241.5	60.6	383	10	Q24472	Q24472 petroselinu
41	1235	60.3	382	10	Q9FW85	Q9FW85 petroselinu
42	1232.5	60.2	383	10	Q9FW91	Q9FW91 petroselinu
43	1232	60.2	384	10	Q9FW88	Q9FW88 petroselinu
44	1230.5	60.1	383	10	Q9FW90	Q9FW90 petroselinu
45	1230	60.1	384	10	Q9FW86	Q9FW86 petroselinu

## ALIGNMENTS

## RESULT 1

ID	Q9SCG2	PRELIMINARY;	PRT;	377 AA.
AC	Q9SCG2;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	(8,11)-linoleoyl desaturase (Fragment).			
GN	DES8.11.			
OS	Calendula officinalis.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae;			
OC	Calendula.			
OX	NCBI_TaxID=41496;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=Immature seed;			
RX	MEDLINE=20086417; PubMed=10622705;			
RA	Fritzsche K., Horning E., Peitzsch N., Renz A., Feussner I.;			
RT	"Isolation and characterization of a calendic acid producing (8,11)-			
RT	linoleoyl desaturase."			
RL	FEBS Lett. 462:249-253(1999).			
DR	EMBL, AJ245938; CAB64256.1.			
DR	GO; GO:0016451; F:oxidoreductase activity; IEA.			
DR	InterPro; IPR005804; FA desat. fam.			
DR	Pfam; PF00487; FA desaturase; 1.			
DR	Prodom; PD001081; FA desat. fam; 2.			
FT	NON TER			
FT	SEQUENCE 377 AA; 43615 MW; 1CBP7650955F26BP CRC64;			

Qy	1	MGAGGRMSDPSEGNILERVVDPPTLSDKAIPTHCFRSTYIRSSYYVHHLLIVAVV	60
Db	1	MGAGGRMSDPSEGNILERVVDPPTLSDKAIPTHCFRSTYIRSSYYVHHLLIVAVV	60

QY 61 FYLLANTYIPLIPPLAYLAMPVTFWCOASITLGTMTVGHGCHHAESDYQIIDDIVGFV 120  
DB 61 FYLLANTYIPLIPPLAYLAMPVTFWCOASITLGTMTVGHGCHHAESDYQIIDDIVGFV 120  
QY 121 LHSALTTFPSWKYSHRNHNANTNSLDNDVYIPRKSXKVTYSKLNNPGRVFTLVFR 180  
DB 121 LHSALTTFPSWKYSHRNHNANTNSLDNDVYIPRKSXKVTYSKLNNPGRVFTLVFR 180  
QY 181 LTLGFPYLITNISGKKGFRANHPDMSPIFNDRERVOVLSDFGLLAVFAIKLVA 240  
DB 181 LTLGFPYLITNISGKKGFRANHPDMSPIFNDRERVOVLSDFGLLAVFAIKLVA 240  
QY 241 KGAAMVIMYAIPLVGVSVFPLITLHTHTLSLPHYSTENMWIKALSTIDRDFGLN 300  
DB 241 KGAAMVIMYAIPLVGVSVFPLITLHTHTLSLPHYSTENMWIKALSTIDRDFGLN 300  
QY 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMREAKECIYI 360  
DB 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMREAKECIYI 360  
QY 361 EPDESEHKGVFWYHKM 377  
DB 361 EPDESEHKGVFWYHKM 377

## RESULT 2

QYXAL3 PRELIMINARY; PRT; 377 AA.  
AC QYXAL3;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Delta12-fatty acid acetylase.  
OS Helianthus annuus (Common sunflower).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;  
OC Helianthus.  
OX NCBI\_TaxID=4232;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22674157; PubMed=12787248;  
RA Cahoon E.B., Schmitt J.A., Hultman E.A., Minto R.E.;  
RT "Fungal responsive fatty acid acetylases occur widely in  
evolutionarily distant plant families."  
RL Plant J. 34:671-683(2003).  
DR EMBL: AY166773; AAC38032.1; -  
SQ SEQUENCE 377 AA; 43750 MW; 832C8A129C6C2A55 CRC64;

Query Match 93.9%; Score 1922; DB 10; Length 377;  
Best Local Similarity 91.8%; Pred. No. 3.5e-158;  
Matches 346; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGAGRMSDPSGKILERVVDPPFTLSDLKKAIPHCERSVIRSSYVVHDLIVAV 60  
DB 1 MGAGRMSDPSGKILERVVDPPFTLSDLKKAIPHCERSVIRSSYVVHDLIVAV 60  
QY 61 FYLLANTYIPLIPPLAYLAMPVTFWCOASITLGTMTVGHGCHHAESDYQIIDDIVGFV 120  
DB 61 FYLLANTYIPLIPPLAYLAMPVTFWCOASITLGTMTVGHGCHHAESDYQIIDDIVGFV 120  
QY 121 LHSALTTFPSWKYSHRNHNANTNSLDNDVYIPRKSXKVTYSKLNNPGRVFTLVFR 180  
DB 121 LHSALTTFPSWKYSHRNHNANTNSLDNDVYIPRKSXKVTYSKLNNPGRVFTLVFR 180  
QY 181 LTLGFPYLITNISGKKGFRANHPDMSPIFNDRERVOVLSDFGLLAVFAIKLVA 240  
DB 181 LTLGFPYLITNISGKKGFRANHPDMSPIFNDRERVOVLSDFGLLAVFAIKLVA 240  
QY 241 KGAAMVIMYAIPLVGVSVFPLITLHTHTLSLPHYSTENMWIKALSTIDRDFGLN 300  
DB 241 KGAAMVIMYAIPLVGVSVFPLITLHTHTLSLPHYSTENMWIKALSTIDRDFGLN 300

QY 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMREAKECIYI 360  
DB 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMREAKECIYI 360  
QY 361 EPDESEHKGVFWYHKM 377  
DB 361 EPDESEHKGVFWYHKM 377

## RESULT 3

QYXAL0 PRELIMINARY; PRT; 326 AA.  
AC QYXAL0;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Delta12-fatty acid acetylase (Fragment).  
OS Rubusckia hirta.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;  
OC Rubusckia.  
OX NCBI\_TaxID=52299;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22674157; PubMed=12787248;  
RA Cahoon E.B., Schmitt J.A., Hultman E.A., Minto R.E.;  
RT "Fungal responsive fatty acid acetylases occur widely in  
evolutionarily distant plant families."  
RL Plant J. 34:671-683(2003).  
DR EMBL: AY166776; AAC38035.1; -  
FT NON-TER 1  
FT NON-TER 1  
SQ SEQUENCE 326 AA; 37861 MW; D3C65BAD9E25783 CRC64;

Query Match 80.3%; Score 1644; DB 10; Length 326;  
Best Local Similarity 92.0%; Pred. No. 3.6e-134;  
Matches 300; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 33 KAIPHCERSVIRSSYVVHDLIVAVFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 92  
DB 1 KAIPHCERSVIRSSYVVHDLIVAVFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 92  
QY 93 TGLWITGHEGCHHAESDYQIIDDIVGFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 152  
DB 93 TGLWITGHEGCHHAESDYQIIDDIVGFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 152  
QY 61 TGLWITGHEGCHHAESDYQIIDDIVGFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 120  
DB 61 TGLWITGHEGCHHAESDYQIIDDIVGFYLLANTYIPLIPPLAYLAMPVTFWCOASITL 120  
QY 153 IPKRSKXKVTYSKLNNPGRVFTLVFRITLGTPLYLITNISGKKGFRANHPDMSPIF 212  
DB 153 IPKRSKXKVTYSKLNNPGRVFTLVFRITLGTPLYLITNISGKKGFRANHPDMSPIF 212  
QY 213 NDRERVOVLSDFGLLAVFAIKLVAAGAMVIMYAIPLVGVSVFPLITLHTHTL 272  
DB 213 NDRERVOVLSDFGLLAVFAIKLVAAGAMVIMYAIPLVGVSVFPLITLHTHTL 272  
QY 273 SLPHYSTENMWIKALSTIDRDFGLN RVHDVTHHTVHLHLISYIPHYHAKARDAIK 332  
DB 273 SLPHYSTENMWIKALSTIDRDFGLN RVHDVTHHTVHLHLISYIPHYHAKARDAIK 332  
QY 333 PVLGEEYKIDRTPIFAMREAKECI 358  
DB 333 PVLGEEYKIDRTPIFAMREAKECI 358  
QY 301 PVLGEEYKIDRTPIFAMREAKECI 326  
DB 301 PVLGEEYKIDRTPIFAMREAKECI 326

## RESULT 4

QYXAL0 PRELIMINARY; PRT; 326 AA.  
AC QYXAL0;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Delta12-fatty acid acetylase (Fragment).  
OS Helichrysum bracteatum.



OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Campanulids; Asterales; Asteroideae; Asteroideae; Gnaphalaceae;  
 OC Helicrysium.  
 NC NCB1\_TaxID=220345;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22674157; PubMed=12787248;  
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;  
 RT "Fungal responsive fatty acid acetyltransferases occur widely in  
 RT evolutionarily distant plant families."  
 RL Plant J. 34:671-683(2003).  
 DR EMBL, AY167778; AAC38037.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 326 AA; 38024 MW; D355816CF4AA2829 CRC64;

Query Match 78.5%; Score 1607; DB 10; Length 326;  
 Best Local Similarity 88.0%; Pred. No. 5.7e-131;  
 Matches 287; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 32 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPLTPLYLAMPVYFCQASI 91  
 DB 1 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPLTPLYLAMPVYFCQASI 60  
 QY 92 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 151  
 DB 61 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 120  
 QY 152 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNISSGKGRFANHPDPSPI 211  
 DB 121 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNISSGKGRFANHPDPSPI 180  
 QY 212 FNDREVOVLISDGLAVFAIKLVAAKGAAMVIMYALPVGVSVFVLITLYLHHTH 271  
 DB 181 FTERERIQVNLSDGIIAVCYALVAAKATVMCMYGVGVNAFVLLITLYLHHTH 240  
 QY 272 LSLPHYSTENMWIKGALSTIDRDFGLNRFVHDVTHVHLHLSYIPHYAKARDAI 331  
 DB 241 LSLPHYSTENMWIKGALSTIDRDFGLNRFVHDVTHVHLHLSYIPHYAKARDAI 300  
 QY 332 KPVIGERYKIDRPIPFAMTBEAKC 357  
 DB 301 NPVLGEYKIDRPIPFAMTBEAKC 326

## RESULT 5

QY 07XA09 PRELIMINARY; PRT; 326 AA.  
 AC 07XA09;  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Delta12-fatty acid acetyltransferase (Fragment).  
 OS Dimorphochea sinuata (African daisy).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Campanulids; Asterales; Asteroideae; Asteroideae; Calenduleae;  
 OC Dimorphochea.  
 NC NCB1\_TaxID=112408;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22674157; PubMed=12787248;  
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;  
 RT "Fungal responsive fatty acid acetyltransferases occur widely in  
 RT evolutionarily distant plant families."  
 RL Plant J. 34:671-683(2003).  
 DR EMBL, AY167777; AAC38036.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 326 AA; 37813 MW; 978706DD144EA3D0 CRC64;  
 Query Match 78.0%; Score 1596; DB 10; Length 326;

Best Local Similarity 87.7%; Pred. No. 5.2e-130;  
 Matches 286; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

QY 32 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPLTPLYLAMPVYFCQASI 91  
 DB 1 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPLTPLYLAMPVYFCQASI 60  
 QY 92 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 151  
 DB 61 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 120  
 QY 152 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNISSGKGRFANHPDPSPI 211  
 DB 121 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNISSGKGRFANHPDPSPI 180  
 QY 212 FNDREVOVLISDGLAVFAIKLVAAKGAAMVIMYALPVGVSVFVLITLYLHHTH 271  
 DB 181 FTERERIQVNLSDGIIAVCYALVAAKATVMCMYGVGVNAFVLLITLYLHHTH 240  
 QY 272 LSLPHYSTENMWIKGALSTIDRDFGLNRFVHDVTHVHLHLSYIPHYAKARDAI 331  
 DB 241 LSLPHYSTENMWIKGALSTIDRDFGLNRFVHDVTHVHLHLSYIPHYAKARDAI 300  
 QY 332 KPVIGERYKIDRPIPFAMTBEAKC 357  
 DB 301 NPVLGEYKIDRPIPFAMTBEAKC 326

## RESULT 6

QY 065771 PRELIMINARY; PRT; 374 AA.  
 AC 065771;  
 DT 01-AUG-1998 (Tremblrel. 07, Created)  
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Delta 12 fatty acid epoxigenase.  
 OS Crepis palaestina.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Campanulids; Asterales; Asteroideae; Cichorioideae; Cichorioideae; Crepis.  
 NC NCB1\_TaxID=72611;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98239771; PubMed=9572738;  
 RA Lee M., Lemman M., Banas A., Bator M., Singh S., Schweizer M.,  
 RA Nilsson R., Liljendberg C., Dahlqvist A., Gummesson P., Sjoedahl S.,  
 RA Green A., Skymne S.;  
 RT "Identification of Non-Heme Diron Proteins That Catalyze Triple Bond  
 RT and Epoxy Group Formation."  
 RL Science 280:915-918(1998).  
 DR EMBL, Y16283; CAA76156.1; -.  
 DR GO:GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro:IPR005804; FA\_desat\_fam.  
 DR Pfam:PF00487; FA\_desaturase; 1.  
 DR ProDom:PD001081; FA\_desat\_fam; 2.  
 SQ SEQUENCE 374 AA; 43323 MW; 7764DB17BC7F426 CRC64;

Query Match 77.7%; Score 1589.5; DB 10; Length 374;  
 Best Local Similarity 75.4%; Pred. No. 2.2e-129;  
 Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGGRSDSEGNILERVVDPEPTLSLTKKAIPTECFERSVRSYVVVDLIVAV 59  
 DB 1 MGAGGR--GRTSEKSVVERSVVDVPTLSLTKKAIPTECFERSVRSYVVVDLIVAV 58  
 QY 60 VFYLIANTYPLIPLTPLYLAMPVYFCQASITGLMVGHECGHAFSDYQIDIDVGF 119  
 DB 59 IFYLIANTYPLIPLTPLYLAMPVYFCQASITGLMVGHECGHAFSDYQIDIDVGF 118  
 QY 120 VLSGALLTPYFSWKYSHRNHANTNSLDNDEVYIPRKSQVNTSKYSLNNPGRVFTLV 179  
 DB 119 ILSFLLTPYFSWKYSHRNHANTNSLDNDEVYIPRKSQVNTSKYSLNNPGRVFTLV 178

```
Qy 180 RLTLGFLYLLTNTSGKKYGFANHFDMSPINFDRERVOYLLSDFGLLAVFYAKLIVA 239
Db 179 MFTLGFLYLLTNTSGKKYGFANHFDMSPINFDRERVOYLLSDFGLLAVFYAKLIVA 238
Qy 240 AKGAAMVIMTAIPVLGVSVFVLLTYLHHTHLSLPHYDSEMMWIKALSTIORDPFL 299
Db 239 NKGAAMVIMTAIPVLGVSVFVLLTYLHHTHLSLPHYDSEMMWIKALSTIORDPFL 298
Qy 300 NRVFHDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGYYKIDPTPIFKAMYTEAKECIY 359
Db 299 NSVFDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGYYKIDPTPIFKAMYTEAKECIY 358
Qy 360 IEPDESEHKGVFWYTHKM 377
Db 359 IEP--DSKLGKGVWYTHKL 374

RESULT 7
082729 PRELIMINARY; PRT; 383 AA.
AC 082729;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta-12 fatty acid desaturase.
OS Borago officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Boraginaceae; Borago.
OC NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RA Sayanova O., Shewry P.R., Napier J.A.;
RT "Fatty acid desaturases from borage.";
RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF074324; AAC31696.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD001081; FA desat. fam; 2.
SQ SEQUENCE 383 AA; 74048 MW; 13DF2BD876E7B5EF CRC64;

Query Match 68.2%; Score 1396.5; DB 10; Length 383;
Best Local Similarity 63.9%; Pred. No. 1.2e-112;
Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

Qy 1 MGAGGRMSDPSSEK---NILERPVDP-PPTLSLQKKAIPTHCERBSVIRSSYYVVDL 55
Db 1 MGAGGRMSVPPPKKSEVLRKVPHSKPPTLQKKAIPHCHGFRSVLSFSYVVDL 60
Qy 56 IVAVFFYIANTYPLIPPTLAYLAMPYWFQASILGLWVIGHGCGHAFSDYQLIDD 115
Db 61 VIALLPFTASRYTHLQHPHSYVAMPYWCQSVLIGVWIAHECGHAFSDYQLIDD 120
Qy 116 IVGFVLSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRSKYKIVSKLNNPGRVF 175
Db 121 TVGLLHLSALVLPYFSWKYSHRHHSNTGSLERDEVFVPKKSGISMSSEYLNPPGRVL 180
Qy 176 TLVRLTYGFPLYLNTISGKKYGFANHFDMSPINFDRERVOYLLSDFGLLAVFYAK 235
Db 181 VLLVOLLTGWPLVYLFNVSGRPYDRFACHYDPGPIYDRERTEIYISDAGVLAAMYGLY 240
Qy 236 LLVAKGAAMVIMTAIPVLGVSVFVLLTYLHHTHLSLPHYDSEMMWIKALSTIORD 295
Db 241 RLVAAGVAMVVCYGVPLLVNGLVLLTYLQHOPSLPHDSEMMWIKALSTIORD 300
Qy 356 ECIYIEPDESEHKGVFWYTHK 374
Db 361 ECIYIEADGDESGKVWYTHK 379
```

```
RESULT 8
08GZC3 PRELIMINARY; PRT; 383 AA.
AC 08GZC3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta 12 oleic acid desaturase FAD2.
OS Vernicia fordii (Tung) (Aleurites fordii).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Aleuritideae;
OC Vernicia.
OC NCBI_TaxID=73154;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=12481086;
RX Dyer J.M., Chapital D.C., Kuan J.-C.W., Mullen R.T., Turner C.,
RA McKeon T.A., Pepperman A.B.;
RT "Molecular Analysis of a Bifunctional Fatty Acid Conjugase/Desaturase
RT from Tung. Implications for the Evolution of Plant Fatty Acid
RT Diversity.";
RL Plant Physiol. 130:2027-2038(2002).
DR EMBL; AF525534; AAN87573.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD001081; FA desat. fam; 2.
SQ SEQUENCE 383 AA; 74152 MW; FSD06112C31B3BC CRC64;

Query Match 67.8%; Score 1387.5; DB 10; Length 383;
Best Local Similarity 63.3%; Pred. No. 7.2e-112;
Matches 241; Conservative 61; Mismatches 74; Indels 5; Gaps 2;

Qy 1 MGAGGRMSDPSSEK---NILERPVDP-PPTLSLQKKAIPTHCERBSVIRSSYYVVDL 55
Db 1 MGAGGRMSVPPPKKSEVLRKVPHSKPPTLQKKAIPHCHGFRSVLSFSYVVDL 60
Qy 56 IVAVFFYIANTYPLIPPTLAYLAMPYWFQASILGLWVIGHGCGHAFSDYQLIDD 115
Db 61 TVAILPFTYIANTYPLIPPLAYLAMPYWFQASILGLWVIGHGCGHAFSDYQLIDD 120
Qy 116 IVGFVLSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRSKYKIVSKLNNPGRVF 175
Db 121 IVGLVHSCLLVLPYFSWKYSHRHHSNTASLERDEVFVPKKSSIRWFSKYLNNPGRVF 180
Qy 176 TLVRLTYGFPLYLNTISGKKYGFANHFDMSPINFDRERVOYLLSDFGLLAVFYAK 235
Db 181 TLVRLTYGFPLYLNTISGKKYGFANHFDMSPINFDRERVOYLLSDFGLLAVFYAK 240
Qy 236 LLVAKGAAMVIMTAIPVLGVSVFVLLTYLHHTHLSLPHYDSEMMWIKALSTIORD 295
Db 241 RLVAAGVAMVVCYGVPLLVNGLVLLTYLQHHSIPHYDSEMMWIKALSTIORD 300
Qy 356 ECIYIEPDESEHKGVFWYTHK 376
Db 361 ECIYIEADGDESGKVWYTHK 381

RESULT 9
09LL17 PRELIMINARY; PRT; 383 AA.
AC 09LL17;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Omega-6 fatty acid desaturase.
```

GN FAD2.  
 OS Sesamum indicum (Oriental sesame) (gingelly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Pedaliaceae; Sesamum.  
 NC NCBITaxID=4182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jin U.H., Chung C.H.;  
 RT "Molecular characterization of a omega-6 fatty acid desaturase cDNA of  
 sesame (Sesamum indicum L.) seeds.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF124466; AAF80560.1; -  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 SQ SEQUENCE 383 AA; 44265 MW; F324272C3D57BBF5 CRC64;

Query Match 67.1%; Score 1374.5; DB 10; Length 383;  
 Best Local Similarity 62.8%; Pred. No. 9.6e-111;  
 Matches 238; Conservative 60; Mismatches 76; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPS-----EGKUIIERVP-VDPPTLSDLKKAIPTHCFERSVIRSSYYVHD 55  
 DB 1 MGAGGRMSDPTTKDEQKNPLQRPVPYAKPPTLGDIKKAIIPHCERSVRSFSYVYDL 60  
 QY 56 IVAVVFYLYANTYIPLIPLTFLAYLAMPVYVFCQASILTGLMVIHGEGHNAFSDYQILD 115  
 DB 61 VIVFLVLYIANTSYHPLPSFYCYLAMPYVAVQGCVCIGVIAHCGHNAFSDYQILD 120  
 QY 116 IVGFVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKVYIKSLNNPPGRV 175  
 DB 121 TVGILHSALLVYFSWKYSHRRHNSNTGSLRDEVFVFKPSRVSYSKYLNPPGRVI 180  
 QY 176 TLVFRLLTGFPLYLITNLSGKKYGRFANHPDPSPIFNDREYQVLLSDFGLLAVFYAI 235  
 DB 181 TLVVTLLTGMPLYLITNLSGKKYGRFANHPDPSPIFNDREYQVLLSDFGLLAVFYAI 240  
 QY 236 LIVAAGAAWVINYVYIPVLGVSVFVLYITLHHTHLSLPHYDSEWMIKALSTIDR 295  
 DB 241 RVALVKGILAMPVYVFCQASILTGLMVIHGEGHNAFSDYQILD 300  
 QY 296 FGLNRFVHDVTHVTLHLISYIPHYAKKADAIKPVLGEEYKIDRTPIFKAMVREAK 355  
 DB 301 YGVANKYFHNITDHTVHTLFTSTPHYAMEATKAIKILQYQFQDTPPYKAMREAK 360  
 QY 356 ECTIYEPDESEHKGVFWY 374  
 DB 361 ECTIYEPDESEHKGVFWY 379

## RESULT 10

Q8W2FO PRELIMINARY; PRT; 383 AA.  
 AC Q8W2FO;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Delta-12 oleate desaturase (EC 1.3.1.35).  
 GN FAD2-2.  
 OS Helianthus annuus (Common sunflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Campanulids; Asterales; Asteroideae; Helianthaceae;  
 OC Helianthus.  
 NC NCBITaxID=4232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Martinez-Rivas J.M., Sperling P., Luehs W., Heinz E.;  
 RT "Spatial and temporal regulation of three different microsomal oleate  
 desaturase genes (FAD2) from normal-type and high-oleic varieties of

RT sunflower (Helianthus annuus L.).";  
 RL Mol. Breed. 8:159-168 (2001).  
 DR EMBL; AF251843; AAL68982.1; -  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 KW Oxidoreductase.  
 SQ SEQUENCE 383 AA; 43991 MW; 7E143AB4B4E23BAF CRC64;

Query Match 66.8%; Score 1366.5; DB 10; Length 383;  
 Best Local Similarity 63.4%; Pred. No. 4.7e-110;  
 Matches 241; Conservative 60; Mismatches 72; Indels 7; Gaps 3;

QY 1 MGAGGRMSDPSGK-----NIIERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVHD 54  
 DB 1 MGAGGRMSNPNGEKKRPDPLQRPVPYAKPPTLGDVYKALIPHCERSVIRSSYYVHD 60  
 QY 55 LIVAVVFYLYANTYIPLIPLTFLAYLAMPVYVFCQASILTGLMVIHGEGHNAFSDYQILD 114  
 DB 61 LTIASIFYLYANNYIALPLSPFLAYVAMPVYVFCQCVLTGVVIAHCGHNAFSDYQILD 120  
 QY 115 DIVGFVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKVYIKSLNNPPGRV 174  
 DB 121 TVGILHSALLVYFSWKYSHRRHNSNTGSLRDEVFVFKPSRVSYSKYLNPPGRVI 180  
 QY 175 FTLVFRLLTGFPLYLITNLSGKKYGRFANHPDPSPIFNDREYQVLLSDFGLLAVFYAI 234  
 DB 181 LTLVTLTGMPLYLITNLSGKKYGRFANHPDPSPIFNDREYQVLLSDFGLLAVFYAI 240  
 QY 235 KIVAAGAAWVINYVYIPVLGVSVFVLYITLHHTHLSLPHYDSEWMIKALSTIDR 294  
 DB 241 FRVAMTKGLTFLVMTAGPLLVNGFLVITLQHTHPSLPHYDSEWMIKALSTIDR 300  
 QY 295 DFGFLNRFVHDVTHVTLHLISYIPHYAKKADAIKPVLGEEYKIDRTPIFKAMVREAK 354  
 DB 301 DYGVANKYFHNITDHTVHTLFTSTPHYAMEATKAIKILQYQFQDTPPYKAMREAK 360  
 QY 355 KECIYEPDESEHKGVFWY 374  
 DB 361 KECIYVDDEEVK-DGVYVY 379

## RESULT 11

Q8H2C3 PRELIMINARY; PRT; 382 AA.  
 AC Q8H2C3;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Delta-12 fatty acid desaturase.  
 OS Persea americana (Avocado).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.  
 NC NCBITaxID=3435;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang X., Richter A., Prusky D.;  
 RT "Isolation of a cDNA Clone Encoding an Avocado (Persea americana)  
 Delta-12 Fatty Acid Desaturase.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY057406; AAL23676.1; -  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR ProDom; PD001081; FA\_desat\_fam; 2.  
 SQ SEQUENCE 382 AA; 43492 MW; 8323B053D86B3B8 CRC64;

Query Match 66.4%; Score 1360; DB 10; Length 382;  
 Best Local Similarity 63.8%; Pred. No. 1.7e-109;  
 Matches 241; Conservative 56; Mismatches 77; Indels 4; Gaps 3;

```

Qy 1 MGAGRMS--DPSEGNILERVV--DPPTLSDLKKAIPTHCFERSVIRSSYYVVDL 57
Db 1 MGAGRMSVTPSVKXVDLERVPKAPPTFEGQLKKAIPKCFNRSIRSSMSYVVDLTI 60
Qy 58 AVVFYLYANTYPLIPTPLAY-LAMPVWFCQASLTGLMWIGHCCHHAASDYQI 116
Db 61 SSILYLYANTYPLIPSPSPSYFIAMPVWFCQASLTGLMWIAHCGHHAASDYQI 120
Qy 117 VGFVLSALITPYFSWKYSHRNHANTNSLDNDEYVIPKRSKYKIVSKLNNPGRVFT 176
Db 121 VGLIHSALVLPYFSWKYSHRRHSNTGSLTSDEYVFKPSQPMWFSKILNPPGRFLT 180
Qy 177 LVFRLTLPPLYLITNIGSKYGRFANFPDMSPIFNDREVOYLISDFGLAVYAIK 236
Db 181 LAFSLITLMPPLYLAVNVSGRKXDRFACHDPGPIYSDBERLQIISDLGVAVYICGLFR 240
Qy 237 LVAAGAAMVINMYAIPVLGVSVPFVLITYLHHTHLSLPHYDSTEMNWKALSTIDRD 296
Db 241 LVAACGLMWVVCVGVPLLVNGFLVLTIFLQHTHPSLPHYDSEMDWLKALATVDYDY 300
Qy 297 GFLENRFHDVTHVTHLHLSYIPHYHAKKARDAIKPVIGEYKIDRTPIFKAMRYAKE 356
Db 301 GVLMNVFNITDTHVAHLHLSFTHPHYHAKKARDAIKPILIGDYHSDGTPVYKAMRYAKE 360
Qy 357 CTYIEPDESEHKGVFWY 374
Db 361 CVYVEPDESGVKGVFWY 378

```

## RESULT 12

```

ID 09SP28 PRELIMINARY; PRT; 383 AA.
AC 09SP28;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN PAD2-2.
OS Vernonia galamensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Cichorioideae; Vernoniaceae;
OC Vernonia.
OC NCBI_TaxID=83960;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10759541;
RA Hage T.G., Seither C., Hildebrand D.;
RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
RT encoding a microsomal oleate desaturase (PAD2) (accession nos.
RT AF188263 and AF188264) and functional expression in Saccharomyces
RT cerevisiae (PCR00-035).";
RL Plant Physiol. 122:1457-1457(2000).
DR EMBL; AF188264; AAF04094.1; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA_desat. fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase.
SQ SEQUENCE 383 AA; 44330 MW; 10D954DC084F7D41 CRC64;

```

Query Match 66.4%; Score 1359.5; DB 10; Length 383;  
 Best Local Similarity 62.9%; Pred. No. 1.9e-109;  
 Matches 239; Conservative 61; Mismatches 73; Indels 7; Gaps 3;

```

Qy 1 MGAGRMSDPSEBK-----NILERVVD--PPPTLSDLKKAIPTHCFERSVIRSSYYVVD 54
Db 1 MGAGRMSNPDPDEKKAHEALQRPYQKPPPTVDDIKKAIPPHCFNRSVIRSSYYVVD 60
Qy 55 LIVAVVFYLYANTYPLIPTPLAYLAMPVWFCQASLTGLMWIGHCCHHAASDYQI 114
Db 61 LTISIFLYLYANTYPLIPPLPPLSVAMPVWIFQCCVLGVAIAHCGHHAASDYQI 120

```

```

Qy 115 DIVEVLSALLTPYFSWKYSHRNHANTNSLDNDEYVIPKRSKYKIVSKLNNPGRV 174
Db 121 DTVGLIHSALVLPYFSWKYSHRRHSNTGSIHEDEYVFPKKNVRSYARVANNPPGRI 180
Qy 175 FTVFRLTLPPLYLITNIGSKYGRFANFPDMSPIFNDREVOYLISDFGLAVYAI 234
Db 181 LTLVTLTGLMPPLYLIMFVNSGRYDRFACHDPSPISNBERAQIFSDGILAVFGL 240
Qy 235 KLVAAKGAAMVINMYAIPVLGVSVPFVLITYLHHTHLSLPHYDSTEMNWKALSTIDR 294
Db 241 FKLMAKGLTWLVCYGGPPLLVNGFLVLTIFLQHTHPSLPHYDTTENDMIRGALATIDR 300
Qy 295 DGFLENRFHDVTHVTHLHLSYIPHYHAKKARDAIKPVIGEYKIDRTPIFKAMRYA 354
Db 301 DYGLNKVFNITDTHVAHLHLSFTHPHYHAKKARDAIKPILIGEYQDFGTSIFAMRYET 360
Qy 355 KCTYIEPDESEHKGVFWY 374
Db 361 KCTIYVDKENVK-DGVYVY 379

```

## RESULT 13

```

ID 08W2E9 PRELIMINARY; PRT; 382 AA.
AC 08W2E9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN PAD2-3.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Helianthus.
OC NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HA89;
RA Martinez-Rives J.M., Sperling P., Luehs W., Heinz B.;
RT "Spatial and temporal regulation of three different microsomal oleate
RT desaturase genes (PAD2) from normal-type and high-oleic varieties of
RT sunflower (Helianthus annuus L.).";
RL Mol. Breed. 8:159-168(2001).
DR EMBL; AF251844; AAL68983.1; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA_desat. fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase.
SQ SEQUENCE 382 AA; 44004 MW; 59B524A3593D624F CRC64;

```

Query Match 66.3%; Score 1357; DB 10; Length 382;  
 Best Local Similarity 63.1%; Pred. No. 3.1e-109;  
 Matches 239; Conservative 59; Mismatches 75; Indels 6; Gaps 3;

```

Qy 1 MGAGRMSDPB-----BGNILER--VPVDPPTLSDLKKAIPTHCFERSVIRSSYYVVDL 55
Db 1 MGAGRMSPRNGKDKGKDEKPELRALHKEKPPPTVDDIKVIRPHCFKSVIRSSYYVVDL 60
Qy 56 IVAVVFYLYANTYPLIPTPLAYLAMPVWFCQASLTGLMWIGHCCHHAASDYQI 115
Db 61 TIASIFYLYANTYPLIPNSLAVAMPVWIFQCCVLGVAIAHCGHHAASDYQI 120
Qy 116 IVGFVLSALITPYFSWKYSHRNHANTNSLDNDEYVIPKRSKYKIVSKLNNPGRV 175
Db 121 TVGILHSALVLPYFSWKYSHRRHSNTGSIHEDEVFPKPKSVRSYARVANNPPGRI 180
Qy 176 TLVFRLTLPPLYLITNIGSKYGRFANFPDMSPIFNDREVOYLISDFGLAVYAIK 235
Db 181 TLVTLTGLMPPLYLIMFVNSGRYDRFACHDPSPISNBERAQIFSDAGILAVFYILF 240
Qy 236 LIVAAGAAMVINMYAIPVLGVSVPFVLITYLHHTHLSLPHYDSTEMNWKALSTIDRD 295

```

```

Db      241 RLASTKGLVWLTWYGCPLLVNNGFLVLTFLQHTPSLPHYDSTEMWMLRGALATVDRD 300
Qy      296 FGLNRRVHDVTHTHVHLHLISYIPHYAKKARDAIKPVLAGYYKIDRTPIFKAMYREAK 355
Db      301 YGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLIGDYQFDGTSIFKAMYREBK 360
Qy      356 ECIYIPEDESEHKGVFWY 374
Db      361 ECIYVDKEDVK-DGVYMY 378

RESULT 14
QSP29  PRELIMINARY:  PRT:  383 AA.
AC      09SP29:
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Delta-12 oleate desaturase (EC 1.3.1.35).
GN      FAD2-1.
OS      Vernonia galamensis.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Campanulids; Asterales; Asteraceae; Cichorioideae; Vernoniaceae;
OC      Vernonia.
OX      NCBI_TaxID=83960;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=10759541;
RA      Hage T.G., Seitcher C., Hildebrand D.;
RT      "Isolation of two cDNAs from Vernonia galamensis (Case.) Less.
RT      encoding a microsomal oleate desaturase (FAD2) (accession nos.
RT      AF188263 and AF188264) and functional expression in Saccharomyces
RT      cerevisiae (FER00-035).";
RL      Plant Physiol. 122:1457-1457(2000).
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      InterPro; IPR005804; F:oxidoreductase; IEA.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Prodom; PD001081; FA_desat_fam; 2.
KW      Oxidoreductase.
SQ      SEQUENCE 383 AA; 44268 MW; C16B93B7F94DA80 CRC64;

Query Match      66.0%; Score 1350.5; DB 10; Length 383;
Best Local Similarity 62.4%; Pred. No. 1.2e-108;
Matches 237; Conservative 62; Mismatches 74; Indels 7; Gaps 3;

Qy      1  MGAGGRMSDPSEGK-----NILERVPVD-PPTLSDLKKAIPTHCFERSVIRSSYYVND 54
Db      1  MGAGGRMSNPDEKKAHEALQRPYQKRPPTVGDICKAIPKCLANSVIKSFYVYVD 60
Qy      55 LIVAVFYLYANTYIPLPITPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLID 114
Db      61 LTISIFYYLYLTNTYIPLPPLPLSYAVAMPVYWFQGCVCVLTGVVIAHECGHAFSDYQWLD 120
Qy      115 DIVGVVLSALLTPYFSWKYSHRNHNANTSLDNDENVYIPKRSKYKYSKLLNPPGRV 174
Db      121 DTVGILHSALLVPIYFSWKYSHRRHSNTGSLERDEVFVPRKKSVRSTARLANNPPGR 180
Qy      175 FTLVFRLLTGFPYLYLTNLSGKKYGRFANHPDPMSPIFNDRERVQVLSDFGLAVFYAI 234
Db      181 LTLVLTLTGLWPLVLMFVVSGRYYRFACHPDNPSPISSNERRAQIFISDGIILAVFYGL 240
Qy      235 KLLVAAGAAVYINMYAIPVLGVSVFVLYLITVLAHHTHLSLPHYDSTENMWIKALSTIDR 294
Db      241 FKLMAKGLTWTWLCMYGGRPLLVNNGFLVLTFLQHTPSLPHYDTEMDWMLRGALATYDR 300
Qy      295 DGFNRRVHDVTHTHVHLHLISYIPHYAKKARDAIKPVLAGYYKIDRTPIFKAMYREA 354
Db      301 DYGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLIGDYQFDGTSIFKAMYRET 360
Qy      355 ECIYIPEDESEHKGVFWY 374

```

```

Db      361 ECIYVDKEDVK-DGVYMY 379

RESULT 15
Q41305  PRELIMINARY:  PRT:  383 AA.
AC      041305:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-NOV-2003 (TREMBLrel. 24, Last annotation update)
DE      D12 oleate desaturase.
OS      Solanum commersonii (Commerson's wild potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Lamiales; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxID=4109;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Consiglio F., Amatrua M.R., Leone A., Costa A., Grillo S.;
RT      Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RL      EMBL; X92847; CAA63432.1; -.
DR      PIR; T10480; T10480.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      InterPro; IPR005804; FA_desat_fam.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Prodom; PD001081; FA_desat_fam; 2.
SQ      SEQUENCE 383 AA; 44101 MW; F17CFAE0C0CC5595 CRC64;

Query Match      65.9%; Score 1348.5; DB 10; Length 383;
Best Local Similarity 61.2%; Pred. No. 1.7e-108;
Matches 232; Conservative 65; Mismatches 77; Indels 5; Gaps 2;

Qy      1  MGAGGRMSDPSEK-----EGNILERVPVD-PPTLSDLKKAIPTHCFERSVIRSSYYVNDL 55
Db      1  MGAGGRMSAPNGETEVKNPLQKVPTSKPPTVGDICKAIPKCFGRSLRISFSYVYDL 60
Qy      56 IVAVFYLYANTYIPLPITPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLID 115
Db      61 ILVSIWYVANTYIPLPILPSPICYTAMPYIWCQGCVCVGIWVNAHECGHAFSDYQWDD 120
Qy      116 IVGVVLSALLTPYFSWKYSHRNHNANTSLDNDENVYIPKRSKYKYSKLLNPPGRV 175
Db      121 TVGILHSALLVPIYFSWKYSHRRHSNTGSLERDEVFVPRKKSQGLWYSKYLNNPPGRV 180
Qy      176 TLVFRLLTGFPYLYLTNLSGKKYGRFANHPDPMSPIFNDRERVQVLSDFGLAVFYAIK 235
Db      181 SLITLTGLWPLYLAFVNSGRPYRFACHYDPYGPYINRRLOIFISDAGVLCYLLY 240
Qy      236 LLLVAKGAAYVINYAIPVLGVSVFVLYLITVLAHHTHLSLPHYDSTENMWIKALSTIDR 295
Db      241 RIALVKGALMAVYGVGFLVNGFLVLTFLQHTPSLPHYDSTEMWMLRGALATYCRD 300
Qy      296 FGLNRRVHDVTHTHVHLHLISYIPHYAKKARDAIKPVLAGYYKIDRTPIFKAMYREAK 355
Db      301 YGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLIGDYQFDGTSIFKAMYREBK 360
Qy      356 ECIYIPEDESEHKGVFWY 374
Db      361 ECIYVDKEDSESGKGVFWY 379

Search completed: June 18, 2004, 17:37:54
Job time : 48 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 17:29:57 ; Search time 59 Seconds  
(without alignments)  
1805.431 Million cell updates/sec

Title: US-10-069-772-2

Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEGNILERV.....IYIPDEDESEHKGVFWYHKM 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2047	100.0	377	4	AAB70946 C. offici
2	1636	79.9	375	2	AAW6793 Crepis al
3	1598.5	78.1	374	2	AAW79743 Crepis sp
4	1589.5	77.7	374	2	AAW79742 Crepis pa
5	1578.5	77.1	384	2	AAW83354 Vernonia
6	1396.5	68.2	383	2	AAW72825 Borago of
7	1332.5	65.0	383	4	AAE13421 Cotton ol
8	1331.5	65.0	387	7	AAE40489 P. granat
9	1325.5	64.8	383	4	AAE13427 Soybean m
10	1323.5	64.7	383	5	AAAG80695 C. offici
11	1318	64.4	384	2	AAW86153 Protein s
12	1318	64.4	384	2	AAW94053 Amino aci
13	1318	64.4	384	3	AAW70114 Braslica
14	1317	64.3	384	2	AAW27329 B. napus
15	1317	64.3	384	5	ABW80028 Rape micr
16	1313	64.1	384	2	AAW27330 B. napus
17	1312	64.1	384	2	AAW24997 Microsoma
18	1312	64.1	384	2	AAW94049 Amino aci
19	1312	64.1	384	3	AAW94457 Protein e
20	1312	64.1	384	5	ABG71327 Braslica
21	1311	64.0	384	8	AAW85752 Microsoma
22	1311	64.0	384	2	AAW85155 Protein s
23	1311	64.0	384	2	AAW94054 Amino aci
24	1311	64.0	384	2	AAW94051 Amino aci
25	1311	64.0	384	3	AAW70115 B. napus

26	1310	64.0	384	2	AAW94055 Amino aci
27	1310	64.0	384	3	AAW70116 B. napus
28	1308	63.9	384	5	ABG71326 Braslica
29	1307	63.8	384	2	AAW86154 Protein s
30	1307	63.8	384	2	AAW94052 Amino aci
31	1305	63.8	384	2	AAW24998 Microsoma
32	1305	63.8	384	2	AAW94050 Amino aci
33	1302.5	63.6	383	3	AAW1517 Arabidops
34	1301	63.6	384	2	AAW27331 B. napus
35	1300.5	63.5	383	2	AAW53697 Sequence
36	1300.5	63.5	383	3	AAW50097 Arabidops
37	1300.5	63.5	383	3	AAW70270 A. thalia
38	1300.5	63.5	383	3	AAW22053 Arabidops
39	1300.5	63.5	383	4	AAE13428 Arabidops
40	1300.5	63.5	383	5	ABW80027 Cress mic
41	1299	63.5	384	2	AAW24995 Microsoma
42	1299	63.5	384	2	AAW94047 Amino aci
43	1299	63.5	384	2	AAW94455 Protein e
44	1299	63.5	384	5	ABG71325 Braslica
45	1299	63.5	384	8	ADW85748 Microsoma

## ALIGNMENTS

## RESULT 1

AAB70946 standard; protein; 377 AA.

AAW70946;

22-AUG-2001 (first entry)

C. officinalis calendulic acid desaturase.

Calendula; calendulic acid desaturase; unsaturated fatty acid; oil; triglyceride; transgenic plant.

Calendula officinalis.

DE19941609-A1.

08-MAR-2001.

01-SEP-1999; 99DE-01041609.

01-SEP-1999; 99DE-01041609.

(IPBP-) IPB INST PFLANZENBIOCHEMIE.

Feussner I, Hornung E, Fritzsche K, Peitzsch N, Renz A;

WPI; 2001-283028/30.

N-PSDB; AAF88311.

New nucleic acid sequence encoding Calendula officinalis calendulic acid desaturase, useful for e.g. producing transgenic plants having oil with an increased unsaturated fatty acid content.

Claim 1c; Page 15-16; 22pp; German.

This invention describes a novel isolated nucleic acid sequence (I) encoding a Calendula officinalis calendulic acid desaturase polypeptide. The invention also describes (1) a process for producing unsaturated fatty acids, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism, isolating oil from the organism and releasing fatty acids from the oil; (2) a process for producing triglycerides with an increased unsaturated fatty acid content, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism; (3) a process for producing saturated fatty acids, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing organism, growing the organism, isolating oil from the organism

CC and releasing fatty acids from the oil; (4) a process for producing  
 CC triglycerides with an increased saturated fatty acid content, comprising  
 CC introducing at least one nonfunctional copy of (i) or (ii) into an oil-  
 CC producing organism, growing the organism and isolating oil from the  
 CC organism; (5) an enzyme capable of converting a diunsaturated fatty acid  
 CC of to a triunsaturated fatty acid. Transgenic organisms (especially  
 CC plants) containing one or more copies of (i) are useful for producing  
 CC oils with an increased unsaturated fatty acid content. Transgenic  
 CC organisms (especially plants) containing one or more nonfunctional copies  
 CC of (i) are useful for producing oils with an increased saturated fatty  
 CC acid content. (i) and fragments of (i) are also useful for isolating  
 CC genomic sequences by homology screening. This sequence represents the  
 CC candelitic acid desaturase described in the method of the invention  
 CC  
 XX  
 SQ Sequence 377 AA;

Query Match 100.0%; Score 2047; DB 4; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-200;  
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAGGRMSDPSGKNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVVDLIYAVV 60  
 DB 1 MGAGGRMSDPSGKNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVVDLIYAVV 60  
 QY 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 120  
 DB 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 120  
 QY 121 LHSALITPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 180  
 DB 121 LHSALITPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 180  
 QY 181 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 240  
 DB 181 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 240  
 QY 241 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 300  
 DB 241 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 300  
 QY 301 RVFHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360  
 DB 301 RVFHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360  
 QY 361 EPEDESEHKGVFWYHKM 377  
 DB 361 EPEDESEHKGVFWYHKM 377

RESULT 2  
 AAM36793  
 ID AAM36793 standard; protein; 375 AA.  
 XX  
 AC AAM36793;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-APR-1998 (first entry)  
 XX  
 DE Crepis alpina delta 12 acetylase.  
 XX  
 KM Crepis alpina delta 12 acetylase; plant; yeast; acetylenic compound;  
 KM fatty acid; coating; plastic; lubricant; oilseed.  
 XX  
 OS Crepis alpina.  
 XX  
 PN .MO9737033-A1.  
 PD 09-OCT-1997.  
 XX  
 PF 14-FEB-1997; 97WO-SE000247.  
 XX  
 PR 29-MAR-1996; 96SE-00001236.  
 XX

PA (BAFO/) BAFOR M.  
 PA (BANAV/) BANAS A.  
 PA (DAHL/) DAHLQVIST A.  
 PA (GUMM/) GUMMESON P.  
 PA (LEEM/) LEE M.  
 PA (LENNM/) LENNAN M.  
 PA (SJOE/) SJOEDAHN S.  
 PA (STYM/) STYME S.  
 PI Bafor M, Banas A, Dahlqvist A, Gummeson P, Lee M, Lenman M,  
 PI Sjoedahl S, Styne S;  
 XX WPI, 1997-503117/46.  
 DR N-PSDB; AAT95688.  
 PT  
 PT New acetylase used for production of crepenynic acid from linoleic acid -  
 PT derived from Crepis alpina, used for production of acetylenic fatty acids  
 PT suited for the production of coatings, plastics and lubricants.  
 XX  
 PS Claim 7; Page 21; 33pp; English.

This is the Crepis alpina delta 12 acetylase. This is used in the  
 CC production of acetylenic compounds. The process comprises treating C18  
 CC fatty acids having a double bond at position delta 12 with an acetylase  
 CC to form 12-ynoic acids. The acetylenic compounds can be produced by  
 CC organisms such as oilseed plants, yeast and fungi which are transformed  
 CC with the acetylase DNA. These organisms can accumulate these acetylenic  
 CC compounds which are chemical feedstocks, particularly for coatings,  
 CC plasticisers and lubricants. The process enables the production of these  
 CC acetylenic compounds from a renewable resource with high purity and at  
 CC reasonable cost. (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SQ Sequence 375 AA;

Query Match 79.9%; Score 1636; DB 2; Length 375;  
 Best Local Similarity 76.9%; Pred. No. 1.6e-158;  
 Matches 289; Conservative 40; Mismatches 45; Indels 2; Gaps 1;

QY 1 MGAGGRMSDPSGKNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVVDLIYAVV 60  
 DB 1 MGAGGRMSDPSGKNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVVDLIYAVV 60  
 QY 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 120  
 DB 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 120  
 QY 59 FYFLADKYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 118  
 DB 59 FYFLADKYIPLIPPLATLAMPVYVFCQASITGLMTVIGHCCHAFSDYQOLIDIVGFV 118  
 QY 121 LHSALITPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 180  
 DB 121 LHSALITPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 180  
 QY 119 LHSPLMTYPSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 178  
 DB 119 LHSPLMTYPSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSKLNNPGRVFTLYER 178  
 QY 181 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 240  
 DB 181 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 240  
 QY 179 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 238  
 DB 179 LTLGFPYLITNLSGKKGPRANHPDPMSPINFDERVOVLLSDGLLAVFYAIKLVA 238  
 QY 241 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 300  
 DB 241 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 300  
 QY 239 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 298  
 DB 239 KGAANVIMYAIPLVUGSVFVLITYLHHTLSLPHYSTENWIKGALSTIDRPFGLN 298  
 QY 301 RVFHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360  
 DB 301 RVFHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360  
 QY 299 SVLHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 358  
 DB 299 SVLHDVTHVLAHLISYIIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 358  
 QY 361 EPEDESEHKGVFWYHKM 376  
 DB 361 EPEDESEHKGVFWYHKM 376

RESULT 3  
 AAM79743  
 ID AAM79743 standard; protein; 374 AA.  
 XX  
 AC AAM79743;  
 XX



DT 02-FEB-1999 (first entry)  
 XX Crepis sp. delta-12-epoxygenase.  
 XX Fatty acid epoxygenase; Crepx gene; delta-12-epoxygenase;  
 KM mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;  
 KM vegetable oil; oilseed.  
 XX Crepis sp.  
 XX Key Location/Qualifiers  
 FH Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 FT Misc-difference 293  
 FT Misc-difference 305 /note= "encoded by AGN"  
 FT Region /note= "encoded by GTN"  
 FT Region /note= "His-rich region"  
 XX MO9846762-A1.  
 PN 22-OCT-1998.  
 PD 09-APR-1998; 98WO-AU000246.  
 XX 15-APR-1997; 97AU-00006223.  
 PR 15-APR-1997; 97AU-00006226.  
 PR 16-APR-1997; 97US-0043706P.  
 PR 20-JUN-1997; 97US-0050403P.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (STYM/) STYMNE S.  
 PA Styenne S, Green A, Singh S, Lenman M;  
 PI WPI; 1998-568734/48.  
 DR N-PSDB; AAV63102.  
 XX New isolated fatty acid epoxygenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.  
 XX Claim 29; Page 84-86; 150pp; English.  
 PS This is the amino acid sequence of a novel epoxygenase of a vernolic acid  
 CC -containing Crepis sp. (not crepis palaestina). It was deduced from  
 CC isolated cDNA clone Crepx (see AAV63102). The deduced sequence contains  
 CC His-rich motifs (see AAW79752-54) that are characteristic of mixed  
 CC function monooxygenases, and shows a high degree of homology to a novel  
 CC delta-12-epoxygenase (see AAW79742) of C. palaestina. The invention  
 CC relates generally to novel genetic sequences (see AAV63101-03) encoding  
 CC fatty acid epoxygenases (see AAW79742-44), especially delta-12-  
 CC epoxygenases or mixed function monooxygenases. These provide the means by  
 CC which fatty acid metabolism can be manipulated in e.g. yeast, mould,  
 CC bacteria, insects, birds, mammals and plants (especially oilseed plants  
 CC such as flax), in particular to convert unsaturated fatty acids to  
 CC epoxygenated fatty acids. The invention includes genetically modified oil  
 CC -accumulating organisms and to the oils derived from them. These oils can  
 CC be used in production of coatings, resins, glues, plastics, surfactants  
 CC or lubricants  
 XX Sequence 374 AA:  
 SQ  
 Query Match 78.1%; Score 1598.5; DB 2; Length 374;  
 Best Local Similarity 75.7%; Pred.No. 1.1e-154;  
 Matches 286; Conservative 41; Mismatches 46; Indels 5; Gaps 3;  
 QY 1 MGAGGRSDPBGKNIILRPVDP-PPTLSLKLKAIPLHCEBVSIVSSYVVDLIVAY 59  
 DB 1 MGAGGR--GRTSEKSVMERVSVDPTVLSLKLKAIPLHCEBVSIVSSYVVDLIVAY 58

QY 60 VFYYIANTYIPLIPTPLAYLAMPYVWFCQASILTGLMWIGHCCHHAFSDYQIIDIYGF 119  
 DB 59 IFYFLANTYIIPNLHPLAYLAMPYVWFCQASVLGLMWIGHCCHHAFSNTVDDTYG 118  
 QY 120 VLHSAULTPTYSKYSRHHNHAATNSLDNDVYIPKRSKXYISKLINPPGRVFTLVF 179  
 DB 119 IHSFLLTPYFSWYSHNHNHNSNTSIDNDVYIPKRSKXYIKLKNPPGRLLVLI 178  
 QY 180 RLTLGFPPLVLLTNSGKKYGRFANHPDPMSPIFNDRERVOLLSDFGLAIFYAIKLIVA 239  
 DB 179 MFTLGFPLVLLTNSGKKYGRFANHPDPMSPIFYEREPQVFLSDGLAIFYAIKLIVA 238  
 QY 240 AKGAAMVIMYAIPLVGVSEFVLLTYLHTLSLPHYDSTEMWIKGALSTIDRDFGL 299  
 DB 239 NKGAAWAAWYGVPLGVFTFDVITPLHHTHQSPPHDSFEMWIRGALAIIDRDFGL 298  
 QY 300 NRVPHDVTHTVHLHLISYIPHYAKARDAIKVLGEYVYKIDRTPIKAMRYREKCY 359  
 DB 299 NSVPHDVTHTVHMLHSYIPHYAKARDAIKPLIDPFYWIIDRTPIKAMRYREKCY 358  
 QY 360 IEPDESEHKGVPWYHMK 377  
 DB 359 IEP--DSKLGKGVWYHKL 374

RESULT 4  
 AAW79742  
 ID AAW79742 standard; protein; 374 AA.  
 XX AAW79742;  
 AC AAW79742;  
 XX 02-FEB-1999 (first entry)  
 DT Crepis palaestina delta-12-epoxygenase.  
 XX Fatty acid epoxygenase; Cpai2 gene; mixed function monooxygenase;  
 KM delta-12-epoxygenase; epoxygenated fatty acid; transgenic plant;  
 KM vegetable oil; oilseed.  
 XX Crepis palaestina.  
 OS  
 XX Key Location/Qualifiers  
 FH Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 FT Region /note= "His-rich region"  
 XX MO9846762-A1.  
 PN 22-OCT-1998.  
 PD 09-APR-1998; 98WO-AU000246.  
 XX 15-APR-1997; 97AU-00006223.  
 PR 15-APR-1997; 97AU-00006226.  
 PR 16-APR-1997; 97US-0043706P.  
 PR 20-JUN-1997; 97US-0050403P.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (STYM/) STYMNE S.  
 PA Styenne S, Green A, Singh S, Lenman M;  
 PI WPI; 1998-568734/48.  
 DR N-PSDB; AAV63101.  
 XX New isolated fatty acid epoxygenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.

PS Claim 29, Page 78-81; 150pp; English.

XX This is the amino acid sequence of a novel mixed function monooxygenase of  
 CC *Crepis palaestrina* that is characterised as having delta-12-epoxygenase  
 CC activity. It was deduced from isolated full-length cDNA clone Cpai2 (see  
 CC AAV63101). The deduced sequence contains His-rich motifs (see AAV79752-  
 CC 54) that are characteristic of delta-12-desaturase enzymes. The Cpai2  
 CC gene was shown to be highly expressed in developing seeds, with no  
 CC expression detectable in leaves. The invention relates generally to novel  
 CC genetic sequences (see AAV63101-03) encoding fatty acid epoxygenases (see  
 CC AAV79742-44), especially delta-12-epoxygenases or mixed function  
 CC monooxygenases. These provide the means by which fatty acid metabolism  
 CC can be manipulated in e.g. yeast, mould, bacteria, insects, birds,  
 CC mammals and plants (especially oilseed plants such as flax), in  
 CC particular to convert unsaturated fatty acids to epoxygenated fatty  
 CC acids. The invention extends to genetically modified oil-accumulating  
 CC organisms and to the oils derived from them. These oils can be used in  
 CC production of coatings, resins, glues, plastics, surfactants or  
 CC lubricants

XX Sequence 374 AA;

XX SQ

Query Match 77.7%; Score 1589.5; DB 2; Length 374;  
 Beat Local Similarity 75.4%; Pred. No. 9e-154; Indels 5; Gaps 3;  
 Matches 285; Conservative 40; Mismatches 48;

QY 1 MGAGGRMSDPSEKGRILRRVDP-PFTLSDLKKAIPTHCFERSYIRSSYYVVDLIYAY 59  
 DB 1 MGAGGR--GRTSKSVMERVSVDPTFSLSEKKAIPHCGRSIVIRSSYYVVDLIYAY 58

QY 60 VFYYLANTYIPLIPPLAYLAMPVYVFCQASITLGLMWYIGHCCHAFSDYQLIDYIGF 119  
 DB 59 IFYYLANTYIPLTPTSLAYLAMPVYVFCQASVLTGLMWYIGHCCHAFSNTYVFPDVTGVF 118

QY 120 VLHSLALTPYPSWKVSHRNHNANTSLNDEYIIPKRSKVIYSKLIANNPGRVPLTVF 179  
 DB 119 ILHSLALTPYPSWKVSHRNHNANTSLNDEYIIPKRSKVIYSKLIANNPGRVPLTVF 178

QY 180 RLTLGFPYLLTNISGKKYGRFANHPDMSPIFNDRERVOVLLSDFGLLAVFYAKLLVA 239  
 DB 179 MFTLGFPYLLTNISGKKYGRFANHPDMSPIFKRERFOVLLSDGLAVFYGKVVAA 238

QY 240 AKGAAMVIMTAIPVLGVSVFVLLTYLHHTLSLPHYDSTEMWIKGALSTIDRPGFL 299  
 DB 239 NKGAMVACMGVPLGVTFPFDDVITFLHHTHQSPPHDSSTEMWIRGALSIDRPFGL 298

QY 300 NRVFDDVTHVTLHHTLSYIPHYHAKKARDAIKPVLGEEYKIDRPIPKAMVREAKECIY 359  
 DB 299 NSVFDDVTHVTHHLLPSYIIPHYHAKKARDAIKPILGDFYMDRPIPKAMVREGRKCY 358

QY 360 IEPDESEHKGVFWYHKM 377  
 DB 359 IEP--DSKLKGVYVYHKL 374

RESULT 5  
 AAM83354  
 ID AAM83354 standard; protein; 384 AA.

XX AAM83354;

XX AC

XX 27-AUG-2003 (revised)

XX DT 10-FEB-1999 (first entry)

XX DE Vernonia galamensis fatty acid epoxidising enzyme.

XX XX Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;  
 XX KM expression; chimeric gene; recombinant enzyme.  
 XX OS Vernonia galamensis.  
 XX XX  
 XX PM US5846784-A.  
 XX XX

PD 08-DEC-1998.

XX 11-JUN-1997; 97US-00872302.

XX 11-JUN-1997; 97US-00872302.

PA (DDPO ) DU POINT DE MEMOURS & CO E I.

PI Hitz MD;

XX WPI; 1999-053065/05.

DR N-PSDB; AAV72550.

XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid  
 PT epoxidising enzyme - used to alter levels of expression of the enzymes in  
 PT transformed host cells or to produce recombinant enzymes.

PS Claim 5; Col 29-32; 21pp; English.

XX The present sequence is Vernonia galamensis fatty acid epoxidising  
 CC enzyme. The present invention also describes: (i) Vernonia galamensis  
 CC fatty acid desaturase; (ii) chimeric genes comprising the fragments  
 CC linked to regulatory sequences; and (iii) transformed host cells  
 CC containing the chimeric genes. The DNA's from the present invention can  
 CC be used to alter levels of expression of the enzymes in transformed host  
 CC cells or to produce the recombinant enzymes by transformation of  
 CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 384 AA;

XX SQ

Query Match 77.1%; Score 1578.5; DB 2; Length 384;  
 Beat Local Similarity 76.5%; Pred. No. 1.2e-152; Indels 3; Gaps 2;  
 Matches 280; Conservative 39; Mismatches 44;

QY 15 NILERVPYD-PFTLSDLKKAIPTHCFERSYIRSSYYVVDLIYAYVFPYLANITYIPLIP 73  
 DB 19 NINERAPYDAAPFSLSDLKKAIPHCGRSIVIRSSYYVVDLIITFLTYLANSYIPLIP 78

QY 74 TPLAYLAMPVYVFCQASITLGLMWYIGHCCHAFSDYQLIDYIGFVLHSLALTPYPSWK 133  
 DB 79 PPLAYLAMPVYVFCQASITLGLMWYIGHCCHAFSEYQWVDNVTGFLHSLALTPYPSWK 138

QY 134 YSHRNHNANTSLNDEYIIPKRSKVIYS--KLIANNPGRVPLTVRRLTLGFPYLLT 191  
 DB 133 YSHRNHNANTSLNEEYIIPKRSQILNNYSNFFLDNTPRITFLIMTLTGFPYLLT 198

QY 192 NISGKKYGRFANHPDMSPIFNDRERVOVLLSDFGLLAVFYAKLLVAKGAAMVIMNYA 251  
 DB 199 NISGKKYGRFANHPDPSPIFSERERIOVLLSDVGLINVFGLKFLVAKKFGWMMRYG 258

QY 252 IPIVGVSFVLLTYLHHTLSLPHYDSTEMWIKGALSTIDRPGFLNRYVPHDVTHTV 311  
 DB 259 APVVGLANFIMITYLHHTLSSPHYDSTEMWIKGALTITIDRPGFLNRYVPHDVTHTV 318

QY 312 LHLISYIPHYHAKKARDAIKPVLGEEYKIDRPIPKAMVREAKECIYIEPDESEHKGV 371  
 DB 319 LHLFPYIPHYHAKKARDAIKPVLGEEYKIDRTPPYKAMREAKECIYIEPDESKRGV 378

QY 372 FMYHKM 377  
 DB 379 YMYHKM 384

RESULT 6  
 AAY72825  
 ID AAY72825 standard; protein; 383 AA.

XX AAY72825;

XX AC

XX 31-MAY-2001 (first entry)

XX DT Borage officinalis fatty acid hydroxylase enzyme.  
 XX DE  
 XX XX

KM Borage; fatty acid hydroxylase; conjugated double bond; delta-9;  
 KM delta-12; transgenic plant; seed oil.  
 XX  
 OS Borage officialis.  
 XX  
 PN WO200112800-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 15-AUG-2000; 2000WO-US022371.  
 XX  
 PR 16-AUG-1999; 99US-0149050P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 XX  
 PI Canoon EB, Hiltz WD, Ripp KG;  
 XX  
 DR WPI; 2001-218351/22.  
 XX  
 PT Novel nucleic acid fragment encoding plant fatty acid modifying enzyme  
 PT associated with modification of delta-9 position of the fatty acid,  
 PT useful for creating transgenic plants having altered lipid profiles.  
 XX  
 PS Disclosure; Fig 2; 96pp; English.  
 XX  
 CC The present invention relates to nucleic acid fragments encoding plant  
 CC fatty acid modifying enzymes associated with conjugated double bond  
 CC formation, comprising a modification of delta-9 position or a delta-12  
 CC position of fatty acids. The nucleic acid fragments are useful for  
 CC creating chimeric gene which is useful for creating transgenic plants  
 CC having altered lipid profiles. They are also useful for producing seed  
 CC oil containing fatty acids comprising a modification at delta-9 position  
 CC or delta-12 position. The seed is useful for improving the carcass  
 CC quality of an animal by supplementing a diet of the animal with animal  
 CC feed. The nucleic acid fragments are useful for isolating nucleic acid  
 CC fragments encoding homologous fatty acid modified enzymes from the same  
 CC or other plant species. The present sequence is Borage officialis fatty  
 CC acid hydroxylase enzyme. It is a fatty acid modifying enzyme associated  
 CC with conjugated double bond formation  
 XX  
 SQ Sequence 383 AA:  
 Query Match 68.2%; Score 1396.5; DB 4; Length 383;  
 Best Local Similarity 63.9%; Pred. No. 5.4e-134;  
 Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;  
 QY 1 MGAGGRMSDSEBK---NILERVPVD-PPTTSLDKKALPTHCERSVIRSSYYVHDL 55  
 DB 1 MGAGGRMPVPPTKGGKSKSDVQRVSEKRPPTVGDLLKVIIPPHCFORSVLHSFSYVVDL 60  
 QY 56 IVAVVFYLLANTYIPLPTPLAYLAMPVYFCQASILTLGLMVGHEGCHAFSDYQLIDD 115  
 DB 61 VIHALFTYASRIYHLOPHPLSYAMPLVWFCQSSVLGVWVIAHEGCHAFSDYQLIDD 120  
 QY 116 IVGFVLHSALLTPFSWKYSHRNHNANTNSLNDDEVYIPKSKSKVKTYSKLANNPGRGVF 175  
 DB 121 TVGGLLSALLVLPFSWKYSHRNHNANTNSLNDDEVYIPKSKSGISMSSEVLANNPGRVYL 180  
 QY 176 TLVRLTLGFPYLLTNIISGKKYGRFANHPDPSPIFDRERRVQVLLSDFGLLAVFAIK 235  
 DB 181 VILVOLTLTGWPVLYLMFNVSGRPRYDFACHFDPKSPYVDRERLQIYISDAIGVAVMYGL 240  
 QY 236 LILVAKGAAYINMYAIPVIGVSFVLYITLHHTHLSLPHYDSTEMWIMGALSTDRD 295  
 DB 241 RLIVAKGAWAVCYGVPPLVANGELVITLQHTQPSLPHYDSSEWMLGALATVDRD 300  
 QY 296 FGLIARVHDVTHVTLHLISYIPHYAKABDAIKFVLEGYKIDRTPIFKAMVREAK 355  
 DB 301 YGFLINKLHNITDTHVHHLFSTWPHYAMATAIKRIIDGYOQCRTPFKAMVREVK 360  
 QY 356 ECIYIEPDESEHKGVFMY 374  
 DB 361 ECIYVEADEGDNKKGVFMY 379

RESULT 7  
 AAB13421  
 ID AAB13421 standard; protein; 383 AA.  
 XX  
 AC AAB13421;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Cotton oleoyl-PC delta12-desaturase (ghPAD2-2) protein.  
 XX  
 KM Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;  
 KM linoleic acid; stearic acid; oleic acid; transgenic plant;  
 KM cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2.  
 XX  
 OS Gossypium hirsutum.  
 XX  
 PN WO200179499-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 18-APR-2001; 2001WO-AU000436.  
 XX  
 PR 18-APR-2000; 2000US-0198124P.  
 XX  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Green A, Singh S, Liu Q;  
 XX  
 DR WPI; 2001-602932/68.  
 DR N-PSDB; AAD22380.  
 XX  
 PT Modifying endogenous oil of cotton plants, to produce cotton seed oil  
 PT with reduced palmitic and/or linoleic acid content, involves producing  
 PT transgenic plants containing a fatty acid biosynthesis gene in a  
 PT construct.  
 XX  
 PS Example 8; Fig 6; 201pp; English.  
 XX  
 CC The invention relates to a method for modifying the endogenous oil of a  
 CC cotton plant, to produce cotton seed oil. The method comprises producing  
 CC a transgenic cotton plant having a gene construct which includes a fatty  
 CC acid biosynthesis gene operably linked to a promoter sequence capable of  
 CC conferring expression of the delta9-desaturase (delta9 stearoyl-ACP  
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-  
 CC desaturase) gene in the seed of a cotton plant. The invention is useful  
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid  
 CC content, and increased stearic and/or oleic acid content. The present  
 CC sequence is cotton oleoyl-PC delta12-desaturase (ghPAD2-2) protein  
 CC related to the invention  
 XX  
 SQ Sequence 383 AA:  
 Query Match 65.1%; Score 1332.5; DB 4; Length 383;  
 Best Local Similarity 60.7%; Pred. No. 1.9e-127;  
 Matches 230; Conservative 70; Mismatches 74; Indels 5; Gaps 2;  
 QY 1 MGAGGRMSDSEBK---NILERVPVD-PPTTSLDKKALPTHCERSVIRSSYYVHDL 55  
 DB 1 MGAGGRMSVPTSPKPKPFNSIKRVYKRPPTTSLBIKAIIPPHCFORSVLHSFSYLLADF 60  
 QY 56 IVAVVFYLLANTYIPLPTPLAYLAMPVYFCQASILTLGLMVGHEGCHAFSDYQLIDD 115  
 DB 61 ILASLFYHVAATNYPNIPQALSNVAMPVWMOCCITLGVWVIAHEGCHAFSDYQLIDD 120  
 QY 116 IVGFVLHSALLTPFSWKYSHRNHNANTNSLNDDEVYIPKSKSKVKTYSKLANNPGRGVF 175  
 DB 121 TVGGLLSALLVLPFSWKYSHRNHNANTNSLNDDEVYIPKSKSGISMSSEVLANNPGRVYL 180  
 QY 176 TLVRLTLGFPYLLTNIISGKKYGRFANHPDPSPIFDRERRVQVLLSDFGLLAVFAIK 235  
 DB 181 SITOLTLTGWPVLYLAFNVAGRPYDRFACHYDVPYPIFSDRERLQIYISDAIGVAVVAVLY 240



XX Modifying endogenous oil of cotton plants, to produce cotton seed oil  
 PT with reduced palmitic and/or linoleic acid content, involves producing  
 PT transgenic plants containing a fatty acid biosynthesis gene in a  
 PT construct.  
 XX  
 PS Example 8; Fig 7, 201pp; English.  
 CC The invention relates to a method for modifying the endogenous oil of a  
 CC cotton plant, to produce cotton seed oil. The method comprises producing  
 CC a transgenic cotton plant having a gene construct which includes a fatty  
 CC acid biosynthesis gene operably linked to a promoter sequence capable of  
 CC conferring expression of the delta9-desaturase (delta9 stearoyl-ACP  
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-  
 CC desaturase) gene in the seed of a cotton plant. The invention is useful  
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid  
 CC content, and increased stearic and/or oleic acid content. The present  
 CC sequence is soybean microsomal omega-6 desaturase, gmfAD2-2 protein  
 CC related to the invention  
 CC  
 SQ Sequence 383 AA;  
 Query Match 64.8%; Score 1325.5; DB 4; Length 383;  
 Best Local Similarity 61.3%; Pred. No. 1e-126;  
 Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;  
 QY 1 MGAGGRMSDPESEK---NLEERVVD--PPTLSDLKKAIPYHCFERSVIRSSYYVVDL 55  
 DB 1 MGAGGRMDVPPANKSEVDPLKRVPEKQFSLGKIKKAIIPHCGRSVLASFVYVDL 60  
 QY 56 IVAVFYLYANTYPLIPLPLAYLAMPVYVFCQASILTGLVWIGHGCHHAFFSDYQILD 115  
 DB 61 TIACLVYVAHYFHLPLPGPLSFRGMALYMAVQGCILGVWVIAHCGHHAFFSDYQILD 120  
 QY 116 IVGVLSALLTPYFSWKSHRNHNANTSLDNDVYI.PKRSKKTYSKTLNPPGRV 175  
 DB 121 IVGLILSHALLVPYFSWKSHRNHNANTSLDNDVYI.PKRSKKTYSKTLNPPGRV 180  
 QY 176 TLVRLTLGFPYLLTNISGKKYGRFANHPDMSPIFNDREVOVLSDFGLLAVFYAIK 235  
 DB 181 TLAVTLTLGMPPLYLALANSGRPYDRFACHYDPGYISYDRERLQIYIDAGVLAFFVLF 240  
 QY 236 LIVAAGAAVYINNYAIPVLGVSVFVLITLHHTLSLPHYSTENWIKGALSTIDR 295  
 DB 241 RLAAKGLAAVYCVGVPLVVGFLVLTFLQHTHPALPHYTSEMDWMLGALATVDRD 300  
 QY 296 FGFLNRPVHDVTHVLAHLISYIPHYAKKARDAIKFVLGELYKIDTPIFKAMRYEAK 355  
 DB 301 YGILNKVFHNITDTHVAHLFSTMPHYAMEATKAIKPIIGEYVRFDETPEVKAMWREAR 360  
 QY 356 ECIYIEPDESEHKGVFWMY 375  
 DB 361 ECIYVDPQSTESKGVFMYN 380

XX 09-MAY-2001; 2001WO-IB001059.  
 PF  
 XX 09-MAY-2000; 2000US-0203027P.  
 PR  
 XX (BIOR-) BIORIGINAL FOOD & SCI CORP.  
 PA  
 XX Qiu X;  
 PI  
 XX WPI; 2002-089796/12.  
 DR N-PSDB; AA169486.  
 DR  
 XX Nucleic acids which encode a conjugase and its related enzyme a delta  
 PT desaturase to be used for the large scale production of conjugated  
 PT linoleic acid and linolenic acid in plants.  
 XX  
 PS Claim 3; Fig 1; 49pp; English.  
 CC This invention describes a novel polypeptide, Cofad2, capable of  
 CC catalyzing the formation of two conjugated double bonds. The products of  
 CC the invention can be used for the large scale production of conjugated  
 CC linoleic acids. The composition may be used for cosmetic or  
 CC pharmaceutical purposes. The conjugated linoleic acids may be used for  
 CC coating, painting or cold weather ester-type lubricant purposes. There is  
 CC not a natural source which is rich in conjugated linoleic acids and  
 CC chemical processes result in a mixture of several isomers. Plant  
 CC biotechnology is cost-effective and renewable with little side effects.  
 CC This sequence represents the Calendula officinalis Cofad2 protein  
 CC  
 SQ Sequence 383 AA;  
 Query Match 64.7%; Score 1323.5; DB 5; Length 383;  
 Best Local Similarity 61.3%; Pred. No. 1.6e-126;  
 Matches 233; Conservative 57; Mismatches 83; Indels 7; Gaps 2;  
 QY 1 MGAGGRMSDPESEKNIIEERVVD-----PPTLSDLKKAIPYHCFERSVIRSSYYVVD 54  
 DB 1 MGAGGRMODPTNGQNKTEPEPIQVPHKPPFTGDIKKAIPHCFNRSVIRSFYSFYVD 60  
 QY 55 LIVAVFYLYANTYPLIPLPLAYLAMPVYVFCQASILTGLVWIGHGCHHAFFSDYQILD 114  
 DB 61 LTIASILYINANNYSTLPSPLAYVAMPVYVAVQCVLTGVWVIAHCGHHAFFSDYQILD 120  
 QY 115 DIVGVLSALLTPYFSWKSHRNHNANTSLDNDVYI.PKRSKKTYSKTLNPPGRV 174  
 DB 121 DTGVLVLSPLVYFWSKSHRNHNANTSLDNDVYI.PKRSKKTYSKTLNPPGRV 180  
 QY 175 FTLVRLTLGFPYLLTNISGKKYGRFANHPDMSPIFNDREVOVLSDFGLLAVFYAI 234  
 DB 181 LTLAVTLTLGMPPLYLALANSGRPYDRFACHDPSPIYSKREARQIFISDAGILAVFVL 240  
 QY 235 KLVVAAAGAAVYINNYAIPVLGVSVFVLITLHHTLSLPHYSTENWIKGALSTIDR 294  
 DB 241 FRLAMTKGLTWVLTMYGSPPLVVGFLVLTFLQHTHPALPHYSTENWIKGALSTIDR 300  
 QY 295 DFGFLNRPVHDVTHVLAHLISYIPHYAKKARDAIKFVLGELYKIDTPIFKAMRYEAK 354  
 DB 301 DYGLNKVFHNITDTHVAHLFSTMPHYAMEATKAIKPIIGDYQDGTISIFKAMRET 360  
 QY 355 KECIYIEPDESEHKGVFWMY 374  
 DB 361 KECIYVDKDEEVK-DGVYMY 379

RESULT 11  
 AA86153  
 ID AA86153 standard; protein; 384 AA.  
 AC  
 XX AA86153;  
 AC  
 XX 04-MAR-1999 (first entry)  
 DT  
 XX Protein sequence of F form of wild-type Fad2 gene.  
 DB

```

DB          361 KECIYVEPDRQEKKGVEWYN 381

RESULT 12
AAW94053
ID          AAW94053 standard; protein; 384 AA.
XX
AC          AAW94053;
XX
DT          06-APR-1999 (first entry)
XX
DE          Amino acid sequence of Brassica wild-type Fad2-F gene product.
XX
KW          Fatty acid desaturase; FAD; Brassicaceae; Helianthus; mutation;
KW          fatty acid; oleic acid; linoleic acid; Fad2 gene.
XX
OS          Brassica napus.
XX
PN          WO9856239-A1.
XX
PD          17-DEC-1998.
XX
PF          11-JUN-1998; 98WO-US012332.
XX
PR          12-JUN-1997; 97US-00874109.
XX
PA          (CRGI ) CARGILL INC.
XX
PI          Debonte LR, Zhegong F, Loh WH, Shorrosh BS;
XX
DR          MPI: 1999-059929/05.
XX
DR          N-PSDB; AAX06619.
XX
PT          New isolated mutant fatty acid desaturase genes - obtained by mutation of
PT          Brassicaceae or Helianthus plants, used for producing plants or seeds
PT          having altered fatty acid compositions.
XX
XX          Example: Page 73-75; 116pp; English.
XX
PS          The invention relates to fatty acid desaturases (FAD) from Brassicaceae
CC          or Helianthus, where the FAD genes comprise at least one mutation in
CC          their sequences. The mutation is in a region encoding the His-Xaa-Xaa-
CC          His motif of the delta-12 or delta-15 fatty acid desaturases. The
CC          invention also provides methods for producing the FAD mutant genes and
CC          gene products. The products can be used for producing plants and seeds
CC          which have altered fatty acid compositions, e.g. an elevated oleic acid
CC          content, a decreased, stabilised linoleic acid content, both elevated
CC          oleic acid and decreased, stabilised linoleic acid content or a
CC          decreased, stabilised level of alpha-linolenic acid and increased level
CC          of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower,
CC          safflower, castor bean or corn. The present sequence represents the amino
CC          acid sequence of the Brassica wild-type Fad2-F gene product
XX
XX
SQ          Sequence 384 AA;

Query Match          64.4%; Score 1318; DB 2; Length 384;
Best Local Similarity 61.2%; Pred. No. 5,9e-126;
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4

QY          1 MCAGGRM--SDPSSEK--NILERVVD--PPTLSDLKRIPTHCPEHSYIRSSYYVHDL 55
DB          1 MCAGGRMOVSPSKSEDTTIRKVCETPPFVIGELKRIIPHCPEKRSIRPSSTYIMDI 60
QY          56 IYAAYFYLLANTYIPLPTPLAYLAMPVYVFCQASITGLAWYIGHCEGHHAFSDYOLID 115
DB          61 IIASCFYVATYTPFLPLPLPSYFAMPPLMAOQCVLTGWTWYIAHCGHHAFFDYOMDD 120
QY          116 IVGFVLHSLALTPYFSWKYSHRNHNANTNSLDNDEVYIIPKRSKVKIYSKLLNNPGRV 175
DB          121 TVGLIFHSFLVYPYFSWKYSHRRHNSNTSLRDEVFVPKKSDIKWYGYLNNPGRV 180
QY          176 TLVFLTLTGFPYLLTNTISGKY--GRFANHPEPMSEIIPNDRERVQYLLDFFGLANFYAL 234

```

Query	Best Local Similarity	Score	DB	Length
Query Match	64.4%	Score 1318	DB 3	Length 384
Best Local Similarity	61.2%	Pred. No. 5,9e-126		

Matches	233: Conservative	61: Mismatches	81: Indels	6: Gaps	4:
QY	1 MGAGGRM--SDPSSECK--NIIERYVPD--PPTTSDLKKAIPTRCPENSIVRSYTVVDL	55			
Db	1 MGAGGRMQVSPSPSKSESTDYIKRVCEPPTPTVGEIKKAIIPPHCFKRSIPRSPSYLIMDI	60			
QY	56 IVAVVFFYTLANTYIPLIPTPLAATLAMPYVWFQASILTLGLWVIGEGCHHAFSDYQLIDD	115			
Db	61 IIAACEFYVATYTPPLPLHPLUSYFWAMPYMACQCGVLGVWVIAHEGCHHAFSDYQLIDD	120			
QY	116 IVGFVLSALTLPEFWSWKYSHRNHNHANTNSLDNDEVYIPKRSKYKYSKLLNPPGRVFE	175			
Db	121 TVGLIFHSFLVLPFWSWKYSHRRHNSNGSLERDEVFPKPKKSDIKM*GKYLNNPLGRTV	180			
QY	176 TLVPLRLTGPPLYLITISGKKY-GREANHPDPMSPFNDERRVOLLSDPGLAVFYAI	234			
Db	181 MLTVQFTLTGMPLTALFNVSGRPYDGGFCFHNPAPIYNDERERLQIYISDGLIIVCYGL	240			
QY	235 KLIVAAKAAAVIMMVAIPVLGVGVFFLTLYLTHHTSLPHYOSTENNWAKGALSTDR	294			
Db	241 FRYAAQGVASMWCFYGVPLIIVGFLVLTLYLQHTHPSLPHYSSBMDMLGALATVDR	300			
QY	295 DFGELNRFVHDVTHTVLAHLISYIPHYAKEARDAIKPLVGEYKKIDRTPIFKAMVREA	354			
Db	301 DYGLINKYFNHITTDTHVAHHLFSTMPPHMAEATKAIKPIIGEYYPQPGITVYAMVREA	360			
QY	355 KECIYIEPDEDESBHKGVPWYH 375				
Db	361 KECIYIEPDRQEKKGVPWYH 381				
RESULT 14					
ID	AAV27329				
XX	AAV27329 standard; protein; 384 AA.				
XX	AAV27329;				
DT	15-NOV-1999 (first entry)				
DE	B. napus delta-12 fatty acid desaturase 2 (FAD2) D form.				
KW	Fatty acid; delta-12 desaturase; fatty acid desaturase; FAD; enzyme;				
KM	linoleic acid; alpha-linolenic acid; mutant; nutritional value;				
XX	genetic mapping; plant breeding.				
OS	Brassica napus.				
XX	EP945514-A1.				
PM	29-SEP-1999.				
PD	26-MAR-1998; 98EP-00302322.				
PF	26-MAR-1998; 98EP-00302322.				
XX	26-MAR-1998; 98EP-00302322.				
PR	(DUPO ) DU PONT DE NEMOURS & CO E I.				
XX	Broglie RM, Miao G, Debonte LR, Reiter RS, Hitz WD;				
PI	WPI, 1999-530050/45.				
DR	N-PSDB; AAX91076.				
PT	Altering fatty acid profiles in plant seeds, useful for changing				
PT	nutritional value of seeds.				
XX	Example; Page 19-21; 44pp; English.				
CC	The invention relates to a method for altering the fatty acid composition				
CC	in plant seeds and comprises transforming a plant with a nucleic acid				
CC	construct (I) comprising a seed-specific regulatory sequence linked to				
CC	either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene				
CC	encoding a protein with a mutation in a His-(asp/Glu)-Cys-(Gly/Ala)-His				
CC	amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15				

CC FAD. Expression of this construct in plants decreases the level of  
 CC activity of these enzymes in the cells of the plant i.e. the construct  
 CC acts as a dominant negative. The construct comprising a mutant delta-12  
 CC gene is used to decrease the level of linoleic acid in the seeds of  
 CC plants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax,  
 CC canola and peanut). Similarly a construct comprising a mutant delta-15  
 CC gene is used to decrease the levels of alpha-linolenic acid in the seeds  
 CC of plants, especially Brassica canola. The new method may also be used to  
 CC transform a plant with both (i) comprising DNA encoding mutant delta-12  
 CC and (i) comprising DNA encoding mutant delta-15 FAD genes, to decrease  
 CC the levels of both linoleic and alpha-linolenic acid simultaneously in  
 CC their seeds. These methods alter the nutritional value of the seeds of  
 CC plants which have been transformed. (i) may also be used as DNA  
 CC diagnostic markers in plant genetic mapping and plant breeding programs.  
 CC In addition (i) may be used to isolate other related FAD genes. The  
 CC present sequence represents a Brassica napus wild type D form of  
 CC microsomal delta-12 fatty acid desaturase 2 (FAD2)  
 XX  
 SQ Sequence 384 AA;  
 Query Match 64.3%; Score 1317; DB 2; Length 384;  
 Best Local Similarity 61.3%; Pred. No. 7.5e-126;  
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;  
 QY 1 MGAGGRM-----SDPSEGNILERVVD-PEPTSLDKKAIPTCFERSVIRSSYVVHD 54  
 DB 1 MGAGGRMOVSPSKSETDNI-KRVPCEPTPTVGLKKAIPHCFKRSIRSFSTYLWMD 59  
 QY 55 LIVAVFYYLANTYIPLIPTPLAYLAMPVWFCQASILITGLMVGHECGHNAFSDYOLID 114  
 DB 60 IILASCFYVATYTFPLLPPLSYFAMPVWACQCVLTIGWVIAHECGHNAFSDYQWLD 119  
 QY 115 DIVGFVLHSAALLTFYFSWKYSHRNHANTNSLNDDEVYIPKRSKVKIYSLNNPGRV 174  
 DB 120 DTVGILFHSPFLVYFWSKYSHRHNSHTGSLERDEVPVKKSDIKMYGATLNNPLGRT 179  
 QY 175 FTLVFRLTLGFPPLYLITNISKGY-GRFANFDPMSPFNDREVOVLISDFGLAVFYA 233  
 DB 180 VMLTVQFTLGWPLVLAFAVNSGRPYDGGPACHFNPAIYNRERLQIYISAGILAVCYG 239  
 QY 234 IKLVAAGAAVMINMVAIPVLGVSVFVLITLYLHTHTLSLPHYDSTEMNMIKALSTID 293  
 DB 240 LYRAAAGVAVASWCFVGPLVINGFLVLTLYLOHTHPSLPHDSSMDWLRGALATVD 299  
 QY 294 RDFGLNRVFDVTHVLAHLISYIPHYAKAADAIRPVLGYYKIDRTPIFKAMTYRE 353  
 DB 300 RDYGLINKVFHNITDTHVAHLFSTMPHYHAMEATKAIKPILGEEYQDGTPIVYVAMWRE 359  
 QY 354 AKECIYIEPDEDESEHKGVFWTH 375  
 DB 360 AKECIYVEPDRQGEKKGVFWYN 381  
 RESULT 15  
 ABB80028 ID ABB80028 standard; protein; 384 AA.  
 XX AC ABB80028;  
 XX DT 26-JUN-2002 (first entry)  
 XX DE Rape microsomal delta-12 desaturase amino acid sequence.  
 XX KW Rape; microsomal delta-12 desaturase; delta-12 hydroxylase;  
 XX KM delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;  
 XX fact; oil; heart disease.  
 XX OS Brassica napus.  
 XX XX US6372965-B1.  
 XX PD 16-APR-2002.  
 XX

PF 14-AUG-1998; 98US-00133962.  
 XX  
 XX 17-NOV-1992; 92US-00977339.  
 PR 15-OCT-1993; 93WO-US009987.  
 PR 20-JUN-1994; 94US-00262401.  
 XX  
 PA (DUPLO) DU PONT DE NEMOURS & CO E I.  
 XX  
 XX Lightner JE, Okuley JU, Hitz W, Kinney AJ, Perez-Grau L;  
 PI Yadav NS;  
 DR WPI; 2002-392229/42.  
 XX N-PSDB; ABL58600.  
 PT  
 PT New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or  
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and  
 PT producing seed oil with altered levels of unsaturated fatty acids.  
 XX  
 XX Example 3; Col 75-76; 54pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid fragment encoding or  
 CC comprising a sequence encoding a plant enzyme that is a delta-12  
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.  
 CC Chimeric genes comprising nucleic acids of the invention are used to  
 CC create transgenic plants with altered levels of unsaturated fatty acids,  
 CC and can modify plant lipid composition. Nucleic acids of the invention  
 CC can be used as hybridization probes to isolate or amplify nucleotide  
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-  
 CC related enzymes. They can also be used in restriction fragment length  
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in  
 CC seed oil of oil producing plant species. They can also be used to produce  
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic  
 CC acids of the invention can combine the high oleate trait of transformed  
 CC seeds with mutations for altered fatty acid compositions to obtain new  
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in  
 CC total saturates and high in monounsaturates would provide significant  
 CC health benefits to consumers (reduced risk of coronary heart disease) as  
 CC well as economic benefits to oil processors. The current sequence  
 CC represents a rape microsomal delta-12 desaturase amino acid sequence  
 XX  
 SQ Sequence 384 AA;  
 Query Match 64.3%; Score 1317; DB 5; Length 384;  
 Best Local Similarity 61.3%; Pred. No. 7.5e-126;  
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;  
 QY 1 MGAGGRM-----SDPSEGNILERVVD-PEPTSLDKKAIPTCFERSVIRSSYVVHD 54  
 DB 1 MGAGGRMOVSPSKSETDNI-KRVPCEPTPTVGLKKAIPHCFKRSIRSFSTYLWMD 59  
 QY 55 LIVAVFYYLANTYIPLIPTPLAYLAMPVWFCQASILITGLMVGHECGHNAFSDYOLID 114  
 DB 60 IILASCFYVATYTFPLLPPLSYFAMPVWACQCVLTIGWVIAHECGHNAFSDYQWLD 119  
 QY 115 DIVGFVLHSAALLTFYFSWKYSHRNHANTNSLNDDEVYIPKRSKVKIYSLNNPGRV 174  
 DB 120 DTVGILFHSPFLVYFWSKYSHRHNSHTGSLERDEVPVKKSDIKMYGATLNNPLGRT 179  
 QY 175 FTLVFRLTLGFPPLYLITNISKGY-GRFANFDPMSPFNDREVOVLISDFGLAVFYA 233  
 DB 180 VMLTVQFTLGWPLVLAFAVNSGRPYDGGPACHFNPAIYNRERLQIYISAGILAVCYG 239  
 QY 234 IKLVAAGAAVMINMVAIPVLGVSVFVLITLYLHTHTLSLPHYDSTEMNMIKALSTID 293  
 DB 240 LYRAAAGVAVASWCFVGPLVINGFLVLTLYLOHTHPSLPHDSSMDWLRGALATVD 299  
 QY 294 RDFGLNRVFDVTHVLAHLISYIPHYAKAADAIRPVLGYYKIDRTPIFKAMTYRE 353  
 DB 300 RDYGLINKVFHNITDTHVAHLFSTMPHYHAMEATKAIKPILGEEYQDGTPIVYVAMWRE 359  
 QY 354 AKECIYIEPDEDESEHKGVFWTH 375  
 DB 360 AKECIYVEPDRQGEKKGVFWYN 381



Thu Jun 24 08:51:45 2004

us-10-069-772-2.rag

Page 11

Search completed: June 19, 2004, 17:36:25  
Job time : 61 secs

---

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 14:45:14 ; Search time 3294 Seconds  
(without alignments)  
4960.633 Million cell updates/sec

Title: US-10-069-772-2  
Sequence: 1 MGAGGRMSDSEGRNLEERV.....IYEPDESEHKGVFWYHKM 377

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O/cgrr 1/USPFO.spool/US10069772/runat 18062004 145512 5284/app query.fasta\_1.519  
-DB=GenBdb1 -QPM=faabcap -SUFFIX=rge -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USBR=US10069772 @CGN 1 1 2527 @runat 18062004 145512 5284 -NCPU=6 -ICPU=3  
-NO MAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenBdb1:  
1: gb\_ba:\*  
2: gb\_ncg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_stc:\*  
12: gb\_ey:\*  
13: gb\_un:\*  
14: gb\_vt:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_stc:\*  
27: em\_un:\*  
28: em\_vt:\*

29: em\_vt:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vtc:\*  
38: em\_ey:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2047	100.0	1152	8 CQF245938	AZ45938 Calendula
2	2047	100.0	1285	8 AX089471	AX089471 Sequence
3	1922	93.9	1419	8 AY166773	AY166773 Helianthu
4	1644	80.3	979	8 AY166776	AY166776 Rudbeckia
5	1629	79.6	1435	8 CAY16285	Y16285 Crepis alpi
6	1607	78.5	979	8 AY166778	AY166778 Helichrys
7	1596	78.0	979	8 AY166777	AY166777 Dimorphot
8	1592.5	77.8	1312	6 AR367438	AR367438 Sequence
9	1592.5	77.8	1312	6 AX031162	AX031162 Sequence
10	1592.5	77.8	1312	6 BD061165	BD061165 Plant fat
11	1589.5	77.7	1358	6 AR367437	AR367437 Sequence
12	1588.5	77.7	1358	6 AX031160	AX031160 Sequence
13	1588.5	77.7	1358	6 BD061164	BD061164 Plant fat
14	1588.5	77.7	1358	6 CPY16283	Y16283 Crepis pala
15	1578.5	77.1	1364	6 AR064128	AR064128 Sequence
16	1541.5	75.3	1406	8 AY462108	AY462108 Stokesia
17	1396.5	68.2	1291	8 AF074324	AF074324 Borago of
18	1387.5	67.8	1516	8 AF252534	AF252534 Vernonia
19	1374.5	67.1	1466	8 AF192486	AF192486 Sesamum i
20	1366.5	66.8	1344	8 HAN292275	AJ292275 Helianthu
21	1366.5	66.8	1345	8 AF251843	AF251843 Helianthu
22	1360	66.4	1250	8 AY057406	AY057406 Persaea am
23	1359.5	66.4	1507	8 AF188264	AF188264 Vernonia
24	1357	66.3	1259	8 AF251844	AF251844 Helianthu
25	1350.5	66.0	1475	8 AF188263	AF188263 Vernonia
26	1348.5	65.9	1472	8 SCD120LDS	X92847 S.commercion
27	1347.5	65.8	1401	8 AY178447	AY178447 Punica gr
28	1339.5	65.4	110900	8 AP006377	AP006377 Lotus cor
29	1337.5	65.3	1350	8 PER437139	AJ373739 Punica gr
30	1337.5	65.3	1398	8 AX700111	AX700111 Sequence
31	1336	65.3	1447	8 PCU86072	U86072 Petroselinu
32	1336	65.3	1627	8 AB094415	AB094415 Spiraciia
33	1336	65.3	7914	8 AF331163	AF331163 Gossypium
34	1335	65.2	1356	8 CPY16284	Y16284 Crepis pala
35	1332.5	65.1	1422	8 CHOMEGA6	Y10112 Gossypium h
36	1325.5	64.8	1536	8 SOYMO6DA	L43921 Glycine max
37	1323.5	64.7	1411	6 AX301157	AX301157 Sequence
38	1323.5	64.7	1411	8 AF343065	AF343065 Calendula
39	1321.5	64.6	1452	8 AY083163	AY083163 Olea euro
40	1318	64.4	1155	6 AR066514	AR066514 Sequence
41	1318	64.4	1155	6 BD261361	BD261361 Plants, s
42	1318	64.4	1155	6 AR184297	AR184297 Sequence
43	1318	64.4	1155	6 AR431239	AR431239 Sequence
44	1318	64.4	1155	6 BD132762	BD132762 Fatty aci
45	1317	64.3	1155	6 AR184295	AR184295 Sequence

RESULT 1

ALIGNMENTS

LOCUS	DEFINITION	1152 bp	mRNA	linear	PLN 22-DEC-1998
COF245938	COF245938	Calendula officinalis partial mRNA for (8,11)-linoleoyl desaturase (des8.11 gene).			
ACCESSION	Accession	AJ245938			
VERSION	Version	AJ245938.1	GI:6634079		
KEYWORDS	Keywords	(8,11)-linoleoyl desaturase; des8.11 gene.			
SOURCE	Source	Calendula officinalis			
ORGANISM	Organism	Calendula officinalis			
		Euxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Calendula.			
REFERENCE	Reference	1			
AUTHORS	Authors	Fritsche, K., Hornung, E., Peitzsch, N., Renz, A. and Feussner, I.			
TITLE	Title	Isolation and characterization of a calendic acid producing (8,11)-linoleoyl desaturase			
JOURNAL	Journal	FEBS Lett. 462 (3), 249-253 (1999)			
MEDLINE	Medline	20086417			
PUBMED	Pubmed	10622705			
REFERENCE	Reference	2 (bases 1 to 1152)			
AUTHORS	Authors	Feussner, I.			
TITLE	Title	Direct Submission			
JOURNAL	Journal	Submitted (02-SEP-1999) Feussner I., Hormonforschung, Institut fuer Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, GERMANY			
FEATRES	Features	Location/Qualifiers			
source	Source	1..1152			

```

gene
  /gene="des8.11"
  1..>1131
  /gene="des8.11"
  /function="production of calendic acid"
  /codon_start=1
  /evidence=experimental
  /product="8,(11)-linoleyl desaturase"
  /protein_id="CAB64256.1"
  /db_xref="GI:6634080"
  /db_xref="GOA:O9SCG2"
  /db_xref="SPTRMBL:O9SCG2"
  /translation="MGAGGRMSDSESGNILLERVVPDPFTLSDLKAIPTHCERSY
  IRSYVYVHDLIVAFYFYLLANTYIPLPTPLAYLAVVYECASILTGAWLVGHEG
  GHNAESDYHDLIDIVGFPLSHALLTPYSMKSRHNHANNSLNDNEVYIPKRSKQ
  KIVAKILNNPGRGVPTLTVFRLTIGPLPLVILINIGSKYGRGANHPDMSPLFNDRR
  QVLSDBGILAVFYAIKILVAKGAAWYINNAIPVGLVSPFUILITLHKAARDAIKP
  YDSLEMNRIKCALSTIDRDFGLUNKRVFHDVTHVHLHLSTIPATHKANRDLAKP
  LGEYKIKDRTPIPFAMRYEAKCYIIEPDEDSHKGVAYHKM"

```

Alignment Scores:	
Pred. No.:	5.23e-183
Scores:	2047.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	8
Gaps:	0
US-10-069-772-2 (1-377)	x CQ2F45938 (1-1152)

QY	1	MetGlyAlaGlyGlyValMetSerAspProSerGluGlyValAsnIleGluGluArgVal	20
Db	1	ATGGTGCTGGTGGTCCGATGTCGATCCATCTGAGGAAAAAATCATCTTGAACGTGTG	60
QY	21	ProValAspProProPheThrIleuSerAspIleuLysValAlaIleProThrHisGlyPhe	40
Db	61	CCAGTCGATCCACCGTTCACGTTAAGCCATCTGAGAAAGAAAGCATTCCTACCCATGCTTT	120
QY	41	GluArgSerValIleArgSerSerTyrThrValAlaHisAspLeuIleValAlaTyrVal	60

Db	121	GAGGAGTCTGTCATCCGGTCATCATCATATGTTGTCATGATCTCATTTGGTGGCTTAATGTC	180
Qy	61	PheTyrTyrIleuAlaLeuThrTyrIleProIleuIleProThrProIleuAlaTyrIleuAla	80
Db	181	TTTCTACTACCTTGGCAACAGGTAAATCCCTTAACTTCTACACCTCGGCTTACCTTGGCA	240
Qy	81	TTrProValTyrTrpPheGlySerIleLeuThrGlyLeuTrpValIleGlyHis	100
Db	241	TGGCCCGTTTACTGGTTTGTGTCAGCTACAGCATCTTCAACCGGCTCTGGGTATGGTCTAC	300
Qy	101	GluGlyGlyHisIleAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPheVal	120
Db	301	GAATGGTGTCACCATGATTTAGGAGCTACACAGTGTGATGATGATGATTTGGATTGGTG	360
Qy	121	LeuHisSerAlaLeuLeuThrProTyrPheSerTrpTyrSerHisValGlyAsnHis	140
Db	361	CTTCATTCGGCTCTCCCTCAACCCCTTAATTTCTCTGGAAATATAGCCACAGGAATCACAC	420
Qy	141	AlaAsnThrAsnSerIleuAspAspGlyValTyrIleProValGlySerLeuVal	160
Db	421	GCCAAACCAATTAATCTCGATGATACAGAGAGTTTAACTTCTTAAACCTTAAGTCCAAAGTC	480
Qy	161	LysIleTyrSerLysIleuLeuAspAsnProGlyArgValPheThrLeuValPheArg	180
Db	481	AAGATTATTTCCAAACTTCTTAAACAATCCACCGGGGAGGTTCACCTTGGTTCGG	540
Qy	181	LeuThrIleuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysTyrGlyArg	200
Db	541	TTGACTTATGAGATTTCGGTATATACCTTAACTAAATATCTCGGGCAAAATATACGGAGG	600
Qy	201	PheAlaAsnHisPheLeuAspProMetSerProIlePheAsnAspArgValArgValGlnVal	220
Db	601	TTTGTCCAAACCACTTGTGATCCCATGAGTCCCAATTTTCAACATCTGTAAACGGGTTCAGTT	660
Qy	221	LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysIleuLeuValAla	240
Db	661	TTGCTATCCGATTTCCGTTCTTCTCGCTGATTTTATTCANATCAAGCTTCTTGATGACGA	720
Qy	241	LysGlyAlaAlaArgValIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe	260
Db	721	AAAGGGGACAGTTGGGTAACTCAACATGTACGAATTCAGACTAGGGTGTAAAGCTGTTC	780
Qy	261	PheAlaLeuIleThrTyrIleuHisHisThrHisIleuSerLeuProHisTyrAspSerThr	280
Db	781	TTCTGTTTGTACAAATATTGACCAACCAACCATCTTCACCTCCCTCAATTGATTTCAACC	840
Qy	281	GluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn	300
Db	841	GAATGGAATCGATCAAAAGCGGCTTATCAACANATCATAGGAGATTTCCGGTTCCTGAAT	900
Qy	301	ArgValPheHisAspValIleThrHisThrHisValLeuHisHisIleuIleSerTyrIlePro	320
Db	901	CGGGTTTTTCCACGACGTTACACACATCAACATCGTCTGCATCATTTGATCTCATACATCCA	960
Qy	321	HisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValLeuGlyGluTyrTyrLys	340
Db	961	CATTATCATGCAAAAGGAACGAAGGAGTCAATCAAGCAAGTGTGGCGAGTACTATAAAA	1020
Qy	341	IleAspArgThrProIlePheLysValMetTyrArgGlnAlaLysGluCysIleTyrIle	360
Db	1021	ATCCACAGGATCTCAATTTTCAAGCAATGATTAAGAGGTATTAAGAAATGATTTACATC	1080
Qy	361	GluProAspGluAspSerGlnHisLysGlyValPheThrTyrHisLysMet	377
Db	1081	GAGCCCGATGAGATACGAGACCAAAAGGTGTGTCTTCGATACCAAAAGATG	1131

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

Calendula officinalis  
Calendula officinalis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Calenduleae; Calendula.  
1  
Feussner, I., Hornung, B., Fritsche, K., Peltzsch, N. and Renz, A.  
Fatty acid desaturase gene from plants  
Patent: WO 0116362-A 1 08-MAR-2001;  
BASF AKTIENGESELLSCHAFT (DE)  
Location/Qualifiers  
1..1285  
/organism="Calendula officinalis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:41496"  
42..1175  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC34898.1"  
/db\_xref="GI:13443733"  
/db\_xref="REFSEQ:NC034898"  
/translation="MGAGGRMSDPSEGNIIERVVPDPEPTLSDKKAIPTHCERSV  
IRSSYYVVDLIVAVVEFYLLANTYIPLIPTPLAYLAMPVYFQASILITGLMVIGHEC  
GHAFFSDYQIDIDIVGFWLHSLALTPTYSMTYSHRNHANNNDNDENVYIPKRSKY  
KIYSLNNPGRVETLVEFLTLGPELTLNISGKKYGRFANHPDPMSPFENDERY  
QVLSDFGLALVFYAIKLLVAKGAAMVNNYAIPLYGSVFPVLITLHHTHLSLPH  
YDSTBMNWKALSTIDRDFPLNRVFDVTHVHLISYIPTHYAKERDAIKPY  
LGEYTKIDRTPIFAMTRAEKCIYEDESEHKGVFWYHKM"

ORIGIN  
Alignment Scores:  
Pred. No.: 6.01e-183 Length: 1285  
Score: 2047.00 Matches: 377  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-069-772-2 (1-377) x AK089471 (1-1285)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyValAsnIleLeuGluArgVal 20  
Db 42 ATGGGTGCTGGTGGCGGATGCGGATCGATCGAGGAAAAAATCATCTTGACGTGTG 101  
QY 21 ProValAspProPheProPheThrLeuSerAspLeuValAlaIleProThrHisCysPhe 40  
Db 102 CCAAGTCGATCCACCGCTTACGTTAAGCGATCTGAAGAAAGCGATTCTTACCATTGCTTT 161  
QY 41 GluArgSerValIleArgSerSerTyrTyrValValIleAspLeuIleValAlaTyrVal 60  
Db 162 GAGCGATGTCATCCGATCATCATCATGTTGTTCAATGATCATGATGTCATATGTC 221  
QY 61 PheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeuAla 80  
Db 222 TTCTACTACCTTGGAAAACAGGATATCCCTCTTATCTTACACCTCGCTTACTACCA 281  
QY 81 TrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTyrValIleGlyHis 100  
Db 282 TGGCCCGTTTACTGGTTTGTCAAGCTGACATCCCTCACCGGCTCTGGGTATCGTAC 341  
QY 101 GluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPheVal 120  
Db 342 GAATGTGTCACCATGATTTAGGACATCAACGTTGATTGATGACATTTGTGATTCTGTG 401  
QY 121 LeuHisSerAlaLeuLeuThrProTyrPheSerTyrGlySerHisArgAsnHisHis 140  
Db 402 CTCATTGCGCTCTCTCCACCCCGATTCTCTTGGAAATATAGCCACAGGATCACAC 461  
QY 141 AlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProValArgValSerIleVal 160  
Db 462 GCCAACCAATTCATCTGATTAAGATGAAGTTTACATTCTTAAACGTAACTGCAAGTTC 521

QY 161 LysIleTyrSerTyrLeuLeuAsnAsnProGluValArgValPheThrLeuValPheArg 180  
Db 522 AAGATTATTATCCAAACTCTTAACATCAACCGGAGAGTTCATCTTGTTCCG 581  
QY 181 LeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSerGlyValSerTyrGlyArg 200  
Db 582 TTGACTTTAGATTTCCTTATACCTCTTAATATCTCGGGCCAGAAATATACGGAG 641  
QY 201 PheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgValGluVal 220  
Db 642 TTTCGCAACCACTTGATCCCATAGATCAATTTTCAACGATCGTGAACGGGTCAAGTT 701  
QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLeuValAlaIle 240  
Db 702 TTGCTATCCGATTTCCGCTTCTCGCTGTATTTATGCAATCAACCTTCTTGACACA 761  
QY 241 LysGlyAlaAlaTyrPvalIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe 260  
Db 762 AAAGGGGAGCTGGGTATCATCATGATGACCAATTCAGATTAAGGTGAAGCGTTC 821  
QY 261 PheValLeuIleThrTyrTrpLeuHisHisThrHisLeuSerLeuProHisTyrAspSerThr 280  
Db 822 TTCGTTTGATCATATTTGACCAACCACTCTCATCTCCCTCATTTATGATTCAC 881  
QY 882 LysTyrAsnThrPheIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300  
Db 882 GAATGGAAGTGGATCAAAAGGCGCTTATCAACATTCATAGGATTCGGTTCCTGAT 941  
QY 301 ArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIlePro 320  
Db 942 CGGGTTTCCAGCAGATTTACACACTCACACTCATCTTGATCATTTGATCTCATATTC 1001  
QY 321 HisTyrHisAlaLysGluAlaArgAspAlaIleLeuProValLeuGlyValTyrTyrIle 340  
Db 1002 CATTATCATGTGAAGGAAGCAAGGATGCAATCAAGCGATGTTGGGAGTACTATTA 1061  
QY 341 IleAspArgThrProIlePhePheValAlaMetTyrArgGluAlaLysGluCysIleTyrIle 360  
Db 1062 ATCGACAGACTCCAAATTTTCAAGCATGTATGAGAGGTTAAGAAATGATCTACATC 1121  
QY 361 GluProAspGluAspSerGluHisLysGlyValAlaPheTyrTyrHisLysMet 377  
Db 1122 GAGCCCGATGAGATAGAGCACAAAGTGTGTTGTTGATCCACAAGATG 1172

RESULT 3  
AY166773  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AY166773 1419 bp mRNA linear PLN 02-JUN-2003  
AY166773.1 GI:31322134  
Helianthus annuus delta12-fatty acid acetylase mRNA, complete cds.  
Helianthus annuus (common sunflower)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
1 (bases 1 to 1419)  
Cañon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.  
Fungal responsive fatty acid acetylases occur widely in  
evolutionarily distant plant families  
Plant J. 34 (5), 671-683 (2003)  
Submitted (18-OCT-2002) Crop Genetics, Dupont, Bldg. 402  
Experimental Station, Wilmington, DE 19880-0402, USA  
Location/Qualifiers  
1..1419  
/organism="Helianthus annuus"  
/mol\_type="mRNA"

CDS

/db\_xref="taxon:4232"  
69..1202  
/codon\_start=1  
/product="delta12-fatty acid acetylase"  
/protein\_id="AA038032.1"  
/db\_xref="GI:31322135"  
/translation="MGAGRWSDPSEKNIIEVPIIDPPTLSLKKAIIPACFERSV  
IRSYVYVHDLIVAVFYFLANTYIPLIPTMAVLAIPVYPCASILITGLWVGHGEC  
GHAAYSDQIIDDIVGVLHSALTPTFSWYSHRNHNHNTSLDNDVYIPKRAKY  
AVSKLANNPGRVETLVRLTGLPPLVNLISGKKYGRFANHPDPLSPTRERI  
QVSDIGILAVLAVATKLIVAKGAAVTCAYLIPIVIGVHMFVLIITLHSLPH  
VSTEMNIRGALSTIDRDFGLNRFVHDVTHVHLISYIPIHYAKKARDALKPV  
LGEFYKIDRTIFKAMREACECTIIEDEDESEHKGYTHYHKM"

ORIGIN

Alignment Scores:

Pred. No.:	3,896-171	Length:	1419
Score:	1922.00	Matches:	346
Percent Similarity:	96.29%	Conservative:	17
Best Local Similarity:	91.78%	Mismatches:	14
Query Match:	93.89%	Indels:	0
DB:	8	Gaps:	0

US-10-069-772-2 (1-377) x AY166773 (1-1419)

QY 1 MetGlyAlaGlyValArgMetSerAspProSerGluGlyValAsnIleLeuGluArgVal 20  
DB 69 ATGGGTGAGGTGGCGGATGTCAGACCATCTGAGGCAAAACATCCTCGAAGCTGTC 128  
QY 21 ProValAspProPheThrLeuSerAspLeuValAlaIleProThrHisCysPhe 40  
DB 129 CCCATGATCCACCATCTCACTAGATGATCTTAAGAAAGCAATCCCTGCTCAGCTTC 188  
QY 41 GluArgSerValIleArgSerSerTyTyValValHisAspLeuIleValAlaIleVal 60  
DB 189 GAAGATGTCATCGTTCATCTTACTATGTTGTTCACTGACCTGATTTGGGCTATGTC 248  
QY 61 PheTyTyLeuAlaAsnThrTyTleProLeuIleProThrProLeuAlaTyLeuAla 80  
DB 249 TTTTACTTCCTTCCACACATATATCCCTCTTCACTACCCCTGGGCTTACTTACCA 308  
QY 81 TrpProValTyTyTrpPheCysGluAlaSerIleLeuThrGlyLeuTrpValIleGlyHis 100  
DB 309 TGGCGGCTTACTGCTTTTGCAAGCTACATCTCACTGGGCTATGGGCTATCGGCTAC 368  
QY 101 GluCysGlyHisAlaPheSerAspTyTyGluLeuIleAspAspIleValGlyPheVal 120  
DB 369 GAATGTGCTCACAGCGCTATAGTACCAATGATTGATGACATTGTTGGTTCGTC 428  
QY 121 LeuHisSerAlaIleLeuThrProTyTyPheSerTyTySerHisArgAsnHisHis 140  
DB 429 CTCGATTAGCTCTTATACCCCTTATTTCTTGGAAATACAGCCATCGGAACACACAC 488  
QY 141 AlaAsnThrAsnSerLeuAspAsnAspGluValTyTyIleProTyArgTyLeuVal 160  
DB 489 GCCAACAAGATTCGCTTGATGATGATGAAGTTTCACTTCTTAAGCGAAGCCAAATTT 548  
QY 161 LysIleTyTySerTyTyLeuLeuAsnAsnProGlyArgValPheThrLeuValPheArg 180  
DB 549 GCAGTTTACTCAAAAGCTTCTTAACAATCCCTGGTGCAGTGTTCACCTTGGTTTTCAGG 608  
QY 181 LeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSerGlyValGlyTyTyArg 200  
DB 609 TTAACCTTCAAGGTTTCTTGTGACTCTTGTGACTAATTTCTGGGCAAAATATACCGGAGG 668  
QY 201 PheAlaAsnHisAspAspProMetSerProIlePheAsnAspArgGluArgValGlnVal 220  
DB 669 TTTCGCAACCACTTTCATTCACATGCGAATTTTCACTGAGCGTGAAGAGGATAGGTT 728  
QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAlaIleTyTyLeuLeuValAla 240  
DB 729 GTTATATCTGATATTGATTTCTCGCGGTTTGTATGACACTTAACCTTGTAGAACGG 788

QY 241 LysGlyAlaAlaIleTrpValIleAsnMetTyTyAlaIleProValIleGluValSerValPhe 260  
DB 789 AAGGGGGAGCTTGCGTACATGATTAATTCGGGCTAGGAGTACATGATTTT 848  
QY 261 PheValLeuIleThrTyTyLeuHisHisThrHisLeuSerLeuProHisTyTyAspSerThr 280  
DB 849 TTCTGTTGATGACGATTTTGGACACACCATCTCTTCTTAACTCATTAATGATTAAC 908  
QY 281 GluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300  
DB 909 GAAAGCAACTGAGACAGGGGGCATTTTCGCAATTTGATGGGATTTTGATTCCTGAT 968  
QY 301 ArgValPheHisAspValIleThrHisThrHisValLeuHisHisLeuIleSerTyTyIlePro 320  
DB 969 AGGCTTTCATGATGTCACACACATCTGATCTTGCATCTGATCTCTTCAATTTCCA 1028  
QY 321 HisTyTyHisAlaLysGluAlaArgAspAlaIleLysProValIleGluGluTyTyTyTy 340  
DB 1029 CATTTATCATGCAAAAGAGGAGGACAGATCAAGCAATCAAGCAATTTTATTAAG 1088  
QY 341 IleAspArgThrProIlePheLeuAlaMetTyTyArgGluAlaLysGluGlyIleTyTyIle 360  
DB 1089 ATCGATAGACCCCTATTTTCAGAGCGATGCGAGAGGCGCAAGATGATCTATCATC 1148  
QY 361 GluProAspGluAspSerGluHisLysGlyValAlaPheTrpTyTyHisLysMet 377  
DB 1149 GAACCGATGAAATGATGAAACACAAAGGACATATTTGATCAATAATG 1199  
RESULT 4  
LOCUS AY166776 979 bp DNA linear PLN 02-JUN-2003  
DEFINITION *Rudbeckia hirta* delta12-fatty acid acetylase gene, partial cds.  
ACCESSION AY166776  
VERSION AY166776.1 GI:31322140  
KEYWORDS  
SOURCE  
ORGANISM  
*Rudbeckia hirta*  
Rudbeckia hirta  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Rudbeckia.  
REFERENCE  
1 (bases 1 to 979)  
Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.  
Fungal responsive fatty acid acetylases occur widely in  
evolutionarily distant plant families  
Plant J. 34 (5), 671-683 (2003)  
AUTHORS  
2 (bases 1 to 979)  
Cahoon, E.B.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (19-OCT-2002) Crop Genetics, Dupont, Bldg. 402  
Experimental Station, Wilmington, DE 19880-0402, USA  
FEATURES  
source  
1..979  
/organism="Rudbeckia hirta"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:52259"  
CDS  
mRNA  
1..>979  
/product="delta12-fatty acid acetylase"  
<1..>979  
/codon\_start=1  
/product="delta12-fatty acid acetylase"  
/protein\_id="AA038035.1"  
/db\_xref="GI:31322141"  
/translation="KAIPHCERSVIRSYVVHDLIVAVFYFLANTYIPLIPTMA  
AYLAMPVYPCASILITGLWVGHGECGHAAYSDQIIDDIVGVLHSALTPTFSWY  
SHRNHNHNTSLDNDVYIPKRAKYAVSKLANNPGRVETLVRLTGLPPLVNLISGKKY  
GRFANHPDPLSPTRERIQVSDIGILAVLAVATKLIVAKGAAVTCAYLIPIVIGVHMFV  
LITLHSLPHVSTEMNIRGALSTIDRDFGLNRFVHDVTHVHLISYIPIHYAKKARDAL  
KPV LGEFYKIDRTIFKAMREACECTIIEDEDESEHKGYTHYHKM"

ORIGIN

Alignment Scores:

Pred. No.:	3,396-145	Length:	979
------------	-----------	---------	-----



```

Db      28 ATGGGTGGCGGTGGCGGT-----GGTGGACTTGGCAAAAACCCCTATGAGAGTGTG 81
Qy      21 ProValaapProPheThrLeuSeraspLeuValaalleProThriCyasphe 40
Db      82 TCAGTGTATCCACCTTACCGGTGATCTCAAGCAAGCAATCCCTCCATTTGCTTC 141
Qy      41 GluAgsSerValaalleAgsSerSerTyrrValValaalleAapLeuValaalleAa 60
Db      142 AAGCATCTGTATTCCTTCTTACATCAAGTCCAGATCTATTATGCGCTTACATC 201
Qy      61 PheTyrrLeuValaalleAaThrTyrrLeuProLeuThriProLeuAlaTyrrLeuAla 80
Db      202 TTCTACTTCTTCTTCCGCAAAATACATTCGATCTTCCCTGCGCCCTTACCTACTGCT 261
Qy      81 TrpProValTyrrTrpPheCysGlnAlaSerilleLeuThriGlyLeuTrpValilleGlyHis 100
Db      262 TGGCCCTTATCTGTTCTGTCAAGCTAGCATCTCCACCGGCTTATGGGTATCGGTAC 321
Qy      101 GluCyagGlyHisHlaAlaPheSeraspTyrrGlnLeuValaAapPheValaGlyPheVal 120
Db      322 GAATGGCGGTCAACAGCTTCAAGCATCAAGTGGGTGACGACACTGTGGGCTTCAATC 381
Qy      121 LeuHisSerAlaLeuLeuThriProTyrrPheSerTrpTyrrSerHisArgAsnHisHis 140
Db      382 CTCCACTGTTCTTCTATGACCCCGATTTCTCTGGAATACAGCCACCGAACCACCAT 441
Qy      141 AlaAenThriAaSerLeuAaAapAaAapGlyValTyrrileProGlyAaGlySerVal 160
Db      442 GCCAACCAAAATTCCTTGCACACATGATGATCCCAAAAGCAAGGCCAAAGTCC 501
Qy      161 LysIleTyrrSerLeuLeuAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 180
Db      502 GCGCTTACTATTAAGTTCTCAACACACACACACACACACACACACACACACACAC 561
Qy      181 LeuThriLeuGlyPheProLeuTyrrLeuThriAaAaAaAaAaAaAaAaAaAaAaAa 200
Db      562 TTCCACCTTACAGCTTCTTACTTACTTCTTACCAATATTTCCGGAAGAAGATGAAG 621
Qy      201 PheAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 220
Db      622 TTTGGCAACCAATTCCTTGCACACATGATGATCCCAAAAGCGTGAACCGGTTTCA 681
Qy      221 LeuLeuSerAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 240
Db      682 TTGCTATCGAGCTTGGCTTCTTGTCTGTCTTGAAGATTAACCTTGGCTTACAGC 741
Qy      241 LysGlyAlaAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 260
Db      742 AAAGCGCGCGCTGCGGTGACGATTCATTCGGAATTCAGATTAGGCGGTATTATCT 801
Qy      261 PheValaLeuIleThriTyrrLeuHisHisThriHisLeuSerLeuProHisTyrrA 280
Db      802 TTTCATATCATCACTTATGCAACACACACACACACACACACACACACACACACAC 861
Qy      281 GluTrpAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 300
Db      862 GAATGAAGATGCGCTCAAGGGCTTGTCAAAATCGATGAGGACTTGGGTCTTGAT 921
Qy      301 ArgValaPheHisAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 320
Db      922 AGTGCGCTCCATGATGATTCACACACTCACTATGATCATCTGTTTCAATACATTC 981
Qy      321 HisTyrrHisAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 340
Db      982 CACTATCATGCGAAGAGGAGGAGGATCAATCAACACAGCTTGGGCGACTTTATTA 1041
Qy      341 IleAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 360
Db      1042 ATCGATAGACTCCCAATTCGTAAGCAATGTGGAAGAGGCCAAGAAATGCAATTC 1101
Qy      361 GluProAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 376
Db      1102 GAGCTGAAGAAAGTGAAGGGGTCAAGGGGTGTATTTGTGTAACATTA 1149

```

```

RESULT 6
AV166778
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS
TITL
JOURNAL
REFERENCE
AUTHORS
TITL
JOURNAL
FEATURES
source
1..979
/organism="Helichrysus bracteatum"
/mol type="genomic DNA"
/db_xref="taxon:220345"
<1..>979
/product="delta12-fatty acid acetylase"
/codon_start=1
/product="delta12-fatty acid acetylase"
/protein_id="AA038037.1"
/db_xref="GI:31322145"
/translation="KKAIPRCFERSYIRSSYYVYHDLIXVYVYLAIXYIPXPAH
LAYAKMVPVFCASITLGLVNIHGECHHAFSYYOLIDVGVGLVLSALTPTFSMK
VNSRSHNANTNSLNDENVYIPKRSKWTISKILNPNPGRFTLAFLTLGFPYLLT
VNSGKKYERFANHPDPLSPJETERERQVLSIDGILAVFAVLAIVAAKGLSWLSM
YVIVIGVHAFVLTIVLHHTHLSLPHYDSRWKVIKGLASTIRDRGFLNRVPHDVT
HTHVLHLILSITPHYAKKARDALNPVLGEYKIKDRPIPFAMRBAKEC"
ORIGIN
Alignment Scores:
Pred. No.: 1.02e-141 Length: 979
Score: 1607.00 Matches: 287
Percent Similarity: 93.56% Conservative: 18
Best Local Similarity: 88.04% Mismatches: 21
Query Match: 78.51% Indels: 0
Gaps: 0
US-10-069-772-2 (1-377) x AV166778 (1-979)
Qy      32 LysAlaValaalleProThriCyaspheGluAgsSerValaalleAgsSerSerTyrrVal 51
Db      1 AAAGAGGTATTCCTTCTTACATCAAGTCCGATCTTATTCATCTTACTTACGCTT 60
Qy      52 ValHisAapLeuValaalleAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 71
Db      61 STTATGATCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 120
Qy      72 IleProThriProLeuAlaTyrrLeuAlaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 91
Db      121 CTCCTGCTATCTCGCTTACTTARCGGCGGTTATGTTGTTGCAAGTATGAT 180
Qy      92 LeuThriGlyLeuTrpValilleGlyHisGlyCyagGlyHisHisAlaPheSeraspTyrr 111
Db      181 CTAAACCGGTTATGAGGATGCTGACGAATGTGKCAACATGCTTTATGATGACTTACAG 240
Qy      112 LeuIleAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 131

```



Db 241 TTTATCGATGACGGTGTGATCGTCTGCATCTGCTCTTTTACACCDTATTCTCA 300  
 Qy 132 TrrlyserSerHisArgAsnHisHisAlaSerThrAsnSerLeuAspAsnProVal 151  
 Db 301 TGGAAATACACCGATCGATCATACCCCAACAACTCTCTGATACGATGAATTT 360  
 Qy 152 TrrileProlySerGlySerLeuValIleTyrSerLeuLeuAsnProPro 171  
 Db 361 TACATTCCTAAACGTAATCCAAAGTCATGATTTATCTCAAAATCTCAACATCCACC 420  
 Qy 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuThr 191  
 Db 421 GGTGAGTTTCACTTGTGCTGCTGAGTTAATCTTGGGTTTCTTATACCTCTTAAC 480  
 Qy 192 AsnIleSerGlyLeuValTyrGlyValArgPheAlaAsnHisPheAspProMetSerProIle 211  
 Db 481 AATGTTCCGGGAAGAAATACGAAAGTTTGGCAACCACTTGTATCCGTGATGCCGATT 540  
 Qy 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe 231  
 Db 541 TTCACCGAGCGCAACGAATTCAGTTGCTCTATCGATCTTGGTATCATTTGCTGATTT 600  
 Qy 232 TyrAlaIleLeuValLeuValAlaAlaValGlyValAlaAlaIleValIleAsnMetTyrAla 251  
 Db 601 TATGCAATAGGCTTCTTGTAGCGCAAGGTTGAGCTTGGCTGCTGATGATG 660  
 Qy 252 IleProValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHis 271  
 Db 661 ATTCTGTATCGAGTCAGCTGACGCTTTCTTCTGTTTGTATCATCTTATTCATCACCCAT 720  
 Qy 272 LeuSerLeuProHisTyrAspSerThrGluTrpAsnTrpIleLeuGlyValAlaLeuSerThr 291  
 Db 721 CTGCTGTAACCTCATATGATGATTCGACCGAATGAAATGATCAAGGAGCTTATCTACG 780  
 Qy 292 IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisHisThrHisVal 311  
 Db 781 ATCGATAGAGATTCGCTTCTGATAGAGATTCGATGATGATGATGATGATGATGATGATG 840  
 Qy 312 LeuHisIleLeuIleSerTyrIleProHisTyrHisAlaValGlyValAlaArgAspAlaIle 331  
 Db 841 TTGCATCATCTGATATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 900  
 Qy 332 LysProValLeuGlyGluTyrTyrLeuValLeuAspArgThrProIlePheValAlaMetTyr 351  
 Db 901 AACCGGTTTGGGAGATATTAATAGATGATGATGATGATGATGATGATGATGATGATG 960  
 Qy 352 ArgGluAlaValGlyGluCys 357  
 Db 961 AGGGAAGCAAAAGATGC 978  
 RESULT 7  
 AY166777 979 bp DNA linear PLN 02-JUN-2003  
 LOCUS AY166777  
 DEFINITION Dimorphotheca sinuata delta12-fatty acid acetylase gene, partial cds.  
 ACCESSION AY166777  
 VERSION AY166777.1 GI:31322142  
 KEYWORDS  
 SOURCE Dimorphotheca sinuata (African daisy)  
 ORGANISM Dimorphotheca sinuata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Dimorphotheca.  
 1 (bases 1 to 979)  
 CAhon, E.B., Schurr, J.A., Huffman, E.A. and Minto, R.E.  
 Fungal responsive fatty acid acetylases occur widely in evolutionarily distant plant families  
 Plant J. 34 (5), 671-683 (2003)  
 JOURNAL 2 (bases 1 to 979)  
 AUTHORS Cahoon, E.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-OCT-2002) Crop Genetics, Dupont, Bldg. 402

FEATURES  
 source  
 Experimental Station, Wilmington, DE 19880-0402, USA  
 Location/Qualifiers  
 1..979  
 /organism="Dimorphotheca sinuata"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:112408"  
 <1..>979  
 /product="delta12-fatty acid acetylase"  
 <1..>979  
 /codon\_start=1  
 /product="delta12-fatty acid acetylase"  
 /protein\_id="AA038036.1"  
 /db\_xref="GI:31322143"  
 /translation="KKAIIPHCERSLRSSVYVVDLIVAVVEYPLANTYIPPLPAP  
 LAYLVVVFCCASILGLMVIHECHGNAFSQOMIGDVGFLISALFPLYSWK  
 YSHSHANNSLNDSEVYIPKRSKRYANKSLNNDPGVFTLVFLTGLPPLYLT  
 NGSKTRERANHDPMSPIFTEBERQVLTSDGLAVCALVIAKATVMCM  
 YGVPIVGHAFVILTYLHHTLSLPHYDSERKMWIKGALSTIDRDFPLRVHDTV  
 HTHVLHLISYIPHYAKKARDALIPVIGERYKIDRPIPFAMWRAKEC"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,11e-140 Length: 979  
 Score: 1596.00 Matches: 286  
 Percent Similarity: 94.48% Conservative: 22  
 Best Local Similarity: 87.73% Mismatches: 18  
 Query Match: 77.97% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-069-772-2 (1-377) x AY166777 (1-979)  
 Qy 32 LysValAlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyrVal 51  
 Db 1 AAGAAGCTATTCGCGCCACATGATGTTGAGGATCTTACCGTTACTTACGCTT 60  
 Qy 52 ValHisAspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeu 71  
 Db 61 GTTCATGATCTCATGTTGCTGATGCTTCTTACTCTCTTGGCAACACTTATATCTCTT 120  
 Qy 72 IleProThrProLeuAlaTyrLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIle 91  
 Db 121 CTCCCGCTCTCTGCTTACTAGCGGCGCTTATCTGTTTGGCAAGTACGATC 180  
 Qy 92 LeuThrGlyLeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGln 111  
 Db 181 CTCACCGTTTATGGTGATTTGTCATGAAGTGTGATCATCATGATTTAGGAACAAG 240  
 Qy 112 LeuIleAspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSer 131  
 Db 241 TGGATTGGTGACACTGTTGATTCATCTTCTGCTCTTACCCCTTATTTCTCT 300  
 Qy 132 TrrlyserTyrSerHisArgAsnHisHisAlaSerThrAsnSerLeuAspAsnProVal 151  
 Db 301 TGGAAATACACCGATCGATCATACCCCAACAACTCTCTGATACGATGAATTT 360  
 Qy 152 TrrileProlySerGlySerLeuValIleTyrSerLeuLeuAsnProPro 171  
 Db 361 TACATTCCTAAACGTAATCCAAAGTCATGATTTATCTCAAAATCTTAAACACCCACC 420  
 Qy 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuThr 191  
 Db 421 GGTGAGCTTCTTACCTTGTGTTTGTAGGTCAGCTGAGGCTTCTTATATCTTAAAC 480  
 Qy 192 AsnIleSerGlyLeuValTyrGlyValArgPheAlaAsnHisPheAspProMetSerProIle 211  
 Db 481 AATGTTCCGGGAAGAAATACGAAAGTTTGGCAACCACTTGTATCCGTGATGCCGATT 540  
 Qy 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe 231  
 Db 541 TTCACAGAGCTGAACGATTCAGTTGTTATCGGATCTGATATTAATGCGTTTGT 600  
 Qy 232 TyrAlaIleLeuValLeuValAlaAlaValGlyValAlaAlaIleValIleAsnMetTyrAla 251

Dd		601	TACGACATMAAAGTCTTGTTGGACGACAAAGAGCCACTGGGTGCATGTGATGTATGA	660
Oy		252	IlleProValIleuGIYValSerValPhePheValIleuIIeTrTYrLeuHisHISThrIs	271
Dd		661	GTTCGCCGATGTAAGGGCATGCGCTTCCTTGTTGGTATGCATTATTTACCACACCCCAT	720
Oy		272	LeuSerLeuProHISLeTYrAspSerThrgluTYrPaenTPriIeysGIYAlaIeuSerThr	291
Dd		721	CTCTCGTTGCCCTCATTAATGATTCGTCGCAATGAACTGATCMAAGAGCCTTATTCACA	780
Oy		292	IleAspArgAspPheGIYPheLeuAsnArgValPheHisAspValIthrHisThrIVal	311
Dd		781	ATCATAGATAGATTTTGGCTCTTGTGAATAGGGATATTCATGACGTATACACACTCACG	840
Oy		312	LeuHisHISleuIIeSerTYrIleProHISTYrHisAlaIysGIYAlaArgAspAlaIle	331
Dd		841	TTGCATCATTTGATTCCTTACATTCACATTCATGCAAGAAGGAAGGACCCCAATC	900
Oy		332	LysProValIleauGIYgluTYrTYrLysIleAspArgThrProIlePheIysAlaMetTYr	351
Dd		901	ATACCAATTTTGGGGGAAATTTATAAGATCGATAGACTCCATCTTTAAAGCAATGTGG	960
Oy		352	ArgGIYAlaIysGIYcys 357	
Dd		961	AGAGAGGCCAARGARTGC 978	
RESULT	8			
LOCUS	AR367438	1312 bp	mRNA	linear PAT 12-SEP-2003
DEFINITION	Sequence 3 from patent US 632518.			
ACCESSION	AR367438			
VERSION	AR367438.1 GI:34600637			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1312)			
TITLE	Green,A., Singh,S., Lemman,M. and Styhme,S.			
JOURNAL	Plant fatty acid epoxigenase genes and uses therefor			
FEATURES	Patent: US 6329518-A 3 11-DEC-2001;			
source	Location/Qualifiers			
	1..1312			
	/organism="unknown"			
	/mol_type="mRNA"			
ORIGIN				
Alignment Scores:				
Pred. No.:	3,44e-140	Length:	1312	
Score:	1592.50	Matches:	285	
Percent Similarity:	86.24%	Conservative:	41	
Best Local Similarity:	75.40%	Mismatches:	47	
Query Match:	77.80%	Indels:	5	
DB:	6	Gaps:	3	
DS-10-069-772-2 (1-377) x AR367438 (1-1312)				
Oy		1	MetGIYalagIYGlyARGMeSerAspProSerGIYGLYSAsnIleuGIYargVal	20
Dd		26	ATGGGTGCGGGCGCGCGT-----GTCGCAATCGAAGAAAGTCGTCATGAGACGTGTC	79
Oy		21	ProValaspPro---ProPheThrIeuSerAspleuLYSLAlalleProThrHisCys	39
Dd		80	TCAGTTGATTCACGTAACCTTCACATCGATGATTTGGAAGCAAGCAATCCCTCCACATTC	139
Oy		40	PheGIYargseValIleArgseSerTYrTYrValIleHisAspleuIIeValAlaTYr	59
Dd		140	TTCCAGCAATCGTATCCGTCATCTTAATTAAGTGTTCAGAGATCTCATTAATTCCTAAC	199
Oy		60	ValPheTYrTYrLeuAlaasnThrTYrIleProleuIIeProthProleuAlaTYrIeu	79
Dd		200	ATCTTCTACTCTTCCTTGCCACACATATATCCCTATCTCCGCATCTCTAGCCACTTA	259
Oy		80	AlatrpProvalTYrtripheCYeqInlaaserIleauthrgIYleuTrpValIlegly	99

D	b		260	GCTTGCGCCGCTTACTGGTTCTGTCAAGTAGCCTCTCACTGGATTATGGATCTCTCGGC	319
O	y		100	Htsglucygslyshhsialapheseraptryglulelleasppillevalglyphe	119
D	b		320	CATGAATGTGTACCAATGCTCATAGACAATCACATGAGTTGACGACCTGTGGCCTTC	379
O	y		120	VallenuisgeralaleulleuthPhrotyrPheSerTrpYstRHisarAsnHis	139
D	b		380	ATCATTCATTAATTTCTCTCAACCCTGATTTCTCTGGANATACAGTCAACCGAATCAC	439
O	y		140	HtsialasnThrAenSerLeuasAsnaspqiluvallyrlleProLySarGlySerLys	159
D	b		440	CATTCACAACAAGATTGGATTGATAGATGAATTTACATTCGAAAGAAGAACATCCAAA	499
O	y		160	VallysileTySerLysleuLeuasnsbnProGlyIargValPheThrLeuValPhe	179
D	b		500	CTCAAGCTATCTATTAACCTTTAAACACCACTGTGTGCACTGGTGTGGTTGATATC	559
O	y		180	ArgleuthrleuglyphetheProleuthLeuethrAnllesergilylvlsyTyrgly	199
D	b		560	ATGTTACCCCTAGAGATTTCTTTATACCTCTTGCAAAATATTTCCGCCAAGAAATAGAT	619
O	y		200	ArPheAlaenHispheAspPrometSerProillePheAsnAspArgGlurValGln	219
D	b		620	AGGTTTGGCAACCACTTGCAGCCCATAGTCCATTTTCAAAGAAGCTGACGGTTTCAG	679
O	y		220	ValleuenseSerapPheglyLeuLeuAlavalPheTyralailelysleuLeuValala	239
D	b		680	GTTCTTCCTTGGATCTTGGCTCTTCTGCTGTGTTTTATGGAATTAAGTTGCTGTAGCA	739
O	y		240	AlalyseglyalalaiatrpvalilleasmetrykrAlalleProvalleuglyvalSerVal	259
D	b		740	AATAAAGAGAGCTGCTGGTGCGCTGCATGATAGAGATTCGGATGAGGCGATATTAC	799
O	y		260	PhePheValleullethrTyLeuHishisthrhisleuSerLeuProHistyrAspSer	279
D	b		800	TTTTTCATGATGATCAGCTTTTACACCAACCACTCATGCTGCTCATTAATGATTTCA	859
O	y		280	ThrglutrpAsentripileylsyglivalaleuSerThrilleAsparGaapPheglyPheleu	299
D	b		860	ACTGATGCACTGGATCAGAGGGGCTTTGTCAACAATCATGATAGATTTGGGCTTCCTG	919
O	y		300	AsnarGValPheHishAspValThnthisthrhisvalleuHishisteUyleSetTyrlle	319
D	b		920	AATAGGTGTTTCCATGATGATNAACAACAATCCATCATGATCATTTGTTTCATACATT	979
O	y		320	ProhistTyrsialalyseglualaryAspAlalleysProvalleuglyglutTyrr	339
D	b		980	COACACTATCATCGAAGAGACAGAGGATGCATCAACCGATCTTGGCGCATTTAT	1039
O	y		340	LysilleAspargthrProillePheHysAlametyrArgreglualalyseUyleTyrr	359
D	b		1040	ATGATCGATAGAGCTCCAAATTTAAAGCAATGCGAGAGAGGCGAGGATGATGTAC	1099
O	y		360	IlegluProAspgluAspsergluHishlyslyvalPhetrptyrHishysMet	377
D	b		1100	ATCGAGCCT-----GATAGCAACGCTCAAGAGTCTTATTTGTTATCAATAATTG	1147
 RESULT 9 AX031162					
LOCUS		AX031162	1312 bp	DNA	linear PAT 24-NOV-2000
DEFINITION		Sequence 3 from Patent WO9846762.			
ACCESSION		AX031162			
VERSION		AX031162.1 GI:10278515			
KEYWORDS					
SOURCE					
ORGANISM		Crepis sp. Crepis sp. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.			
REFERENCE 1					



ORIGIN /db\_xref="taxon:137775"

## Alignment Scores:

Pred. No.: 3,44e-140 Length: 1312  
 Score: 1592.50 Matches: 285  
 Percent Similarity: 86.24% Conservative: 41  
 Best Local Similarity: 75.40% Mismatches: 47  
 Query Match: 77.80% Indels: 5  
 Gaps: 3

US-10-069-772-2 (1-377) x BD061165 (1-1312)

Qy 1 MetGlyAlaGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20  
 Db 26 ATGGGTGCGGCGGCGGT-----GTCGACATCGGAAAAGTCGATGGAACGTGTC 79  
 Qy 21 ProValAspPro---ProPheThrLeuSerAspLeuLysValAlaIleProThrHisCys 39  
 Db 80 TCAGTGTATCCAGTAACCTTCTCACTAGTAGATTTGAAGCAAGCATCCCTCCACATTGC 139  
 Qy 40 PheGluArgSerValIleArgSerSerTyTyValValHisAspLeuIleValAlaTyx 59  
 Db 140 TTCAGGCAATCTGTATCCGTTCACTTATTAAGTTTCAGAGATCTCATATTCCTAC 199  
 Qy 60 ValPheTyTyLeuAlaAsnThrTyxIleProLeuIleProThrProLeuAlaTyxLeu 79  
 Db 200 ATCTTCACTTCTCTGCAACATATATCCCTATCTCCCTCATCTCTAGCCTACTTA 259  
 Qy 80 AlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99  
 Db 260 GCTTGCGCGCTTACTGTGTCTGTCACAGTACCGCTCCACAGGTTATGATCTCGGC 319  
 Qy 100 HisGluCysGlyHisAlaPheSerAspTyxGlnLeuIleAspAspIleValGlyPhe 119  
 Db 320 CATGATGTGTGTCACCATGCTCATATGACATACATGGGTTGACGACATGGGCTTC 379  
 Qy 120 ValLeuHisSerAlaLeuLeuThrProTyxPheSerTrpLysSerHisArgAsnHis 139  
 Db 380 ATCATCCATTCATTTCTCTCCACCCCGTATTTCTTGGAATATACAGTCACCGGAAATC 439  
 Qy 140 HisAlaAsnThrAsnSerLeuAspAsnArgIleValTyxIleProLysArgLysSerHis 159  
 Db 440 CATTCACACACAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499  
 Qy 160 ValLysIleTyxSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPhe 179  
 Db 500 CTCAAGCGTATCTATAAAGCTTCTTAACAACCACTGTCAGCTGTGTTTGGTTATC 559  
 Qy 180 ArgLeuThrLeuGlyPheProLeuTyxIleLeuThrAsnIleSerGlyLysLysTyxGly 199  
 Db 560 ATGTTCACTTACCTGATTTCTTATTAACCTTGAACAAATATTTCCGGGACAGAAATACAT 619  
 Qy 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgIleArgValGln 219  
 Db 620 AGGTTTGCACACCTTGAACCCCAAGTCAATTTCCAAAGAACGTAAGCGGCTTACG 679  
 Qy 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyxAlaIleLysLeuValAla 239  
 Db 680 GTCCTCTTGGGATCTTGCTTCTTCTGCTGTTTATGAAATTAAGTTGGCTTACCA 739  
 Qy 240 AlaLysGlyAlaAlaTrpValIleAsnMetTyxAlaIleProValLeuGlyValSerVal 259  
 Db 740 AATAAGAGAGCGCTTGCGTGCATGATGATGATGATGATGATGATGATGATGATGAT 799  
 Qy 260 PhePheValLeuIleThrTyxLeuHisIleHisIleSerLeuProHisTyxAspSer 279  
 Db 800 TTTTTCATGTGATACGTTTACACACACATCAGTGTGCTCGCTCATTTATGATTTCA 859  
 Qy 280 ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299  
 Db 860 ACTGAATGGAAGTGAATGAGAGGCGCTTGTCAAGAAATGATAGAGACTTTGGGTTCTG 919

Qy 300 AsnArgValPheHisAspValThrHisThrIleValLeuHisIleLeuIleSerTyxIle 319  
 Db 920 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979  
 Qy 320 ProHisTyxHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyLysTyx 339  
 Db 980 CCACATCTATGCAAG 1039  
 Qy 340 LysIleAspArgTrpProIlePheLysAlaMetTyxArgIleValAlaLysGlyCysIleTyx 359  
 Db 1040 ATGATCGATGAGCTCCATTTTAAAGCATGTGAGAGAGAGAGAGAGAGAGAGAGAGATGAC 1099  
 Qy 360 IleGluProAspGluAspSerGluHisLysGlyValPheTrpTyxIleLysMet 377  
 Db 1100 ATTCAGGCT-----GATAGCAAGCTCAAGGTGTATTTAGTATCAATAAATTTG 1147  

RESULT 11  
 AR367437  
 LOCUS AR367437 1358 bp DNA linear PAT 12-SEP-2003  
 DEFINITION Sequence 1 from patent US 6329518.  
 ACCESSION AR367437  
 VERSION AR367437.1 GI:34600636  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 Unclassefied.  
 1 (bases 1 to 1358)  
 REFERENCES  
 1 Green, A., Singh, S., Lemman, M. and Styenne, S.  
 TITLE Plant fatty acid epoxigenase genes and uses therefor  
 JOURNAL Patent: US 6329518-A 11-DEC-2001;  
 FEATRES Location/Qualifiers  
 1. 1358  
 source /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN /db\_xref="taxon:137775"

Alignment Scores:

Pred. No.: 6.88e-140 Length: 1358  
 Score: 1589.50 Matches: 285  
 Percent Similarity: 85.98% Conservative: 40  
 Best Local Similarity: 75.40% Mismatches: 48  
 Query Match: 77.65% Indels: 5  
 Gaps: 3

US-10-069-772-2 (1-377) x AR367437 (1-1358)

Qy 1 MetGlyAlaGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20  
 Db 30 ATGGGTGCGGCGGCGGT-----GTCGACATCGGAAAAGTCGATGGAACGTGTC 83  
 Qy 21 ProValAspPro---ProPheThrLeuSerAspLeuLysValAlaIleProThrHisCys 39  
 Db 84 TCAGTGTATCCAGTAACCTTCTCACTAGTAGATTTGAAGCAAGCATCCCTCCCATTTGC 143  
 Qy 40 PheGluArgSerValIleArgSerSerTyTyValValHisAspLeuIleValAlaTyx 59  
 Db 144 TTCAGAGATGTGATTCGCTCATCTTCACTAGTGTTCAGAGATCTCATAGTACGCTACTTA 203  
 Qy 60 ValPheTyTyLeuAlaAsnThrTyxIleProLeuIleProThrProLeuAlaTyxLeu 79  
 Db 204 ATCTTCACTTCTCTGCAACATATATCCCTATCTCTCACTAGTACGCTACTTA 263  
 Qy 80 AlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99  
 Db 264 GCTTGCGCGCTTACTGTGTCTGTCACAGTACGCTCCCTCATCTTATGATGATCTCGGC 323  
 Qy 100 HisGluCysGlyHisAlaPheSerAspTyxGlnLeuIleAspAspIleValAlaTyxPhe 119  
 Db 324 CACGAATGTGTGTCACATGCTTATGACATACATGATGATGATGATGATGATGATGATGAT 383  
 Qy 120 ValLeuHisSerAlaLeuLeuThrProTyxPheSerTrpLysSerHisArgAsnHis 139  
 Db 384 ATCTTCACTATTTCTCTCAACCCCGTATTTCTTGGAATTCAGTACCGGAAATC 443



QY	260	thePheValleuileThyTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSer	275
Db	804	TTTTTCAGTGTGATCACCCTTTCTTGACACACACCATCATGTCGTGGCTCATTTATGATTTCA	863
QY	280	ThrglUTPAsnTrrPileIleGlyValAlaLeuSerThrIleAspArgAspPheGlyPheLeu	299
Db	864	ACTGATATGAACTGATGTACAGAGGGCCCTTGTCACGATTCGATAGGACTTTGGATTCCTG	923
QY	300	AsnArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIle	319
Db	924	AATAGTGTTCCTTCAGATGTTTACACACACTCATGTCAATCATATTTGTTTCATATACATT	983
QY	320	ProHisTyrHisAlaIleGlyValAlaArgAspAlaIleLeuProValLeuGlyGluTyrTyr	339
Db	984	CCACACTATCATGCAAGAGGCAAGGATGTGATCAAGCCATCTTGTGGAGCATTTAT	1043
QY	340	LysIleAspArgTThrProIlePheIleValIleMetTyrArgGluValAlaGlyCysIleTyr	359
Db	1044	ATGATCGACAGACCTCCATTTTAAACATGTCGAGAGAGGAGGAGGATGATGTATC	1103
QY	360	IleGluProAspGluAspSerGluHisGlyGlyValPheTrrTyrHisIleMet	377
Db	1104	ATCGAGCCT-----GATACGACAGCTCAAGGTGTTTATGTGATCATTAATATG	1151
RESULT 13			
LOCUS	BD061164	1358 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Plant fatty acid epoxxygenase gene and uses therefor.		
ACCESSION	BD061164		
VERSION	BD061164.1	GI:22606770	
KEYWORDS	JP 2001518797-A/1.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 1358)		
TITLE	Stymne,S., Green,A., Singh,S. and Lemman,M.		
JOURNAL	Plant fatty acid epoxxygenase gene and uses therefor		
COMMENT	Patent: JP 2001518797-A 1 16-OCT-2001; COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN STYMNE		
FEATURES	source		
ORIGIN			
Alignment Scores:			
Pred. No.:	6,88e-140	Length:	1358
Score:	1589.50	Matches:	285
Percent Similarity:	85.98%	Conservative:	40
Best Local Similarity:	75.40%	Mismatches:	48
Query Match:	77.65%	Indels:	3
DB:	6	Gaps:	3
US-10-069-772-2 (1-377) x BD061164 (1-1358)			
QY	1	MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyValAsnIleLeuGluArgVal	20

Db	30	ATGGGTGCGCGCGGTCTG-----GGTCCGACATCGAAAAATCGGTCATGGAACGTCTC	83
QY	21	ProValAspPro---ProPheThrLeuSerAspLeuLysAlaIleProThrHisCys	39
Db	84	TCAGTTGATCCAGAACCTTCTCTCAGTGAAGTGAAGCAAGAACTCCCTCCCAATTGC	143
QY	40	PheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyr	59
Db	144	TYTCAGAGATCTGTAAATCCGCTCATCTTAAGTGTGTTCGAAAGTTCATTATGGCTTAC	203
QY	60	ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProTyrProLeuAlaTyrLeu	79
Db	204	ATCTTCTACTCTCTTGCCACACATATATCCCTACTTCTCTACTAGCTAGCTACTTA	263
QY	80	AlaIrrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeuIrrProValIleGly	99
Db	264	GCTTGGCCCGGTTTACTGGTTCGTGCAAGTACGAGTCTCTCACTGGCTTATGAGTCTGGC	323
QY	100	HisGluCysGlyHisHisAlaIlePheSerAspTyrGlnLeuIleAspAspIleValGlyPhe	119
Db	324	CACGAATGTGGTCCACATGACCTTTCAGCACTACATGATTTTGACGACACTGTGGGCTTC	383
QY	120	ValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSerHisArgAsnHis	139
Db	384	ATCTCCACCTATTTCTCTCTCACCCCGATATTTCTTGGAATATTCAGTCCCGAATCAC	443
QY	140	HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLys	159
Db	444	CATTCCAACACAAATTCGATTGATTAAGATGAAGATTACATTCGGAAACAGATCCAA	503
QY	160	ValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPhe	179
Db	504	CTCCGCGGTATCTATTAACCTTTCMAACCCACTGGTGGCGGTGGTTGATTAATC	563
QY	180	ArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnLieserGlyLysTyrGly	199
Db	564	ATGTTCACCTTCAGATTTCTTACTTGTACAAATATTTCCGGCAGAAATACGAC	623
QY	200	ArgPheAlaAsnHisAspAspProMetSerProIlePheAsnAspArgLysArgValGln	219
Db	624	AGGTTTGGCAACGACTTCGACCCCATGATGATTCATTTTCMAAGAACGTGACGGTTTCAG	683
QY	220	ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAla	239
Db	684	GCTCTCTCTTCGGATCTTGTCCTTCCTTCGCGTGTTCATGGAATTAAGTTCGTGATGCA	743
QY	240	AlaLysGlyAlaAlaTrrPValIleAsnMetTyrAlaIleProValLeuGlyValSerVal	259
Db	744	AATAAAGAGGTGCTTGAGTGGCTGCATGATGAGATTCGGATATTAAGCGATTTTACC	803
QY	260	PhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSer	279
Db	804	TTTTTTCATGTCACCTTCTTGCACACACCCATCAGTCGTGGCTCATTTATGATTTAC	863
QY	280	ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyLeu	299
Db	864	ACTGAATGGAAGTGCATGACAGGAGGCGCTGTGCAGCAATCATATGGGACTTTGGATTCCTG	923
QY	300	AsnArgValPheHisAspArgValThrHisThrHisValLeuLeuHisHisLeuIleSerTyrIle	319
Db	924	AATAGTGTTCATGATGATGATACACACATCATGATGATTCATTTGTTTTCATACATTT	983
QY	320	ProHisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValLeuGlyLysTyrTyr	339
Db	984	CCACACTATCATGCAAGAGAGGCAAGGAGATGCATCAAGCAATCTTGGGCACTTTTAT	1043
QY	340	LysIleAspArgThrProIlePheLeuAlaMetTyrArgGluAlaLysGluCysIleTyr	359
Db	1044	ATGATTCGACAGAGATTCGAATTTTAAAGCAATGTGAGAGAGGCGACGAGATGATGTAC	1103
QY	360	IleGluProArgLysAspSerGlnHisLysGlyValPheThrTyrHisLysMet	377
Db	1104	ATCGAGGCT-----GATAGGCACTGAAGAGGTGTTATATGGTATCTAATAATTTG	1151

RESULT 14  
 CPY16283 1358 bp mRNA linear PLN 13-MAY-1998  
 LOCUS Crepis palaestina mRNA for delta 12 fatty acid epoxigenase.  
 DEFINITION Y16283 GI:3135017  
 VERSION Y16283.1  
 KEYWORDS delta 12 fatty acid epoxigenase.  
 SOURCE Crepis palaestina  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.  
 REFERENCE 1  
 AUTHORS Lee, M., Lemman, M., Banas, A., Bafar, M., Singh, S., Schweizer, M., Nilsson, R., Liljenberg, C., Dahlqvist, A., Gummesson, P., Stoeckli, S., Green, A. and Styhne, S.  
 TITLE Identification of non-heme diron proteins that catalyze triple bond and epoxy group formation  
 JOURNAL Science 280 (5365), 915-918 (1998)  
 MEDLINE 98239771  
 PUBMED 9572738  
 REFERENCE 2 (bases 1 to 1358)  
 AUTHORS Lemman, M.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-JAN-1998) M.E. Lemman, Dept of Plant Breeding Research, SLU, Herman Ehles V 2-4, 26831 Svalov, SWEDEN  
 FEATURES  
 SOURCE location/Qualifiers  
 1..1358  
 /organism="Crepis palaestina"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:72611"  
 /clone="pCpal2"  
 /clone\_lib="lambda ZAP"  
 /dev\_stage="developing seed"  
 30..1154  
 /codon\_start=1  
 /product="delta 12 fatty acid epoxigenase"  
 /protein\_id="CA76156.1"  
 /db\_xref="GI:3135018"  
 /db\_xref="GOA:O65771"  
 /db\_xref="SPRMBL:O65771"  
 /translation="MGAGRGRTSEKSVMERVSVDYPTFSLSEKQAIIPPHCFORSVI RSYVYVDLIAYFYFLANTYIPLPTSLAYLAMPYVWCOASVLTGLWILHEG HARSNTWPDVTGFIHSRLPYPSWKSRRHNSNSINDRDVYIPKSKIA RIYULNNPGRLLVLIIMTFLGPIYILNITSGKTRDRAHNPDPSPFKERRO VFLSDGLAVFYGIKVAIVANKGAWACMGVPLGVFTFDVITPLAHTHQSSPHY DSTEMNIRGLAISIDRDPGLNSVDFHDVTHVMHLFSYIPHYHAKKARDAIKPIL GDFYMDITRPIIKAMREGRRCMYIEPDSKLKGVYVYHKL"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 6.88e-140 Length: 1358  
 Score: 1589.50 Matches: 285  
 Percent Similarity: 85.98% Conservative: 40  
 Best Local Similarity: 75.40% Mismatches: 48  
 Query Match: 77.65% Indels: 5  
 Gaps: 3  
 US-10-069-772-2 (1-377) x CPY16283 (1-1358)  
 QY 1 MerglYlaagiYgiYarMetSerAspProSerGluGlyIysAenileLeuGluAryal 20  
 DB 30 ATGGAGTCCCGCGGCTCGT-----GCTCGACATCGCAAAATCGGTATGAAACGATC 83  
 QY 21 ProValAspPro---ProPheThrLeuSerAspLeuYslyAalileProThrHisCys 39  
 DB 84 TCAAGTTATCCAGTAACCTTCTCACTGAGTGAATTTGAAGCAAGCAATCCCTCCCATTC 143  
 QY 40 PheGluArgSerValileArgSerSerTyTyValValHisAspLeuileValAlaTy 59  
 DB 144 TTCAGAGATCTGTAAATCCGCTCATCTTAATGTGTTCAAAGATCATATATGCGCTAC 203

QY 60 ValPheTyTyLeuAlaAsnThrTyriileProLeuileProthrProLeuAlaTyriLeu 79  
 DB 204 ATCTTCTACTCTTCCTGGCAACATATATCCCTACTCTTCTAGCTAGCTAGCTACTTA 263  
 QY 80 AlaTrpProValTyTrpPheCysGlnAlaSerileLeuThrGlyLeuTrpValileGly 99  
 DB 264 GCTTGGCCCGTCTTCTGCTGTGCAAGCTAGCGCTCACCTGCTTATGATCTCTCGC 323  
 QY 100 HisGluCysGlyHisAlaPheSerAspTyGlnleuileAspAspIleValGlyPhe 119  
 DB 324 CACGAATGTGTACCAATGCTTGTAGCACTACACATGCTTGTAGCACTGTGGCTTC 383  
 QY 120 ValLeuHisSerAlaLeuLeuThrProTyPheSerTrpTySerHisArgAsnHis 139  
 DB 384 ATCTCCCACTATTTCTTCTTCAACCCCGATTTCTTCTGGAATTCAGTACCGGATCAC 443  
 QY 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyriileProTyArgLysSerLys 159  
 DB 444 CATTCCAACACAAAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
 QY 160 ValIysIleTySerTyLeuLeuAsnAspProGlyArgValPheThrLeuValPhe 179  
 DB 504 CTCGGCGGTATCTATTAACCTTAAACACCACCTGCTGCTGCTGCTGCTGCTGCTGCT 563  
 QY 180 ArgLeuThrLeuGlyPheProLeuTyriLeuLeuThrAsnIleSerGlyLysLeTyGly 199  
 DB 564 ATGTTCACCCATAGATTTCTTATATCTTGTGACAAATATTTCCGCAAGAAATATGAC 623  
 QY 200 ArgPheAlaAsnHisAspAspProMetSerProIlePheAsnAspArgLysValGln 219  
 DB 624 AGTTTGGCAACCACTTCGACCCCATGATGATGATGATGATGATGATGATGATGATGAT 683  
 QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyriAlaileLeuLeuValAla 239  
 DB 684 GCTTCTCTTGGATCTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743  
 QY 240 AlaIysGlyAlaAlaTrpValileAsnMetTyriAlaileProValleuGlyValSerVal 259  
 DB 744 AATAAAGAGAGCTGCTGGGTAGCGTCATGATGATGATGATGATGATGATGATGATGAT 803  
 QY 260 PhePheValLeuileThrTyriLeuHisThrHisLeuSerLeuProHisTyTrpAspSer 279  
 DB 804 TTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
 QY 280 ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspAspAspPheGlyPheLeu 299  
 DB 864 ACTAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 923  
 QY 300 AsnArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyriile 319  
 DB 924 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 983  
 QY 320 ProHisTyriHisAlaLysGlyAlaArgAspAlaileLysProValleuGlyLysTyTr 339  
 DB 984 CCACACTATCATGCAAGAGAGGCAAGGATCATATCAAGCAATCTTGGCGGCACTTTAT 1043  
 QY 340 LysIleAspArgThrProIlePheLysAlaMetTyriArgGluAlaLysGluCysIleTy 359  
 DB 1044 ATGATTCACAGACTCCAAATTTTAAAGCAATGAGAGAGGCGAGGAGTGTGATGATAC 1103  
 QY 360 IleGluProAspGluAspSerGluHisIleLysGlyValPheTrpTyriHisLysMet 377  
 DB 1104 ATCGAGCT-----GATACGACACTCAAGGTGTTATTTGTTATCATTAATTTG 1151  
 RESULT 15  
 AR064128 1364 bp DNA linear PAT 29-SEP-1999  
 LOCUS Sequence 3 from patent US 5846784.  
 DEFINITION AR064128  
 ACCESSION AR064128  
 VERSION AR064128.1 GI:5993436  
 KEYWORDS unknown.

ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 1364)  
 AUTHORS Hitez, W.D.  
 TITLE Fatty acid modifying enzymes from developing seeds of Vernonia  
 JOURNAL galatensis  
 Patent: US 5846784-A 3 08-DEC-1998;  
 FEATURES Location/Qualifiers  
 source 1..1364  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	7,49e-139	Length:	1364
Score:	1578.50	Matches:	280
Percent Similarity:	87.16%	Conservative:	39
Best Local Similarity:	76.50%	Mismatches:	44
Query Match:	77.11%	Indels:	3
DB:	6	Gaps:	2

US-10-069-772-2 (1-377) x AR064128 (1-1364)

QY 15 AsnIleLeuGluValProValAsp--ProProPheThrLeuSerAspLeuLys 33  
 |||||  
 DB 157 AATATAAACGACCGGATGATCGGACCATTCGTTAAGGATCTAAAGAA 216  
 |||||

QY 34 AlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValHis 53  
 |||||  
 DB 217 GCATTCCTCCGCAATGCTTCAGGATCTGCATCTGCTAGCTGTTCAAG 276  
 |||||

QY 54 AspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIlePro 73  
 |||||  
 DB 277 GATCTCATTAATACCTCTTTATACAGCTCGGCAACTCTTACATTCCTCTCTCT 336  
 |||||

QY 74 ThrProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThr 93  
 |||||  
 DB 337 CCTCCTTACCTTCTTATGACATGCGCTGTTTACGATCTGCAATCTGATCTCTACT 396  
 |||||

QY 94 GLeuLeuTyrValIleGluHisGluCysGluHisIleAlaPheSerAspTyrGlnLeuIle 113  
 |||||  
 DB 397 GGTATTAGGCTCATTTGGCAGATGATGCGCATCTCTTATAGGATACCAAGGGTT 456  
 |||||

QY 114 AspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLys 133  
 |||||  
 DB 457 GATAACACCGTGTGATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 516  
 |||||

QY 134 TyrSerHisArgAsnHisIleAlaAsnThrAsnSerIleuAspAsnArgLysValTyrIle 153  
 |||||  
 DB 517 TACAGCCATCGAAGACACCATGCAACAGATTCATCGAAGAGAGGTTTACAT 576  
 |||||

QY 154 ProLysArgLysSerLysValLysIleTyrSer-----LysLeuLeuAsnAsnProPro 171  
 |||||  
 DB 577 CTTAAAGCCAGTCCCACTCAGGAATTCCTCAATTCTTGAACAACACCCCT 636  
 |||||

QY 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThr 191  
 |||||  
 DB 637 GGTGGAATCTCATTTGCTTATCATGTTGACCTTGCGCTTCTTATACCTCTTGACC 696  
 |||||

QY 192 AsnIleSerGlyLysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIle 211  
 |||||  
 DB 697 AATATTTCAGGCAAGAAATACCAAGGTTTGCAACACCTTGAATCCGTTGAGCCCATC 756  
 |||||

QY 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe 231  
 |||||  
 DB 757 TTCAGTGAAGCGTGAACGAATCCAGTCTGCTATCGATGCGATCTCATCTGTGTTT 816  
 |||||

QY 232 TyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAla 251  
 |||||  
 DB 817 TACGGGCTTAAGTTCTTGTAGCAAAAGGTTGCGTGAATGCGCATGTACGGA 876  
 |||||

QY 252 IleProValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrHis 271  
 |||||

DB 877 GCCCCAGTGGTGGCTGAATGCTTCAATAATGATCACTTATCTCCACACACCAT 936  
 QY 272 LeuSerLeuProHisTyrAspSerThrGluTyrAsnTrpIleLysGlyAlaLeuSerThr 291  
 |||||  
 DB 937 CTGCTTCGCTCATTTACGATTCGACCGAATGAGATCGAATCAAGGCTTGAATCA 996  
 |||||

QY 292 IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValIleThrHisVal 311  
 |||||  
 DB 997 ATCGATGAGATTTGCGGTCTCTGAATGAGGTGTTCAATGCGTCACTACACACACG 1056  
 |||||

QY 312 LeuHisIleLeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIle 331  
 |||||  
 DB 1057 TTGCATCTTTGTTCCCGTACATTCACATTAATGCAAGAGGCGAGGAGGACATA 1116  
 |||||

QY 332 LysProValLeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyr 351  
 |||||  
 DB 1117 AAGCCGGTGTAGGGAGATCGGATGATCGATGAGACTCGTTTCAAGCAATGTGG 1176  
 |||||

QY 352 ArgGluAlaLysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyVal 371  
 |||||  
 DB 1177 AGAGAGGCGAAGATGATCTTACATCGAGCAATGAGTAAAGACCAAGGTGTA 1236  
 |||||

QY 372 PheTrpTyrHisLysMet 377  
 |||||  
 DB 1237 TATTGTRACATAAATG 1254  
 |||||

Search completed: June 23, 2004, 16:53:19  
 Job time : 3312 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:50:48 ; Search time 425 Seconds  
(without alignment)  
12844.552 Million cell updates/sec

Title: US-10-069-772-1

Perfect score: 1285

Sequence: 1 aaaaagcctctctctgtga.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002s:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1285	100.0	1285	4	AAF88311
2	718.6	55.9	1128	2	AAT95688
3	715.8	55.7	1358	2	AAV63101
4	705.4	54.9	1312	2	AAV63102
5	699.8	54.5	1364	2	AAV72550
6	455.6	35.5	1369	6	ABL58599
7	455.6	35.5	1372	2	AAO66068
8	455.6	35.5	1372	3	AAZ51315
9	455.6	35.5	1411	3	AAZ51315
10	454.4	35.4	1476	2	AAV72549
11	454	35.3	1152	2	AAZ32636
12	454	35.3	1451	3	AAZ32636
13	454	35.3	2973	6	AAO66074
14	454	35.3	2973	6	ABL58607
15	453.6	35.3	1451	3	AAZ32636
16	453.4	35.3	1390	3	AAZ32636
17	453.4	35.3	1580	7	ABZ22026
18	450.8	35.1	1152	2	AAZ32637
19	445.8	34.7	1422	5	AAZ22380
20	444.8	34.6	1411	5	AAZ22379
21	436.8	34.0	1411	5	AAZ22379
22	436	33.9	1662	2	AAT88864
23	432	33.6	1423	6	ABL58600

24	432	33.6	1464	2	AAZ91076
25	431.8	33.6	1216	4	AAZ89457
26	431	33.5	1155	2	AAV84678
27	431	33.5	1155	2	AAZ06617
28	431	33.5	1155	2	AAZ51118
29	429.4	33.4	1155	2	AAV84677
30	429.4	33.4	1155	2	AAV84676
31	429.4	33.4	1155	2	AAV84676
32	429.4	33.4	1155	2	AAZ51119
33	427.8	33.3	1155	2	AAZ06619
34	427.8	33.3	1155	2	AAZ51120
35	426.8	33.2	1164	7	ABZ58386
36	426.8	33.2	1155	2	AAZ91077
37	426.2	33.2	1155	2	AAZ06620
38	426.2	33.2	1155	2	AAZ06621
39	426.2	33.2	1155	3	AAZ51121
40	426.2	33.2	1155	3	AAZ51122
41	425.2	33.1	1155	2	AAT85846
42	425.2	33.1	1155	2	AAZ06613
43	425.2	33.1	1155	3	AAZ27144
44	425.2	33.1	1155	6	ABZ55809
45	425.2	33.1	1155	10	ABZ85747

#### ALIGNMENTS

RESULT 1

AAF88311

ID AAF88311 standard; DNA; 1285 BP.

XX

AC AAF88311;

DT 22-AUG-2001 (first entry)

XX

DE C. officinalis calendulic acid desaturase encoding DNA.

XX

KW Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;

XX

triglyceride; transgenic plant; de.

XX

OS Calendula officinalis.

XX

Key Location/Qualifiers

FT 42..1175

FT CDS /\*tag= a

FT /product= "calendulic acid desaturase"

FT

XX

DE19941609-A1.

XX

PD 08-MAR-2001.

XX

PE 01-SEP-1999; 99DE-01041609.

XX

PR 01-SEP-1999; 99DE-01041609.

XX

PA (IPBP-) IPB INST PFLANZENBIOCHEMIE.

XX

PI Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;

XX

WP1; 2001-283028/30.

DR P-PSDB; AAB70946.

XX

PT New nucleic acid sequence encoding Calendula officinalis calendulic acid

PT desaturase, useful for e.g. producing transgenic plants having oil with

PT an increased unsaturated fatty acid content.

XX

PS Claim 1b; Page 13-15; 22pp; German.

XX

CC This invention describes a novel isolated nucleic acid sequence (i)

CC encoding a Calendula officinalis calendulic acid desaturase polypeptide.

CC The invention also describes (i) a process for producing unsaturated

CC fatty acids, comprising introducing at least one copy of (i) or (ii) into

CC an oil-producing organism, growing the organism, isolating oil from the

organism and releasing fatty acids from the oil; (2) a process for producing triglycerides with an increased unsaturated fatty acid content, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism; (3) a process for producing saturated fatty acids, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing organism, growing the organism, isolating oil from the organism and releasing fatty acids from the oil; (4) a process for producing triglycerides with an increased saturated fatty acid content, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism; (5) an enzyme capable of converting a diunsaturated fatty acid of to a triunsaturated fatty acid. Transgenic organisms (especially plants) containing one or more copies of (I) are useful for producing oils with an increased unsaturated fatty acid content. Transgenic organisms (especially plants) containing one or more nonfunctional copies of (I) are useful for producing oils with an increased saturated fatty acid content. (I) and fragments of (I) are also useful for isolating genomic sequences by homology screening. This sequence encodes the calendulic acid desaturase described in the method of the invention

Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 1285; DB 4; Length 1285;  
Best Local Similarity 100.0%; Pred. No. 1.2e-306;  
Matches 1285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAAGCTACTTCTCTGTGAGGGTAATTATATCAACAATGGGTCGTGGTCCGA 60  
1 AAAAGCTACTTCTCTGTGAGGGTAATTATATCAACAATGGGTCGTGGTCCGA 60  
61 TGTGGATCCATCTGAGGAAAAAATCCTTGAACGTGTGCGACATCCATCCGTTCA 120  
61 TGTGGATCCATCTGAGGAAAAAATCCTTGAACGTGTGCGACATCCATCCGTTCA 120  
121 CGTTAAGGATCTGAAGAAAGGATTCCTACCATTTGTTGAGGATCTGATCCGGT 180  
121 CGTTAAGGATCTGAAGAAAGGATTCCTACCATTTGTTGAGGATCTGATCCGGT 180  
181 CATCATATGATGTTGATGATGATCATGTTGCTTACCTTCTTACTACCTTGCAACA 240  
181 CATCATATGATGTTGATGATGATCATGTTGCTTACCTTCTTACTACCTTGCAACA 240  
241 CGTATATCCCTTATATCTTACACCTCTGCTTACCTTACCTTACCTTACCTTACCT 300  
241 CGTATATCCCTTATATCTTACACCTCTGCTTACCTTACCTTACCTTACCTTACCT 300  
301 GTCAAGCTAGATCCTCAACGGGCTCTGGGTCATGCTCAAGAAATGATGATCCATGAT 360  
301 GTCAAGCTAGATCCTCAACGGGCTCTGGGTCATGCTCAAGAAATGATGATCCATGAT 360  
361 TTAAGGACTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
361 TTAAGGACTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
421 CCCCGTATTTCTTGGAAATATAGCCACAGAAATCACCGCAACAAATTTACTCG 480  
421 CCCCGTATTTCTTGGAAATATAGCCACAGAAATCACCGCAACAAATTTACTCG 480  
481 ATAAAGATGAAGTTTACATCTTAAACGTAAGTCAAGATTAATTTTCAAACTTC 540  
481 ATAAAGATGAAGTTTACATCTTAAACGTAAGTCAAGATTAATTTTCAAACTTC 540  
541 TTAACAATCAACCGGGGAGTGTCACTTGGTGTTCGTTGATCTTTAGGATTTCCGT 600  
541 TTAACAATCAACCGGGGAGTGTCACTTGGTGTTCGTTGATCTTTAGGATTTCCGT 600  
601 TATACCTTTAATATATCTGCGCAAGAAATACGGAAGTTTCCACCACTTTGATC 660  
601 TATACCTTTAATATATCTGCGCAAGAAATACGGAAGTTTCCACCACTTTGATC 660  
661 CCATGAGTCAATTTTCAAGATGCTGAACGGCTTCAAGTTTGTATCCGATTTCCGTC 720  
661 CCATGAGTCAATTTTCAAGATGCTGAACGGCTTCAAGTTTGTATCCGATTTCCGTC 720

661 CCATGAGTCAATTTTCAAGATGCTGAACGGCTTCAAGTTTGTATCCGATTTCCGTC 720  
721 TTTCTGCTGTAATTTTATGCAATCAAGCTTTTGTAGCAGCAAAAGGGCAGCTTGGTAA 780  
721 TTTCTGCTGTAATTTTATGCAATCAAGCTTTTGTAGCAGCAAAAGGGCAGCTTGGTAA 780  
781 TCAACATGTAAGCAATTCAGTACTAGGTGTAAGCGTGTCTTGTGATTCATATT 840  
781 TCAACATGTAAGCAATTCAGTACTAGGTGTAAGCGTGTCTTGTGATTCATATT 840  
841 TGCAACACACCATCTCTCACTCCCTCATATGATTCACCGAATGAAATGATCAAAAG 900  
841 TGCAACACACCATCTCTCACTCCCTCATATGATTCACCGAATGAAATGATCAAAAG 900  
901 GCGCCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
901 GCGCCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
961 CACACACTCAGTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
961 CACACACTCAGTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
1021 CAAGGATGCAATCAAGCAGTGTGGGCGAGTACTATTAATGACAGACATCCATTT 1080  
1021 CAAGGATGCAATCAAGCAGTGTGGGCGAGTACTATTAATGACAGACATCCATTT 1080  
1081 TCAAGCAATGATATGAGAGGCTTAAGAAATCACTACATGAGCCCATGAGATGACG 1140  
1081 TCAAGCAATGATATGAGAGGCTTAAGAAATCACTACATGAGCCCATGAGATGACG 1140  
1141 AGCAAAAGGCTGTCTGTAACCAAGATGATCAAAAGGATGATCAATGCAAT 1200  
1141 AGCAAAAGGCTGTCTGTAACCAAGATGATCAAAAGGATGATGATCAATGCAAT 1200  
1201 TGTATGCTTAATTAAGTTTAACTTTCTATTCCTGTAATTAATTAATTAATTAATTAAG 1260  
1201 TGTATGCTTAATTAAGTTTAACTTTCTATTCCTGTAATTAATTAATTAATTAATTAAG 1260  
1261 AAAAAAAAAAAAAAAAAAAAAA 1285  
1261 AAAAAAAAAAAAAAAAAAAAAA 1285

RESULT 2  
AAT95688  
ID AAT95688 standard; DNA; 1128 BP.  
AC AAT95688;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1998 (first entry)  
XX  
DE Crepis alpina delta 12 acetylase encoding DNA.  
XX  
KW Crepis alpina delta 12 acetylase; Plant; Yeast; acetylenic compound;  
XX fatty acid; coating; plastic; lubricant; oilseed; ss.  
OS Crepis alpina.  
XX  
FH Key location/Qualifiers  
FT CDS 1..1128  
FT /tag= a  
FT /product= "Crepis alpina delta 12 acetylase"  
XX  
PD W09737033-A1.  
XX  
PD 09-OCT-1997.  
XX  
PF 14-FEB-1997; 97WO-SE000247.  
XX  
PR 29-MAR-1996; 96SE-00001236.  
XX  
PA (BAFO/) BAFOR M.

PA	(BANAI/ BANAS A.
PA	(DAHL/ DAHLQVIST A.
PA	(GUMM/ GUMMESON P.
PA	(LEEM/ LEE M.
PA	(LENM/ LENMAN M.
PA	(SJOE/ SJOEDAHL S.
PA	(STYM/ STYME S.
XX	
P1	Bafor M., Banas A., Dahlqvist A., Gunmeson P., Lee M., Lenman M,
P1	Sjoedahl S., Styhme S;
XX	
DR	WPI; 1997-503117/46.
XX	P-PsDB; AAM36793.
PT	New acetylase used for production of crepenynic acid from linoleic acid -
PT	derived from Crepis alpina; used for production of acetylenic fatty acids
PT	sulted for the production of coatings, plastics and lubricants.
PS	Claim 7; Page 21; 33pp; English.
XX	
CC	This DNA encodes the Crepis alpina delta 12 acetylase. This is used in
CC	the production of acetylenic compounds. The process comprises treating
CC	C18 fatty acids having a double bond at position delta 12 with an
CC	acetylase to form 12-ynoic acids. The acetylenic compounds can be
CC	produced by organisms such as oilseed plants, yeast and fungi which are
CC	transformed with this acetylase DNA. These organisms can accumulate
CC	these acetylenic compounds which are chemical feedstocks, particularly
CC	for coatings, plasticisers and lubricants. The process enables the
CC	production of these acetylenic compounds from a renewable resource with
CC	high purity and at reasonable cost. (updated on 25-MAR-2003 to correct PA
CC	field.)
SO	Sequence 1128 BP; 270 A; 308 C; 237 G; 313 T; 0 U; 0 Other;
Query Match	55.9%; Score 718.6; DB 2; Length 1128;
Best Local Similarity	77.4%; Pred. No. 4,7e-167;
Matches	871; Conservative 0; Mismatches 254; Indels 0; Gaps 0
Dy	51 GGTGGTCGAGATCGCATCTGAAGGAAAAACATCTTGAACGTGTGCAGTGAT 110 
Dd	4 GGTCGGGCGGCCGCGTGCAGCTTCGCAAAACCCTCATGGAAGTGTCTCAGTTGAT 63 
Oy	111 CCACCGTTCACTTAAGCATGTGAAGAAAGCATTCCTAACCCATTGCTTTGAGCATCT 170 
Dd	64 CCACCTTCACCGTAGTGATCTCAAGCAAGAATCCCTCCCATGTCTCAAGCATCT 123 
Oy	171 GTCATCGSGTATCAACTATGTTGTTCAATGATGTTGTCGTCATGCTTTTATCAAC 230 
Dd	124 GTAATCCGTTCTCTTACTACAAATGTCACAGATGCTATTATGCTTCAACTTTTCACTTC 183 
Oy	231 CTTCGAACAACGATATATCCCTTATTCCTPACACCTCTGGCTTACCTAGATGACCCGTT 290 
Dd	184 CTTCGCGACAATAATACATTCGATTCCTCCTGCCCCCTTAGCTACTCTGCTTGGCCCCCTT 243 
Oy	291 TACTGTTTTGTCAAGCTTAGCATCTCACCGGCTCTTGGGTCATCGGTCAGCAATGTGGT 350 
Dd	244 TACTGTTCTGTCAGTAGCATCTCACCGGCTTATGGGTATCGGTACAGAAATCGGT 303 
Oy	351 CACCATGATTTAAGGACATCAACAGTTGATTATGACATTTGTGATTTGCTGCTCATTTG 410 
Dd	304 CACCATGCTTCAAGGACATCAACAGTGGTTGACGACATGTTGGCTTCACTTCCACTTG 363 
Oy	411 GCCTCCTCACCCCGTATTTCTTTGAAAATTAAGCAAGGAATCAACAGCGCAACACA 470 
Dd	364 TTTCCTCATGACCCCGTATTTCTTCCTGGAATACAGCCACCGAATCCATGECACACACA 423 
Oy	471 AATTCATCTGATACGATGAAGTTTACATCTCTAAACGTAACTGAAAGTCAAGATTAT 530 
Dd	424 AATTCGCTTGACAAAGATGAATTAATATCCCAAAGCAAGCAAGTTCGGCTTTAC 483 
Oy	531 TCCAACTTTCTTAACAATCAACCCCGGAGAGTTTCACTTGGTGTGTTGACTTTA 590 
Dd	484 TATAAGTTCTCAACACCCCACTTGGCGGACGTGATTATGTTATCAACCTTCAACCCCTA 543 

Accession	Gene	Species	Position	Sequence	Length
QY	591	GGATTTCGGTATACCTCTTAACATAATCTCGGCAAGAAATACGGAAGGTTGGCCAC	650		
Db	544	GGCTTCCTCTATACCTTTTACCATAATTTTCGGCAAGAAATATGAAGGTTTGGCAAC	603		
QY	651	CACATTGATCCCATGATGTCGAATTTTCAACGATCGTGAAACGCGTTCAAGTTTGGTATCC	710		
Db	604	CATTTCGACCCCATATGATCCGATTTTCAAAAGCGGTGACGGTTTCAGGTCTTGGTATCG	663		
QY	711	GATTTCGGTCTTTCGCTGTATTTTATGCAATCAAGCTTCTTTATGACGCAAAAGGGCA	770		
Db	664	GATCTTGGCCTTTCGTGTCTTATCGAATTTAACTTTCGGATGACGCAAGGCGCC	723		
QY	771	GCTTGGGATCAACATGATGACCAATTCAGTACCTAGGTGTAAAGCGTTCCTCGTTTG	830		
Db	724	GCTTGGGATGAGTGATTTACGGAAATTCAGATTTTAAAGCGTGTATCTTTTTCGATATC	783		
QY	831	ATCATATATTTTGCACACACACCACATCTCTCACTCCCTCATTAATGATTCACCGAATGAAAC	890		
Db	784	ATCACCTTACTTGCACACACACCACATCTGTCTTGCCTCATTAATGATTCATGAAATGAAAC	843		
QY	891	TGATTCAAAGGCGCTTATCAACAATGATAGGATTTGGGTTCTTGAATCGGTTTTC	950		
Db	844	TGGCTCAAGGGGCTTTGTCTTAAACAATCATATGAGGACTTTGGGTTCTTGAATATGTGTCTC	903		
QY	951	CACGACGTTACACACACTCAGCTGTGATCATTTGATCTGATCATTCATTCACATTATCAT	1010		
Db	904	CATGATGTTTACACACACTCAGCTTATGATCATATCTGTTTCAATACATTCACACATATAT	963		
QY	1011	GCAAGAGAACGAGGAGATGCAATCAAGCCAGTGTGGCGAGTACTATTAATCGACAGG	1070		
Db	964	GCGAAGGAGGCAAGGATGCAATCAACACAGTCTTGGGCGACTTTATTAAGATCGATAGG	1023		
QY	1071	ACTCCATTTTCAAGCAATGTATATGAGAGGCTTAAGAAATGATCTATACATGAGGCCAT	1130		
Db	1024	ACTCCAAATTTGAAAGCAATGTGAGAGAGGCGCAAGAGATCATCTTCATGAGGCTGAA	1083		
QY	1131	GAGGATGCGAGCAAAAGGTGTGTCTGTGATGACCAAGATGTAA	1175		
Db	1084	AAAGGTAGGAGTCCAAAGGTGTATATTGTATCAATTAATTCTGA	1128		
RESULT 3					
AAV63101					
ID	AAV63101	standard; cDNA; 1358 BP.			
AC	AAV63101;				
DT	02-FEB-1999	(first entry)			
DE	Crepis palaestina delta-12-epoxygenase cDNA clone Cpa12.				
XX					
XX					
KW	Fatty acid epoxygenase; Cpa12 gene; mixed function monooxygenase;				
KW	delta-12-epoxygenase; epoxygenated fatty acid; transgenated plant;				
KW	vegetable oil; oilseed; ss.				
OS	Crepis palaestina.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	30..1154			
FT		/*leg= a			
XX					
XX					
XX					
PF	09-APR-1998;	98WO-AU000246.			
XX					
PD	22-OCT-1998.				
XX					
PR	15-APR-1997;	97AU-00006223.			
PR	15-APR-1997;	97AU-00006226.			
PR	16-APR-1997;	97US-0043706P.			
PR	20-JUN-1997;	97US-0050403P.			
XX					

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (STYM/) STYMNE S.  
 PI Styenne S, Green A, Singh S, Lemman M;  
 XX WPI: 1998-568734/48.  
 DR P-PSDB; AAW79742.  
 XX  
 PT New isolated fatty acid epoxigenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.  
 XX  
 PS Claim 15, Page 78-81; 150pp; English.  
 XX  
 CC This full-length cDNA clone, designated Cpal2, codes for a novel mixed  
 CC function monooxygenase (see AAW79742) of Crepis palaestina that is  
 CC characterised as having delta-12-epoxigenase activity. It was isolated  
 CC from a C. palaestina cDNA library using a Crepis alpina acetylase  
 CC partial gene sequence (see AAW63104) as probe. The encoded protein  
 CC contains His-rich motifs (see AAW79752-54) that are characteristic of  
 CC mixed function monooxygenases. The Cpal2 gene was shown to be highly  
 CC expressed in developing seeds, with no expression detectable in leaves.  
 CC The invention relates generally to novel genetic sequences (see AAW63101-  
 CC 03) encoding fatty acid epoxigenases (see AAW79742-44), especially delta-  
 CC 12-epoxigenases or mixed function monooxygenases. These provide the means  
 CC by which fatty acid metabolism can be manipulated in e.g. yeast, mould,  
 CC bacteria, insects, birds, mammals and plants (especially oilseed plants  
 CC such as flax), in particular to convert unsaturated fatty acids to  
 CC epoxigenated fatty acids. The invention extends to genetically modified  
 CC oil-accumulating organisms and to the oils derived from them. These oils  
 CC can be used in production of coatings, resins, glues, plastics,  
 CC surfactants or lubricants  
 CC  
 SQ Sequence 1358 BP; 358 A; 308 C; 278 G; 414 T; 0 U; 0 Other;  
 Query Match 55.7%; Score 715.8; DB 2; Length 1358;  
 Best Local Similarity 78.2%; Pred. No. 2,4e-166;  
 Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;  
 QY 29 ATATATCAACAACATGGGTGCTGTCGATGTCGATCATCTGAGGAAAAACAT 88  
 DB 17 ATCATTTTCAACATGGGTGCTGTCGATGTCGATCATCTGAGGAAAAACAT 70  
 QY 89 CTTTGAACGTGTGCGATGTCATC---ACCGTTCAGTTAAGAGATCGAAGAACAT 145  
 DB 71 CATGGAACGTGTGCGATGTCATC---ACCGTTCAGTTAAGAGATCGAAGAACAT 130  
 QY 146 TCCATCCATGCTTGTGAGCATCTGTGATCCGGTCATCATATATGTTTTCATGATCT 205  
 DB 131 CCTCCCATGCTTGTGAGCATCTGTGATCCGGTCATCATATATGTTTTCATGATCT 190  
 QY 206 CATGTTGCTTATGCTTCTACTACTGCAAAACGATATACCTCTTATTTCTACAC 265  
 DB 191 CATTTATGCTTATGCTTCTACTACTGCAAAACGATATACCTCTTCTCTACTAG 250  
 QY 266 TCTGGCTTACCTAGCATGCGCGTTTACTGTTTGTCAAGCTAGCATCTCACCGGCT 325  
 DB 251 TCTAGCTTACTTATGCTTGTGCGGTTTACTGTTTGTCAAGCTAGCATCTCACCGGCT 310  
 QY 326 CTGGGTATCGGTGCAAGATGTGTGACCATGATTTAGCGACTACAGTTGATTGATGA 385  
 DB 311 ATGATTCCTCGGCAAGATGTGTGACCATGATTTAGCGACTACAGTTGATTGATGA 370  
 QY 386 CATTTGATGATTCGTGCTCATTCGGCTCTCCTGACCCCGATATTTCTCTGGAATATAG 445  
 DB 371 CACTGTGGCTTCACTCTCTCACTCATTTCTCTCAACCCCGATATTTCTCTGGAATATAG 430  
 QY 446 CCACAGATATCAACGCGCAACAATTCATCTGATTAAGATGAAGTTTACATTCCTTA 505  
 DB 431 TCACCGGATATCAACGCGCAACAATTCATCTGATTAAGATGAAGTTTACATTCCTTA 490  
 QY 506 ACGTATGTCGAAGGTCGAAGATTTATTCAAACTTTTAAACAATTCACCCGGCGAGTGT 565

DB 491 AAGCAATGCCAAATCCGGCGTATCTATTAACCTTTAACAACCCACTGCTGCTGT 550  
 QY 566 CACTTTGGTGTGGTGTGATCTTTAGATTTCCGTATACCTTTAACTAATATCTCGG 625  
 DB 551 GCTTTTGTATATCAGTTTCAACCTTAGATTTCTTTATACCTTTGACAAATATTTCCG 610  
 QY 626 CAAAGATATCGGAGGTTTGGCAACCACTTTGATCCCATGATGTCATTTTCAACGATCG 685  
 DB 611 CAAAGATATCGGAGGTTTGGCAACCACTTTGATCCCATGATGTCATTTTCAACGATCG 670  
 QY 686 TGAAGCGCTTCAAGTTTGTATCCGATTTGCGATTTGCGTCTTCTATTTTATGACATCA 745  
 DB 671 TGAAGCGCTTCAAGTTTGTATCCGATTTGCGATTTGCGTCTTCTATTTTATGACATCA 730  
 QY 746 GCTTCTGTATGACCAAAAGGCGGAGCTTGGGTATATCAATGATGCAATTCAGTACT 805  
 DB 731 AGTTGCTGTATGACCAAAAGGCGGAGCTTGGGTATATGATGATGATGATGATGAT 790  
 QY 806 AGGTGTATGCGGTGTTCTTCTGTTTGTATCATATTTTGTACCAACCACTCTCTCACTCC 865  
 DB 791 AGGCGTATTTTACCTTTTGTATGATCATCTTCTGTACCAACCACTCTCTCACTCC 850  
 QY 866 TCATTATGATTTCAACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 925  
 DB 851 TCATTATGATTTCAACCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 910  
 QY 926 TTTGCGGTTTCTGATATCGGTTTTCACAGAGTTTACACACTGATCATCTTGTGATCATTT 985  
 DB 911 CTTTGAATCTGATATGATGTTTTCATGATGATGATGATGATGATGATGATGATGAT 970  
 QY 986 GATCTCATATCTTCACTTATTCATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1045  
 DB 971 GTTTTCAATCATCTTCACTTATTCATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030  
 QY 1046 GGGGAGTACTATTAATATGACAGAGCTCAATTTTCAAGCAATGATATGAGAGGCTAA 1105  
 DB 1031 GGGGAGTACTATTAATATGACAGAGCTCAATTTTCAAGCAATGATATGAGAGGCTAA 1090  
 QY 1106 GGAATGATCTTACATCGAGCCGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 1165  
 DB 1091 GGAATGATCTTACATCGAGCC---TGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144  
 QY 1166 CAAATGATATCAAA 1180  
 DB 1145 TAAATGTGATCATTA 1159  
 RESULT 4  
 AAW63102  
 ID AAW63102 standard; cDNA; 1312 BP.  
 XX  
 AC AAW63102;  
 XX  
 DT 02-FEB-1999 (first entry)  
 XX  
 DE Crepis sp. delta-12-epoxigenase cDNA clone Crepx.  
 XX  
 KW Fatty acid epoxigenase; Crepx; delta-12-epoxigenase;  
 KW mixed function monooxygenase; epoxigenated fatty acid; transgenic plant;  
 KW vegetable oil; oilseed; ss.  
 OS Crepis sp.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 26..1150  
 FT /tag= a  
 XX  
 XX W08846762-A1.  
 XX  
 XX 22-OCT-1998.  
 XX  
 XX 09-APR-1998; 98MO-AU000246.

PR 15-APR-1997; 97AU-00006223.  
 PR 15-APR-1997; 97AU-00006226.  
 PR 16-APR-1997; 97US-0043706P.  
 PR 20-JUN-1997; 97US-0050403P.  
 XX  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (STYM/) STYME S.  
 PI Skymne S, Green A, Singh S, Lenman M;  
 PI MPI: 1998-5568734/48.  
 DR P-PSDB; AAV79743.  
 XX  
 PT New isolated fatty acid epoxigenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.  
 XX  
 PS Claim 16; Page 84-86; 150pp; English.  
 XX  
 CC This cDNA clone, designated Crepx, codes for a novel epoxigenase (see  
 CC AAV79743) of a Crepis sp. (not Crepis palaestina) that has a high  
 CC vernolic acid content. The Crepx gene shows a high degree of homology to  
 CC the novel Crep12 delta-12-epoxigenase gene (see AAV63101) of C.  
 CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using  
 CC a Crepis alpina acetyltransferase partial gene sequence (see AAV63104) as  
 CC probe. The invention relates generally to novel genetic sequences (see  
 CC AAV63101-03) encoding fatty acid epoxigenases (see AAV79742-44).  
 CC especially delta-12-epoxigenases or mixed function monooxygenases. These  
 CC provide the means by which fatty acid metabolism can be manipulated in  
 CC e.g. yeast, mould, bacteria, insects, birds, mammals and plants  
 CC (especially oilseed plants such as flax), in particular to convert  
 CC unsaturated fatty acids to epoxigenated fatty acids. The invention  
 CC extends to genetically modified oil-accumulating organisms and to the  
 CC oils derived from them. These oils can be used in production of coatings,  
 CC resins, glues, plastics, surfactants or lubricants  
 XX  
 SQ Sequence 1312 BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;  
 Query Match 54.9%; Score 705.4; DB 2; Length 1312;  
 Best Local Similarity 78.6%; Pred. No. 8,76-164;  
 Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;  
 QY 77 GGGAAAAAATCATCTTGAAGCTGTGCAATGATCC--ACCGTTACGTTAAGCGATCT 133  
 DB 55 GGAAGAGTCGCTCATGAGAGCTGTCTCAGTATGATCAAGTAACTTTCATGAGTATTT 114  
 QY 134 GAAGAAAGCGATCTCTACCCATTTGCTTGAAGCATCTGTATCCGGTCAATATCTATGT 193  
 DB 115 GAAGCAAGCAATCCCTCCATCTTCCAGCGATCTGTATCCGTTCACTTATTAAGT 174  
 QY 194 TGTTCATGATCTCATGTGTCCTTATGCTTCTTACTACCTTGCAAAAGATATCCCTCT 253  
 DB 175 TGTTCAGATCTCTAATTTGCTTCACTTCTTCTTCCCAACATATATATCCCTTA 234  
 QY 254 TATTCCTACACCTCTGCTTACCTAGACATGCGCGTTACTGCTTTGTCAAGCTAGAT 313  
 DB 235 TCTCCCTCATCTCTTACCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 294  
 QY 314 CTTCAACCGGCTCTGGGTCTATCGGTCAAGATGTGTGTCACATGATTTAGCACTTCA 373  
 DB 295 CTTCACTGGGTATGATCTCTCGGCATGATGTGTGTCACATGATTTAGCACTTCA 354  
 QY 374 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433  
 DB 355 ATGGGTTGAGACACTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 414  
 QY 434 TTGAAATATATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 493  
 DB 415 TTGAAATATATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
 QY 494 TTATCTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553  
 DB 475 TTATCTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534

QY 554 CGGCGAGTGTTCATTTGGTGTGTTCCGTTGACTTATGATTTCCGTTATACCTTTAAC 613  
 DB 535 TGTTCAGCTGTGTTGGTTTGGTTATCATGTTTCACTTGAATTTCTTTATATCCTTTGAC 594  
 QY 614 TATATCTCGGGCAAGAAATACGGAGGTTTGGCCATCCATTTGATCCATGATCCAT 673  
 DB 595 AATATATTTCCGGCAAGAAATACGGAGGTTTGGCCATCCATTTGATCCATGATCCAT 654  
 QY 674 TTTCAAGATGCTGAAGCGCTTCAAGTTTGTCTATCCGATTTGGTCTTCTGCTGATTT 733  
 DB 655 TTTCAAGATGCTGAAGCGCTTCAAGTTTGTCTATCCGATTTGGTCTTCTGCTGATTT 714  
 QY 734 TTATGATCAATCAAGCTTTCTTGTAGACGAAAAGGGGACCTTGGTAAATCAATGATACGC 793  
 DB 715 TTATGATCAATCAAGCTTTCTTGTAGACGAAAAGGGGACCTTGGTAAATCAATGATACGC 774  
 QY 794 AATTCAGTACTAGCTGTAAAGCGTGTCTTCTTGTATGATCAATATTTGACACACCCA 853  
 DB 775 AGTTCGGGTGTAGCGCTATTTTACCTTTTCTGATGATGATCACTTCTTACACACCCA 834  
 QY 854 TCTCTCACTCCCTCATATATATGATCAACGAAATGGAATGGAATGGAATGGAATGGAAT 913  
 DB 835 TCACTCTGCTCTATATATGATCACTGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 894  
 QY 914 AATGATAGGATTTTGGGTTTCTGAAATCGGCTTTTCCACGACCTTACACACTCACT 973  
 DB 895 AATGATAGGATTTTGGGTTTCTGAAATCGGCTTTTCCACGACCTTACACACTCACT 954  
 QY 974 CTTGATCATTTTGTATCTATCATTCATTCACATTTATCATGCAAAAGGAGGATGCAAT 1033  
 DB 955 CATCATCATTTTGTATCTATCATTCATTCACATTTATCATGCAAAAGGAGGATGCAAT 1014  
 QY 1034 CAACCCAGTGTGGGCGAGTAACTATTAATGCAAGAGATCCATTTTCAAGGAATGTA 1093  
 DB 1015 CAACCCAGTGTGGGCGAGTAACTATTAATGCAAGAGATCCATTTTCAAGGAATGTA 1074  
 QY 1094 TAGAGAGCTTAAGATGATCATCTTACATCGAGCCGATGAGATGAGATGAGATGAGATG 1153  
 DB 1075 GAGAGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128  
 QY 1154 GTTCTGTACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1180  
 DB 1129 TTATTTGATCATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1155  
 RESULT 5  
 AAV72550  
 ID AAV72550 standard; cDNA; 1364 BP.  
 XX  
 AC AAV72550;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 10-FEB-1999 (first entry)  
 XX  
 DE Vernonia galamensis fatty acid epoxidising enzyme encoding cDNA.  
 XX  
 KM Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;  
 KM expression; chimeric gene; recombinant enzyme; ss.  
 OS Vernonia galamensis.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 103..1257  
 FT /\*tag= a  
 XX  
 XX US5846784-A.  
 XX  
 PD 08-DEC-1998.  
 XX  
 PF 11-JUN-1997; 97US-00872302.  
 XX  
 PR 11-JUN-1997; 97US-00872302.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Hiltz WD;  
 XX WPI, 1999-059065/05.  
 DR P-PSDB; AAM83354.  
 XX  
 PT DNA encoding *Vernonia galamensis* fatty acid desaturase and fatty acid  
 PT epoxidising *Vernonia* - used to alter levels of expression of the enzymes in  
 PT transformed host cells or to produce recombinant enzymes.  
 XX  
 PS Claim 6, Col 25-29, 21pp; English.  
 XX  
 CC The present sequence encodes *Vernonia galamensis* fatty acid epoxidising  
 CC enzyme. The present invention also describes: (i) *Vernonia galamensis*  
 CC fatty acid desaturase; (ii) chimeric genes comprising the fragments  
 CC linked to regulatory sequences; and (iii) transformed host cells  
 CC containing the chimeric genes. The DNA's from the present invention can  
 CC be used to alter levels of expression of the enzymes in transformed host  
 CC cells or to produce the recombinant enzymes by transformation of  
 CC microbial host cells. (updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;  
 Query Match 54.5%; Score 699.8; DB 2; Length 1364;  
 Best Local Similarity 75.8%; Pred. No. 2.1e-162;  
 Matches 894; Conservative 0; Mismatches 277; Indels 8; Gaps 2;

QY 112 CACCGTTCAGCTTAAAGCATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTG 171  
 DB 188 CACATCTCTCGTTAAGCATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTG 247  
 QY 172 TCATCCGGTTCATCTATGATGTTGTCATGATCTCATGTTGCTGCTTCTTCACTAC 231  
 DB 248 CCAATCCGTTATCGTGTGATGTTGTCATGATCTCATGTTGCTGCTTCTTCACTAC 307  
 QY 232 TTGCAACACGATATATCCCTTATCTTACACCTCTGCTTACCTAGCAGGCGCTTT 291  
 DB 308 TCGCAACTCTTATACCT 367  
 QY 292 ACTGTTTTCAGCTAGCATCTGACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 351  
 DB 368 ACTGTTTTCAGCTAGCATCTGACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 427  
 QY 352 ACCATGATTTAGGACATACCATGATGATGATGATGATGATGATGATGATGATGATG 411  
 DB 428 ATCATGCTTATAGTACGACGAGTGGTGTGATGATGATGATGATGATGATGATGATG 487  
 QY 412 CTCTCTCACCCTGATTTCTTGGAAATATAGCCAGAAATCACAAGCCCAACACAA 471  
 DB 488 TTCTCTTCACACTTACTTTCTTGGAAATATAGCCAGAAATCACAAGCCCAACACAA 547  
 QY 472 ATTGACCTGATAGAGTAAAGTTTATCTTCTTAAACGTAAGCAAGGTCGAAGTTT 528  
 DB 548 ATTGACCTGATAGAGTAAAGTTTATCTTCTTAAACGTAAGCAAGGTCGAAGTTT 607  
 QY 529 ---ATTCCAACTCTTAAACATCCACCCGGGCGAGTGTCACTTTGGTGTTCGGTTGA 585  
 DB 608 CCAATTTCAAATTTCTTGAACAACCCCTGTGCAATCTTCACTTTTGTCTTATCATGTGA 667  
 QY 586 CTTTAGATTTCCGTTATACCTCTTAACTAAATCTCGGGGAGAAATACGGAGGTTTG 645  
 DB 668 CTTTAGGCTTTCTTATACCTCTTGAACAATATTTCAAGGCAAGAAATACCAAGGTTTG 727  
 QY 646 CCAACCACTTTGATGCCATGAGTCCAAATTTTCAAGATCGGGAAGCGCTTCAAGTTTGC 705  
 DB 728 CCAACCACTTTGATGCCATGAGTCCCAATTTTCAAGATCGGGAAGCGCTTCAAGTTTGC 787  
 QY 706 TATCGATTTGGTCTTCTCGCTGATTTTATGCAATCAAGGCTTTGTAGAGCAAAAG 765  
 DB 788 TATCGATTTGGTCTTCTCGCTGATTTTATGCAATCAAGGCTTTGTAGAGCAAAAG 847

QY 766 GGGGAGCTTGGGTATCATCAATGATGACCAATTCAGATCTAGGTGTAAGGTGTTCTCG 825  
 DB 848 GGTTCGGTGGTATATCGATGATGACGAGCCGATGGTGGCTGAATGCCCTTCAATA 907  
 QY 826 TTTTATCATATTTTGCACACACCATCTCTCATCTCCCTCATATGATTAACCGAAT 885  
 DB 908 TAATGATCATCTTATCTTCAACCAACCATCTCTCTTTCGCCCTCATATGATTAACCGAAT 967  
 QY 886 GGAATCGATCAAAAGGCGCTTATCAACAATCGATGAGATTTGGGTTCTGTAATGGG 945  
 DB 968 GGAATCGATCAAAAGGCGCTTATCAACAATCGATGAGATTTGGGTTCTGTAATGGG 1027  
 QY 946 TTTTCCAGAGCTTACACACATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1005  
 DB 1028 TGTTCATGAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1087  
 QY 1006 ATCATGCAAAAGGAGCAAGGATGATCAATCAAGCAGTGTGGCGAGTATTAATAATCG 1065  
 DB 1088 ATCATGCAAAAGGAGCAAGGATGATCAATCAAGCAGTGTGGCGAGTATTAATAATCG 1147  
 QY 1066 ACAGAGCTCCAAATTTTCAAGCAATGATGAGAGGCTTAAGGAATGATCTTCAATCGAGC 1125  
 DB 1148 ATAGAGCTCCGTTTATCAAAAGCAATGAGAGAGGCGAAGGAATGATCTTCAATCGAGC 1207  
 QY 1126 CCGATGAGATGAGGACACAAAGGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1185  
 DB 1208 CAGATGAGATGAGGACACAAAGGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267  
 QY 1186 GTATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1245  
 DB 1268 GTACGT--AGTACGTTGTATGCTTTTGTATGATGATGATGATGATGATGATGATGAT 1325  
 QY 1246 TTATCATTAAGAGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA 1284  
 DB 1326 ATGAAGATTAAGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA 1364

RESULT 6  
 ABL58599  
 ID ABL58599 standard; cDNA; 1369 BP.  
 XX  
 AC ABL58599;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Cress microsomal delta-12 desaturase cDNA.  
 XX  
 KW Cress; microsomal delta-12 desaturase; delta-12 hydroxylase;  
 KW delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;  
 KW fat; oil; heart disease; gene; de.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key location/Qualifiers  
 FT CDS 93..1244  
 FT /\*tag= a  
 FT /product= "microsomal delta-12 desaturase"  
 XX  
 PD US6372965-B1.  
 PD 16-APR-2002.  
 PD 14-AUG-1998; 98US-00133962.  
 PD 17-NOV-1992; 92US-00977339.  
 PD 15-OCT-1993; 93WO-US009987.  
 PD 20-JUN-1994; 94US-00262401.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Lightner JE, Okuley JD, Hiltz W, Kinney AJ, Perez-Grau L;  
 PI Yadav NS;  
 XX

DR WPI; 2002-392229/42.  
 DR P-PSDB; ABB80027.  
 PT New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or  
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and  
 PT producing seed oil with altered levels of unsaturated fatty acids.  
 XX  
 PS Claim 1; Col 65-70; 54pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid fragment encoding or  
 CC comprising a sequence encoding a plant enzyme that is a delta-12  
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.  
 CC Chimeric genes comprising nucleic acids of the invention are used to  
 CC create transgenic plants with altered levels of unsaturated fatty acids,  
 CC and can modify plant lipid composition. Nucleic acids of the invention  
 CC can be used as hybridization probes to isolate or amplify nucleotide  
 CC sequences encoding other fatty acid desaturase or fatty acid desaturase-  
 CC related enzymes. They can also be used in restriction fragment length  
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in  
 CC seed oil of oil producing plant species. They can also be used to produce  
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic  
 CC acids of the invention can combine the high oleate trait of transformed  
 CC seeds with mutations for altered fatty acid compositions to obtain new  
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in  
 CC total saturates and high in monounsaturates would provide significant  
 CC health benefits to consumers (reduced risk of coronary heart disease) as  
 CC well as economic benefits to oil processors. The current sequence  
 CC represents a cress microsomal delta-12 desaturase cDNA  
 XX  
 SQ Sequence 1369 BP; 324 A; 358 C; 302 G; 385 T; 0 U; 0 Other;  
 Query Match 35.5%; Score 455.6; DB 6; Length 1369;  
 Best Local Similarity 63.9%; Pred. No. 3.4e-102;  
 Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

QY 109 ATCCACCGTTTACGTTAAGGATCTGAAGAAAGCGATTCTTACCGATTCTTTAGCGAT 168  
 DB 175 AACCGCTTTCTCCGTTGAGATCTGAAGAAAGCGATCCCGCATTTGTTCAAGCGT 234  
 QY 169 CTGTCATCCGGTATCATATGATGTTGTCATGATGTCATGTTGCGCATATCTTAACT 228  
 DB 235 CAATCCCTCGCTCTTCTCTCACTTACATGATGATCATATTAAGCCATGCTTCACT 294  
 QY 229 ACCTTGCAACACGATATATCCCTTATTTCTTACACCTCTGCTTACCTAGCATGCGCG 288  
 DB 295 ACGTGGCACAATTAATCT 354  
 QY 289 TTTACTGTTTGTCAAGCTAAGATCTTACCGGCTCTGCGTCAATCGTCAAGATGTG 348  
 DB 355 TCTATTGGGCTGTCAAGGCTGTCTCTTCACTGATCTGGGTCAATGACCAAGATGCG 414  
 QY 349 GTACCAATGATTTAAGGACATCAAGATGATGATGATGATGATGATGATGATGATGAT 408  
 DB 415 GTACCAATGATTTAAGGACATCAAGATGATGATGATGATGATGATGATGATGATGAT 474  
 QY 409 CGGCTCTCTCAACCCGATTTCTTCTTGAATAATAGCAAGAAATCAACGCAACA 468  
 DB 475 CTTTCT 534  
 QY 469 CAATTCATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
 DB 535 CTGGATCCCTCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594  
 QY 529 ATTCCAAATCTTAAATCAATCAACCGGCGAGTTCATCTTGGTGTGTTGATGACTT 588  
 DB 595 ACGGGAATATGCTCAACAACCTCTTGGACATCAATGATGATGATGATGATGATGATGAT 654  
 QY 589 TAGGATTCGTTATACCTTTAATATATCTCGGCAAGAAATCAACGGAAGTTTGCA 648  
 DB 655 TCGGCTGCT 714  
 QY 649 ACCACTTGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708

DB 715 GCCATTTCTTCCCAACGCTCCCATCTAATGACCAAGAAAGCGCTCCATATATCTCT 774  
 QY 709 CCGATTTGCGTCTCTCTGCTGATATTTATGCAATCAAGCTTCTGTAGCAAGAAAGGCG 768  
 DB 775 CTGATGGGGGATTTCTAGCCGTCTGTTTGGTCTTTACCGTTAGCGTGTGCAAGGGA 834  
 QY 769 CAGCTTGGGTATCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
 DB 835 TGGCTCGATGATCTGCTCTTACGAGATACCGCTTCTGATGATGATGATGATGATGATGAT 894  
 QY 829 TGATCAATATTTGACACACCAACCATCTCTCACTCCCTCATTAATGATTAACCAAGTGA 888  
 DB 895 TGATCACTTACTTTCAGACACCTATCTCTGCTTGTGCTCTCACTAGATTCATCAAGTGG 954  
 QY 889 ACTGATCAAAAGGCGCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGAT 948  
 DB 955 ACTGGCTCAGGAGGCTTTGGCTACCGTACAGACAGATCAAGATCTTGAACAAGTGT 1014  
 QY 949 TCCACGAGTTTACACACACTCAGCTTGTGATCATGATGATGATGATGATGATGATGATGAT 1008  
 DB 1015 TCCACAACTTACAGACACACAGCTGCTCATCTGCTTCTGACAAATGCGCATATATA 1074  
 QY 1009 ATGCAAGGAAGCAAGGATGATCAAGCCAGTGTGGGAGTACTATTAATTCAGCA 1068  
 DB 1075 ACGCAATGGAAGCTTCAAAAGCGATTAAGCCAAATCTTGGAGACTATTAACAGTTGATG 1134  
 QY 1069 GAGCTCCAAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128  
 DB 1135 GAACACCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194  
 QY 1129 ATGAGATAGGACACAAAGGTGTCTGTGATCAACAAGATGATTAACAAAGGTG 1186  
 DB 1195 ACAAGGAAGTGAACAAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1252

RESULT 7  
 AA06068  
 ID AA06068 standard; cDNA; 1372 BP.  
 XX  
 AC AA06068;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-NOV-1994 (first entry)  
 XX  
 DE Sequence encoding microsomal delta-12 desaturase.  
 XX  
 KM Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.  
 XX  
 OS Arabidopsis thaliana.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 93..1244  
 FT /\*tag= a  
 PN M09411516-A1.  
 XX  
 PD 26-MAY-1994.  
 XX  
 PF 15-OCT-1993; 93MO-US009987.  
 XX  
 PR 17-NOV-1992; 92US-00977339.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Lightner JE, Okuley JU;  
 XX  
 DR WPI; 1994-183515/22.  
 DR P-PSDB; AAR53697.  
 XX  
 PT Genes for fatty acid desaturase enzymes - permit alteration of plant  
 PT lipid composition.  
 XX  
 PS Claim 3; Page 112-114; 147pp; English.

XX The gene corresp. to AA066068 was isolated by screening Arabidopsis  
CC genomic DNA library using radiolabeled pSF2b cDNA insert, purifying  
CC positively-hybridising plaque, and subcloning a 6kb Hind III insert  
CC fragment from the phage DNA in pluescript vector. Comparison of the  
CC sequences of the gene (AA066074) and the cDNA (AA066068) revealed the  
CC presence of a single intron of 1134 bp at a posn. between nucleotides 88  
CC and 89 of the cDNA, which is 4 nucleotides 5' to the initiation codon.  
CC The cDNA is contained in clone AAP92103. Plasmid AAP92103 was deposited  
CC on October 16, 1992 with the ATCC and bears accession number ATCC 69095.  
CC An isolated nucleic acid fragment where in the nucleic acid identity is  
CC 90% or greater to AA066068 or AA066074 is claimed. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 1372 BP; 324 A; 358 C; 303 G; 387 T; 0 U; 0 Other;  
Query Match 35.5%; Score 455.6; DB 2; Length 1372;  
Best Local Similarity 63.9%; Pred. No. 3.4e-102;  
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;  
QY 109 ATCCAGCGTTACGTTAAGCGATCTGAAGAAAGCGATTCTACCCATTCTTTAGAGCAT 168  
DB 175 AACCGCTTTCTCGTGAGGATCTGAAGAAAGCAATCCCGCATTTTCAAGCGCT 234  
QY 169 CTGTCATCCGTCATCATATATGTTGTCATGATCTGATGTCCTATCTTACT 228  
DB 235 CAATCCCTGCTCTTCTCTTACCTTATCAGTGCATATATATAGCTCATGCTTCTACT 294  
QY 229 ACCTTGCAACAGCATATATCCCTCTTATCTTACACCTCTGCTTACCTAGCATGCGCG 288  
DB 295 ACGTCGCAACAATTAATCTTCTCTCTCCCTCAGCCTCTCTTACTTGGCTGGCCAC 354  
QY 289 TTTAAGTGTGTTGTCAGATGATCATCTACCGGCTCTGAGTCATGCGTCACGATGTG 348  
DB 355 TCFATTTGGGCTGTCAGAGGCTGTGCTTACCTGATCTGAGTCATAGCCCAAGATCG 414  
QY 349 GTCAACATGATTTAGGACATCAACAGATTTGATGATGATGTTGATGTCGTCCTCA 408  
DB 415 GTCAACAGCATTTAGGACATCAACATGCGTGAAGATGATGTTGATCTTCACTT 474  
QY 409 CGGCTCTCTACCCCGGATTTCTTGGAAATATAGCCAGAAATACCAAGCCCAACA 468  
DB 475 CTTCTCTCTGCTCTTCTTACTTCTCTGGAATATAGTCATCGCCGTACCATTCACA 534  
QY 469 CAAATTCATCTGATACAGATGAAGTTTCAATTCCTAAACGTAAGTCGAAGTCAAGATT 528  
DB 535 CTGATCCCTCGAAAGATGAAGTATTTGCCAAACAAATCAACATCAAGTGT 594  
QY 529 ATTCCAACTCTTAAGCAATCAACCCGGGAGGTTCACTTGGTGTGTTGATGACTT 588  
DB 595 ACGGAATATACCTCAACACCTCTTGGAGCATATCATATGTTAACGTCACATGTTGTC 654  
QY 589 TAGGATTTCCGTTATACCTCTTAACTAATATCTCGGGCAAGAAATACGGAGGTTTGCA 648  
DB 655 TCGGTTGGCCCTTGAATTAAGCTTAAAGCTCTGGGAGACCGTATAGACGGGTTGCTT 714  
QY 649 ACCACTTGTATCCATGATGATCAATTTCAACGATGTAAGCGGTTCAAGTTTGTCTAT 708  
DB 715 GCCATTTCTTCCCAACGCTCCCATCTCAATGACCGGAAGCGCTCCAGATATACCTCT 774  
QY 709 CGGATTTGGTCTCTGCTGATTTTATGCAATCAACCTCTTGTACCAAAAGGGG 768  
DB 775 CTGATGCGGGTATTTAGCCGCTGTGTTGCTTATCCGTTACCTCTGACAAAGGGA 834  
QY 769 CAGCTTGGGATATCAACATGATGCAATTTCAAGTACTAGTGAAGCTGTGTTCTGTTT 828  
DB 835 TGGCTCATGATCTGCTCTTACGGAATACCGCTTCTATATGTAATGCTTCTCGTCT 894  
QY 829 TGATTCATATTTGACACACCACTCTCACTCTCATATGATTTCAACCGAATGGA 888  
DB 895 TGATTCATATTTGACACACCACTCTCACTCTCATATGATTTCAACCGAATGGA 954  
QY 889 ACTGATCAAAAGGCGCTTATCAACATCATGATGAGGATTTGGGTTCTGATGCGGTTT 948

DB 955 ACTGCTCAAGGAGGCTTTGGCTTACCGTAGACAGACTACGATCTTGAAACAAGGCT 1014  
QY 949 TCACAGAGCTTACACACACTACGCTTTCATCATATTTGATCTTACATTTCCATTATC 1008  
DB 1015 TCACACATTTACAGACACACAGCTGCTCATCTGTTCTTCACATGCGGATTATA 1074  
QY 1009 ATGCMAAGAAAGCAAGGATGCAATCAAGCCAGTGTGGCGGAGTACTATTAATTCACA 1068  
DB 1075 ACGCAATGGAAGCTTCAAAAGCGATTAAGCCCAATTTGGGAGACTATTTACGATTCG 1134  
QY 1069 GAATCCCAATTTTCAAGCAATGATATAGAGGCTAAGGATGATGATCATTCAGGCCG 1128  
DB 1135 GAACACCTGTATATGATGCGATGATATAGGAGGCAAGGATGATATCTATTAACCGG 1194  
QY 1129 ATGAGATAGGAGACACAAAGGTGTGTTGTTGTCACCAAGATGTAATCAAAAAGTG 1186  
DB 1195 ACAGGAAGTGAACAAAGAGTGTGATCTGTAACAATTAAGTATGACATGATG 1252  
RESULT 8  
AAZ51315  
ID AAZ51315 standard; DNA; 1372 BP.  
XX  
AC AAZ51315;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE A. thaliana FAD2 gene encoding delta12-desaturase.  
XX  
KW Arabidopsis FAD2 gene; delta12-desaturase; yeast delta-9 desaturase;  
KW pl-olef gene; transgenic plant; oil plant; mono-unsaturated fatty acid;  
KW Foodstuff; ss.  
XX  
OS Arabidopsis thaliana.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT CDS 93..124  
FT /tag= a  
FT /product= "delta12 desaturase"  
PN WO200011012-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 24-AUG-1999; 99WO-US019443.  
XX  
PR 24-AUG-1998; 98US-0097586P.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Martin CE, Mitchell A;  
XX  
DR WPI; 2000-237610/20.  
DR P-PSDB; AAY70270.  
XX  
PT New synthetic desaturase gene, useful to obtain transgenic plants that  
PT produce a higher yield of unsaturated fatty acids, is customized for  
PT expression in a plant cytoplasm.  
XX  
PS Example 4; Page 72-73; 77pp; English.  
XX  
CC The present sequence is Arabidopsis thaliana FAD2 gene encoding delta12  
CC desaturase. Substitution of N-terminal Ole1 protein coding sequences with  
CC the N-terminal sequence derived from the Arabidopsis FAD2 gene is done to  
CC optimise gene expression, membrane targeting and ER (endoplasmic  
CC reticulum) retention of the chimeric enzyme. Modified yeast delta-9  
CC desaturase pl-olef gene comprising a desaturase domain and a cyr b5  
CC domain, is customized for expression in a plant cytoplasm. This gene is  
CC modified for expression in Arabidopsis and related species to obtain  
CC transgenic plants that produce a higher yield of unsaturated fatty acids.  
CC Transgenic plants, especially oil plants, are produced by this method



CC which have increased amounts of unsaturated, particularly mono -  
CC unsaturated fatty acids, to obtain foodstuff that is more healthy and has  
CC improved flavour

XX Sequence 1372 BP; 324 A; 358 C; 303 G; 387 T; 0 U; 0 Other;

Query Match 35.5%; Score 455.6; DB 3; Length 1372;  
Best Local Similarity 63.9%; Pred. No. 3.4e-102;  
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

```
QY 109 ATCCACGGTTCAGCTTAAGCATCTGAAGAAAGGATTCCTACCATTCCTTTAGCGAT 168
DB 175 AACCGCTTCTCGGTGGAGATCTGAAGAAAGATCCCGCATTTGTTCAAGCGT 234
QY 169 CTGTCATCCGGTTCATCATCTATGTTGTTGATGATCTATGTTGCTTCTTACT 228
DB 235 CAATCCCTCGCTTCTTCTCTACCTTATGATGATCATTTATAGCTTCTTACT 294
QY 229 ACCTTGCAACACGATATATCCCTTATTCCTTACACCTTGGCTTACCTAGCAGCCG 288
DB 295 ACGTCGACCAATTAATCTTCTCTCTCCCTCAGCCTCTCTTACTTGGCTGGCCAC 354
QY 289 TTTACTGTTTGTGACGATAGCATCTCAACCGCCTTGGGTGATCGGTACGAAATGTG 348
DB 355 TCTATTGGGCTGTCAAGCTGTGTCTTAACTGATCTGGGTATGAGCCGCAATATGCG 414
QY 349 GTCCACATGATTTAGGAGCTACCACTGATTTGATGATCATTTGATTTGCTGCTCAT 408
DB 415 GTACACAGCATTAAGGAGCTACCAATGGCTGATGATGACAGATTTGTTCTTCAAT 474
QY 409 CGGCTCTCTCAACCCGATTTCTTTGAAATATAGCAGAAATACACGCCAACA 468
DB 475 CTTCTCTCTCTGCTTACTTCTCTGAAATATGATGATGATGATGATGATGATGAT 534
QY 469 CAATTCATCTCGAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 535 CTGATCTCTCGAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
QY 529 ATTCCAATCTTCAATCAATCCCGGAGATGATGATGATGATGATGATGATGATGAT 588
DB 595 ACGGAAATACCTCAACCTCTTGAAGCATGATGATGATGATGATGATGATGATGAT 654
QY 589 TAGGATTCGGTATATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 648
DB 655 TCGGATGAGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
QY 649 ACCACTTGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
DB 715 GCCATTTCTTCCCAAGCTTCCATGATGATGATGATGATGATGATGATGATGATGAT 774
QY 709 CCGATTTCCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
DB 775 CTGATGAGGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
QY 769 CAGCTTGGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
DB 835 TGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 829 TGAATCAATTTGACACACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 888
DB 895 TGAATCAATTTGACACACCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 954
QY 889 ACTGATCAAGGAGGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 948
DB 955 ACTGATCAAGGAGGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 1014
QY 949 TCCACAGGTTACACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
DB 1015 TCCACAGGTTACACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074
QY 1009 ATGCAAGGAAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
DB 1075 ACGCAATGAGGATCAAAAGGCTTAAAGCAATTTGGGAGATTAACATTAAGTTGATG 1134
```

```
QY 1069 GAATCCAAATTTCAAAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
DB 1135 GAACACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
```

```
QY 1129 ATGAGGATAGCGACACAAAGGTGTCTTCTGATCCCAAGATTAATCAAAAGGTG 1186
DB 1195 ACAGGAAAGGTGACAAAGAAAGGTGTCTGATCAACAAATTAAGTTAGACATGATG 1252
```

## RESULT 9

AC35456  
ID AAC35456 standard; DNA, 1411 BP.

AC35456;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 10262.

Hybridisation assay; genetic mapping; gene expression control;

protein identification; signal transduction pathway; metabolic pathway;

promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.

05-MAR-1999; 99US-0123180P.

09-MAR-1999; 99US-0123548P.

23-MAR-1999; 99US-0125788P.

25-MAR-1999; 99US-0126264P.

29-MAR-1999; 99US-0126785P.

01-APR-1999; 99US-0126785P.

06-APR-1999; 99US-0128234P.

08-APR-1999; 99US-0128714P.

16-APR-1999; 99US-0129845P.

19-APR-1999; 99US-0130077P.

21-APR-1999; 99US-0130449P.

23-APR-1999; 99US-0130510P.

23-APR-1999; 99US-0130891P.

28-APR-1999; 99US-0131449P.

30-APR-1999; 99US-0132048P.

30-APR-1999; 99US-0132407P.

04-MAY-1999; 99US-0132484P.

05-MAY-1999; 99US-0132485P.

06-MAY-1999; 99US-0132486P.

06-MAY-1999; 99US-0132487P.

07-MAY-1999; 99US-0132863P.

11-MAY-1999; 99US-0134256P.

14-MAY-1999; 99US-0134218P.

14-MAY-1999; 99US-0134219P.

14-MAY-1999; 99US-0134221P.

14-MAY-1999; 99US-0134370P.

18-MAY-1999; 99US-0134768P.

19-MAY-1999; 99US-0134941P.

20-MAY-1999; 99US-0135124P.

21-MAY-1999; 99US-0135353P.

21-MAY-1999; 99US-0135629P.

24-MAY-1999; 99US-0136021P.

25-MAY-1999; 99US-0136392P.

27-MAY-1999; 99US-0136782P.

28-MAY-1999; 99US-0137222P.

01-JUN-1999; 99US-0137528P.

03-JUN-1999; 99US-0137502P.

04-JUN-1999; 99US-0137724P.

07-JUN-1999; 99US-0138094P.

08-JUN-1999; 99US-0138540P.

10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 16-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 26-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.

PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149358P.  
PR 17-AUG-1999; 99US-0149375P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 18-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149920P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 23-AUG-1999; 99US-0150566P.  
PR 25-AUG-1999; 99US-0150884P.  
PR 26-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 30-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 26-SEP-1999; 99US-0156458P.  
PR 26-SEP-1999; 99US-0156596P.  
PR 29-SEP-1999; 99US-0157117P.  
PR 04-OCT-1999; 99US-0157753P.  
PR 05-OCT-1999; 99US-0157865P.  
PR 06-OCT-1999; 99US-0158029P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159320P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 35.5%; Score 455.6; DB 3; Length 1411;  
Best Local Similarity 63.9%; Pred. No. 3.4e-102;  
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;  
Cyt 109 ATCCACGTTACGTTAAGCATCTGAAGAAGGATTCCACCATGCTTTGAGCAT 168  
|||||

```

Db 243 AACGCTTTCTCGTGGAGATCTGAAGAAAGCAATCCGCCGATGTTTCAAGCCT 302
Qy 169 CTGATCCGGTCAATCACTATGTTGTTCAATGTTCAATGTTGCTTCTACT 228
Db 303 CAATCCCTCGCTTTTCTCTACTTATCAATGATCAATATATAGCTTCTTACT 362
Qy 229 ACCTTGAAACAGATATATCCCTTATTCCTAGACCTGCTGCTTACCTAGCCGCG 288
Db 363 ACGTGGCAACCAATTAATCTTCTCTCCCTCCTGAGCCCTCTCTTACTTGGCTGGCAC 422
Qy 289 TTTACTGTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTGATCGGTACGAAATGTG 348
Db 423 TCTATGGGCTGTCAAGGCTGTGTCTTACTGTATCTGGGTCAATGCCCAATGTGCG 482
Qy 349 GTCAACATGATTAAGGACTACCAAGTATGATGATGATGATGATGATGATGATGATGAT 408
Db 483 GTCAACATGATTAAGGACTACCAAGTATGATGATGATGATGATGATGATGATGATGAT 542
Qy 409 CGGCTCTCTCAACCCGATTTTCTTGGAAATATAGCCAGAAATCACCAGCCACA 468
Db 543 CTTCTCTCTGCTCTTACTTCTCTGGAATATAGTATGATGATGATGATGATGATGATGAT 602
Qy 469 CAATTCATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
Db 603 CTGATCCCTCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
Qy 529 ATTCAAACTCTTAAACATCAACCCGCGAGATGATGATGATGATGATGATGATGATGAT 588
Db 663 ACGGAAATATCTTAAACATCAACCCCTTTGAGCAATGATGATGATGATGATGATGATGAT 722
Qy 589 TAGGATTTCCGTTATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 648
Db 723 TCGGGTGGCCCTTGTACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 782
Qy 649 ACCACTTGTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Db 783 GCCATTTCTTCCCAAGCTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 842
Qy 709 CCGATTTCCGCTCTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGCAAAAGGGG 768
Db 843 CTGATGGGGTATCTAGCCCTCTGTTTGTCTTAACTTAACTTAACTTAACTTAACTTAACT 902
Qy 769 CAGCTTGGTATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 903 TGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962
Qy 829 TGATCAATTTTGAACACCACTCTCTCACTCTCTCACTTATGATGATGATGATGATGAT 888
Db 963 TGATCACTTACTTGCAGACACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1022
Qy 889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 948
Db 1023 ACTGCTCAAGGGGCTTGTGCTACCTGATGATGATGATGATGATGATGATGATGATGAT 1082
Qy 949 TCCACGATTTACACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
Db 1083 TCCACGATTTACACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1142
Qy 1009 ATGCAAGAAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
Db 1143 ACGCAATGAAAGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
Qy 1069 GGAATCAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
Db 1203 GAATACCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
Qy 1129 ATGAGATGAGCAACAAAGTGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 1186
Db 1263 ACGGAGAGTGAACAAGAAAGTGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 1320

```

RESULT 10  
AAV72549

```

ID AAV72549 standard; cDNA; 1476 BP.
XX
AC AAV72549;
XX
DT 27-AUG-2003 (revised)
DT 10-FEB-1999 (first entry)
XX
DE Vernonia galamensis fatty acid desaturase enzyme encoding cDNA.
XX
KW Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;
KW expression; chimeric gene; recombinant enzyme; ss.
XX
OS Vernonia galamensis.
XX
FH Key location/Qualifiers
FT CDS 134..1282
FT /*tag= a
XX
XX US5846784-A.
XX
XX 08-DEC-1998.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
XX Hitz WD;
XX
XX WPI; 1999-059065/05.
XX
XX P-PSDB; AAW83353.
XX
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid
XX epoxidising enzyme - used to alter levels of expression of the enzymes in
XX transformed host cells or to produce recombinant enzymes.
XX
XX Claim 2; Col 21-24; 21pp; English.
XX
XX The present sequence encodes Vernonia galamensis fatty acid desaturase.
XX The present invention also describes: (i) Vernonia galamensis fatty
XX acid epoxidising enzyme; (ii) chimeric genes comprising the fragments
XX linked to regulatory sequences; and (iii) transformed host cells
XX containing the chimeric genes. The DNA's from the present invention can
XX be used to alter levels of expression of the enzymes in transformed host
XX cells or to produce the recombinant enzymes by transformation of
XX microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 1476 BP; 373 A; 337 C; 346 G; 420 T; 0 U; 0 Other;

Query Match 35.4%; Score 454.4; DB 2; Length 1476;
Best Local Similarity 64.2%; Pred. No. 6.8e-102;
Matches 683; Conservative 0; Mismatches 381; Indels 0; Gaps 0;

Qy 109 ATCCACGCTTCAAGCTTAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 168
Db 213 AACCTCTTACCATGAGGACTCAAAAAGCAATTCCTCCCACTGTTTCAAGGCTT 272
Qy 169 CTGATCCGGTCAATCACTATGTTGTTCAATGATGATGATGATGATGATGATGATGATGAT 228
Db 273 CCTTATCCGTTCTCTTATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 332
Qy 229 ACCTTGAAACAGATATATCCCTTATTCCTAGACCTGCTGCTTACCTAGCCGCG 288
Db 333 ATGAGACCGCATCTTACTTCAACATGCTGCAAAACCTTCTCTCTCTCTCTCTCTCTCT 392
Qy 289 TTTACTGTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTGATCGGTACCAATGTG 348
Db 393 CTATATGGGTGTTCAAGGCTGTGTGCTTACAGAGTGTGGGTCAATGATGATGATGAT 452
Qy 349 GTCAACATGATTAAGGACTACCAAGTATGATGATGATGATGATGATGATGATGATGAT 408
Db 453 GTCAACATGATTAAGGACTACCAATGATGATGATGATGATGATGATGATGATGATGAT 512

```



Db 323 GTACACGAGTTCAGCAGTACCAATGGCTGATGACACAGTGGTCTTATCTTCATT 382  
Qy 409 CGGCTCTCTCAACCCCGATTTCTTGGAAATATAGCCAGGATCAACCGCAACA 468  
Db 383 CTTCTCTCTCTGCTTACTTCTCGAAGTATAGTCATGCCGTACCATTCACACA 442  
Qy 469 CAAATTCACTGATAGAGTAAAGTTTACATTCCTAAACGTAAGTCGAAGTCAAGATT 528  
Db 443 CTGATCTCTCGAAGAGATAGATATTTGTCCAAAGCAAAATCAAGCAATCAAGTGT 502  
Qy 529 ATTCCAACTCTTAATCAATCCACCCGGGAGGTTCACCTTGGTGTGGTGAATT 588  
Db 503 ACGGAAATACCTCAACACCTCTTGGACGATCATATGTATACCGTCAAGTTTCTC 562  
Qy 589 TAGATTTCCGTTATACCTCTTAATATATCTCGGCAAGAAATACCGGAGTTTCCCA 648  
Db 563 TCGGTTGGCCCTTATCTTACCTTTAAGCTCTGCGAGACCGTATGACGGTTTCGTT 622  
Qy 649 ACCACTTGTATCCATGATGTCAAATTTTCAACGATCGTGAACGGTTCAGTTTGTAT 708  
Db 623 GCCATTTCTTCCCAACGCTCCCATCTACATGACCGAAGACGCTCCAGATATACCTCT 682  
Qy 709 CCGATTTCCGTTCTCTGCTGTATTTATGCAATCAAGCTCTTGTAGACCAAAAGGG 768  
Db 683 CTGATGCGGGTATCTAGCCGCTGTGTTGGTCTTTACCGTTACGCTGCTCACAAAGGA 742  
Qy 769 CAGCTTGGGTATCAACATGACCAATTCAGTACTAGTGTAGCGTGTCTTCTGTTT 828  
Db 743 TGGCTGTATGATGTGCTCTTACGGAATCCGCTTCTGATAGTAAAGCTTCTCTCT 802  
Qy 829 TGATCAATATTTGACACCAACCATCTCTGACTCCCTCATTTATGATTTCAACGAAATGA 888  
Db 803 TGATCACTTACTTGACAGACACTCATCCCTGTTGCTCACTACGATTCATCAAGTGG 862  
Qy 889 ACTGGATCAAAAGGGCGCTTATCAACATTCGATAGGAGATTTGGGTTCTGATGGGTTT 948  
Db 863 ACTGGCTCAGGGGAGCTTTGGCTACCGTGAACAAGATTAAGGAACTTTGAACAAGGTGT 922  
Qy 949 TCCAGACGTTACACACACTGACGCTTGTGATCTCATTTGATCTCAATTCACATTTATC 1008  
Db 923 TCCCAACATTTACAGACACACGTTGCTCATCTGTTTTCGACAATGCCGATTTATA 982  
Qy 1009 ATGCAAAAGAAAGAGGATGCAATCAAGCCAGTGTGGGAGTACTATATAATTCACA 1068  
Db 983 ACGCAATGAAAGTACAAAGGCGATTAAGCCATTTCTGGAGACATATACAGTTGATG 1042  
Qy 1069 GGAATCCATTTTCAAAAGCATGATATAGAGGCTTAAAGATGCACTTACATCGACCCG 1128  
Db 1043 GAACACCGTGTATGTAGCGATGTATAGGAGGCAAGAGATGTATGTATAGAAACCGG 1102  
Qy 1129 ATGAGATTAGGAGACAAAGGTGTCTGTGTAACAAGATGTAATCA 1178  
Db 1103 ACAGGGAAGGTGACAAAGAAAGTGTGTACTGTACAAATTAAGTTATGA 1152

RESULT 12  
AAC39493  
ID AAC39493 standard; DNA; 1451 BP.  
XX  
AC AAC39493;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24835.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic pathway;  
XX promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
XX

PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0133180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.

PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 13-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 18-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 35.3%; Score 454; DB 3; Length 1451;  
Best Local Similarity 63.8%; Pred. No. 8.5e-102;  
Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;

QY 109 ATCCACGGTTCACGTTAAGCATGTGAAGAAAGCATTCCTACCATTCCTTTAGGCAT 168  
DB 235 AACCGCTTCTCCGTGGAGATCGAAGAAAGCATCCGCCCATGTTTCMAAGCCT 294  
QY 169 CTGTACCCGGTATCATATGTTGATCATGTATCATTCATTCATTCATTCATTCATTCAT 228  
DB 295 CAATCCCTGCTCTTCTCTCACTTATCATGTATCATTCATTCATTCATTCATTCATTCAT 354  
QY 229 ACCTTGCAACACGTATATCCCTTATTCCTACACCTCTGGCTTACCTAGATGGCCG 288  
DB 355 ACGTGGCAACAATTAATTCCTCTCTCTCCCTAGCCCTCTTACTTGTGGCTTGGCCAC 414  
QY 289 TTTACTGGTTTGTCAAGCTAAGCATTCCTACCGGCTCTGGGTATCGGTACGAATGTG 348  
DB 415 TCTATTGGGCTGTCAAGGCTGTGTCTTACTGTATCTGGGTATGCTCCACGAATGCG 474  
QY 349 GTCAACATGATTTAGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408  
DB 475 GTCAACAGCATTAAGGACATCAACATGCTGATGACACAGTTGGTCTTATTCATTT 534  
QY 409 CGGCTCTCTCACCCCGTATTTCTTGAATATATAGCAGAGATTCACGACGCAACA 468  
DB 535 CTTCTCTCTCTGCTCTTACTTCTCTGGAAGTATGATGATGATGATGATGATGATGATGAT 594  
QY 469 CAAATTCATCTGATPAAGATGAAGTTTACATTCCTTAAAGTAAGTGAAGGTCAAGATT 528  
DB 595 CTGATCCCTCGAAGAGATGAAGTATTTGTCCCAAGACAGAAATACGAATCAAGTGTGT 654  
QY 529 ATTCAAACTTTAAAGATCCACCGGCGAGGTTCATTTGTGTGTGTGTGTGTGTGTGTGT 588

Db 655 ACGGAAATACCTCAACACCCCTTGGACGATGANTGTAAACCGTCCAGTTTGTCC 714  
 Qy 589 TAGATTTCCGTTATACCTTTAATAATATCTGGGCAAGAAATACGGAGATTGGCA 648  
 Db 715 TCGGGTGGCCCTTTACTTACCTTTAAACGCTCTCTGGAGACCGATAGACGGGTTCCGTT 774  
 Qy 649 ACCACTTTGATCCCATGATGCAATTTTCAAGATCGTGAACGGCGTTCAAGTTTGTCTAT 708  
 Db 775 GCCATTTCTTCCCAACGCTCCCATCTACATGACCGGAAACGCTCCAGATATACCTCT 834  
 Qy 709 CCGATTTCCGTTCTTGGCTGTATTTATGCAATCAAGCTTCTGTAGACCAAAAGGG 768  
 Db 835 CTGATGGGGGATTTAGCCGCTGTTTGGCTTTACCGTTACCGCTGCTGCAAGGGA 894  
 Qy 769 CAGCTTGGGTATCAATGATGACCAATTCAGTACTAGGTGTAAGCGTTTCTTCTGTT 828  
 Db 895 TGGCTTGATGATTTGCTCTTACGAGATCCGCTTGTATGTGAATGCGTTCTCTCT 954  
 Qy 829 TGATCAATATTTGACACCAACCCATCTCTGCTCCATTTATGATTTCAACCGAATGGA 888  
 Db 955 TGATCACTTACTTACGACACACTCATCCCTGTTGCTCACTACGATTCATGAGATGGG 1014  
 Qy 889 ACTGGATCAAAAGGCGCTTATCAACATGATAGGATTTGGGTTCTGTAATGGGTTT 948  
 Db 1015 ACTGGCTCAGGGAGCTTTGGCTACCGTACAGAGACTAGGAATCTTGAACAAGGTGT 1074  
 Qy 949 TCCACAGAGTTACACACACTCAGCTTGTGATCTGATCTGATTCATTCACATTTATC 1008  
 Db 1075 TCCCAACATTTACAGACACACAGCTGCTCATCACTGTTTTCACAAATGCCGATTTATA 1134  
 Qy 1009 ATGCAAGAAAGCAAGGAGTGCATCAAGCCAGTGTGGGCGAGTACTATTAATTCAGCA 1068  
 Db 1135 ACGCAATGGAAGTCAACAAGCGATTAAGCCATTTGGGAGACTATTAACAGTTTCATG 1194  
 Qy 1069 GGAATCCAAATTTTCAAGCAATGATATGAGAGGCTAAGGATGATCTACATCGAGCCG 1128  
 Db 1195 GAAACCGGTGATGTGCGCATGTATAGGAGGCAAAAGAGTGTATCTATGTAGAACCCG 1254  
 Qy 1129 ATGAGATAGGAGACAAAGGTGTGTCTGTGACCAAGATGTAAATCAAAAGGTG 1186  
 Db 1255 ACAGGGAAGGTGACAAAGAGGTGTACTGTACAACTAATGATTATGAGATGATG 1312  
 RESULT 13  
 ID AA066074 standard; DNA: 2973 BP.  
 AC AA066074;  
 DT 25-MAR-2003 (revised)  
 DT 09-NOV-1994 (first entry)  
 XX Sequence of microsomal delta-12 desaturase gene.  
 DE Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.  
 OS Arabidopsis thaliana.  
 XX Key Location/Qualifiers  
 FT exon 433..520  
 FT intron 521..1654  
 FT /\*tag= a  
 FT /\*tag= b  
 PN MO9411516-A1.  
 PD 26-MAY-1994.  
 PF 15-OCT-1993; 93WO-US009987.  
 PR 17-NOV-1992; 92US-00977339.  
 XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lightner JE, Okuley JU;  
 XX WPI; 1994-183515/22.  
 DR Genes for fatty acid desaturase enzymes - permit alteration of plant  
 XX lipid composition.  
 PT Claim 3; Page 136-138; 147pp; English.  
 XX The gene corresp. to AA066068 was isolated by screening Arabidopsis  
 CC genomic DNA library using radiolabeled pSF2b cDNA insert, purifying  
 CC positively-hybridizing plaque, and subcloning a 6kb Hind III insert  
 CC fragment from the phage DNA in pBluescript vector. Comparison of the  
 CC sequences of the gene (AA066074) and the cDNA (AA066068) revealed the  
 CC presence of a single intron of 1134 bp at a posn. between nucleotides 88  
 CC and 89 of the cDNA, which is 4 nucleotides 5' to the initiation codon.  
 CC The cDNA is contained in clone AAP92103. Plasmid AAP92103 was deposited  
 CC on October 16, 1992 with the ATCC and bears accession number ATCC 69095.  
 CC An isolated nucleic acid fragment where in the nucleic acid identity is  
 CC 90% or greater to AA066068 or AA066074 is claimed. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX Sequence 2973 BP; 762 A; 637 C; 569 G; 1005 T; 0 U; 0 Other;  
 SQ  
 Query Match 35.3%; Score 454; DB 2; Length 2973;  
 Best Local Similarity 63.8%; Pred. No. 1e-101;  
 Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;  
 Qy 109 ATCCACCGTTACGTTAAGGATGTAAGAAAGCATTTCTACCATTTGCTTGGAGCAT 168  
 Db 1741 AACCGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCCGATTTTCAAGGCT 1800  
 Qy 169 CTGTCACTCGGTATCATATGTTGTGATATGATATGATTTGCTTGTGCTTCTACT 228  
 Db 1801 CAATCCTCGCTCTTCTCTTCTTCACTTATCACTGATCATATTAATGCTTCACTTCTACT 1860  
 Qy 229 ACCTTGCAACAGATATATCCCTTATCTTACACCTCTGCTGCTTACCTAGATGGCCG 288  
 Db 1861 ACGTGGACACCAATTAATTTCTCTCTCTCTCTAGCCTCTCTTACTTGGCTTGGCAC 1920  
 Qy 289 TTATCTGTTTGTCAAGTACATCTCAACCGGCTCTGCTGCTATGCTGCTCAAGATGTG 348  
 Db 1921 TCTATGGGCTGTGCAAGGCTGTGTCTTACTGATCTGCTGCTATGCTGCTCAAGATGTG 1980  
 Qy 349 GTCAACATGATTTAGGATCTACCACTGATGATGATGATTTGATTTGCTGCTCATTT 408  
 Db 1981 GTCAACAGCATTCAGGACTACCAATGCTGATGACACAGTTGATCTTATCTTCAATT 2040  
 Qy 409 CGGCTCTCTACCCCGTATTTCTTCTGAAATATATAGCAAGGAATCACACGCAACA 468  
 Db 2041 CTTCTCTCTCTGCTTCTTCTTCTCTGAAATATATGATCTGCTGCTGCTGCTGCTGCT 2100  
 Qy 469 CAATTCATCTGATTAACGATGAATTTTCACTTCTTAAACGTAAGTCAAGATTT 528  
 Db 2101 CTGATCCCTCGAAAGATGAGATATTTGTCGAAGCAAGATTCAGATCAAGTGT 2160  
 Qy 529 ATTCCAATCTTAAATCAATCAACCGGGGAGGTTCACCTTGTGTGTGCTT 588  
 Db 2161 ACGGGAATATCTTCMAAACCTCTTGGACGATCAAGATTTAAACGTCAGATTTGTCC 2220  
 Qy 589 TAGATTTCCGTTATACCTCTTAACTAATTTCTCGGGCAAGAAATACGGAGTTTGGCA 648  
 Db 2221 TCGGGTGGCCCTTTACTTACCTTTAAGCTCTCTGACACACCGTATGACGGGTTCCCTT 2280  
 Qy 649 ACCACTTTGATCCCATGATGCAATTTTCAAGATCGTGAACGGCGTTCAAGTTTGTAT 708  
 Db 2281 GCCATTTCTTCCCAAGCTTCCATCTACATGACGGAAGACGCTCCATATATACCTCT 2340  
 Qy 709 CCGATTTCCGTTCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTAGCAAGAAAGGG 768  
 Db 2341 CTGATGGGGGATTTTACGCTGTTTGTGTCTTAAACGTTACGCTGCTGCAAGGGA 2400

QY 769 CAGCTGGGTAATCAACATGTAACCAATTCAGTAAGTGTAAAGCTTTCTTCGTT 828  
 Db 2401 TGGCCTCGATATCTGCTCTTACGAGATACCGCTTGTAGTAATGCTTCTCGCT 2460  
 QY 829 TGATCATATTTTGGACACCAACCATCTCTCACTCCCTCATTTATGATCAACCAATGGA 888  
 Db 2461 TGATCATCTTACTTGACAGACACTCTCTCTGTTGCTTCACTACATGATCAAGTGG 2520  
 QY 889 ACTGGATCAAAAGCGCCTTATCAACATGATGATGATTTGGGTTCTGTAATCGGTTT 948  
 Db 2521 ACTGGCTCAGGGAGGCTTTGGCTACCGTAGACAGAGACTTGAACAAAGGTGT 2580  
 QY 949 TCCGACAGTTCACACACTAGCCTTGACATCTTATGATCTTCACTTCACTTATC 1008  
 Db 2581 TCCACAAATTCACACACACACGCTGCTATCCTGTTCTTCACAAATGCGCATTTATA 2640  
 QY 1009 ATGCAAGAAGCAAGGATGATCAATCAAGCAGTGTGGGAGATATTAATAATGACA 1068  
 Db 2641 ACGCATGGAAGCTTACAAAGGCGATTAAGCCATTTGGGAGACTTATACAGTTGATG 2700  
 QY 1069 GGAATCCATTTTCAAAAGCAATGTATAGAGAGGCTTAAGAAATGCACTTACATGACCCG 1128  
 Db 2701 GAACACCGTGTATGTGCGATGTATAGGAGGCAAGAGTGTATGTATGAGAACCGG 2760  
 QY 1129 ATGAGATAGGAGACCAAGAGTGTGTCTGTGTACCAAAATGTAATCAAAAGGTG 1186  
 Db 2761 ACAGGAGAGTGACAAAGAAAGTGTGTACTGTATCAAAATTAAGTTATGAGATGATG 2818

RESULT 14

ABL58607  
 ID ABL58607 standard; DNA; 2973 BP.

AC ABL58607;

DT 26-JUN-2002 (first entry)

DE Cress genomic fragment containing microsomal delta-12 desaturase gene.

XX Cress; microsomal delta-12 desaturase; delta-12 hydroxylase;

KW delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;

XX fat; oil; heart disease; gene; ds.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

FT exon 433..520

FT intron 521..1654

FT misc\_signal 1659..1661

FT /note= "this represents the ATG start codon for the delta-12 desaturase gen, the cDNA for which is given in record ABL58599"

XX US6372965-B1.

XX 16-APR-2002.

XX 14-AUG-1998; 98US-00133962.

XX 17-NOV-1992; 92US-00977339.

XX 15-OCT-1993; 93WO-US009987.

XX 20-JUN-1994; 94US-00262401.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Lightner JE, Okuley JJ, Hitz W, Kinney MJ, Perez-Grau L;

XX Yadau NS;

XX WPI; 2002-392229/42.

DR P-PSDB; ABB80027.

XX New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or  
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and  
 PT producing seed oil with altered levels of unsaturated fatty acids.  
 XX  
 PS Claim 1; Col 99-102; 54pp; English.  
 CC The invention relates to an isolated nucleic acid fragment encoding or  
 CC comprising a sequence encoding a plant enzyme that is a delta-12  
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.  
 CC Chimeric genes comprising nucleic acids of the invention are used to  
 CC create transgenic plants with altered levels of unsaturated fatty acids,  
 CC and can modify plant lipid composition. Nucleic acids of the invention  
 CC can be used as hybridization probes to isolate or amplify nucleotide  
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-  
 CC related enzymes. They can also be used in restriction fragment length  
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in  
 CC seed oil of oil producing plant species. They can also be used to produce  
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic  
 CC acids of the invention can combine the high oleate trait of transformed  
 CC seeds with mutations for altered fatty acid compositions to obtain new  
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in  
 CC total saturates and high in monounsaturates would provide significant  
 CC health benefits to consumers (reduced risk of coronary heart disease) as  
 CC well as economic benefits to oil processors. The current sequence  
 CC represents a cress genomic fragment containing microsomal delta-12  
 CC desaturase gene  
 XX  
 SQ Sequence 2973 BP; 762 A; 637 C; 569 G; 1005 T; 0 U; 0 Other;

Query Match 35.3%; Score 454; DB 6; Length 2973;  
 Best Local Similarity 63.8%; Pred. No. 1e-101;  
 Matches 688; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 109 ATCCACCGTTCACGTTAAGCATGTAAGAAAGCATTCCTACCATTCCTTTGAGCAT 168  
 Db 1741 AACCGCTTTCTCGGTGGAGATCTGAAGAAAGCATCCGCGCATTTGTTCAAGCT 1800  
 QY 169 CTGTATCCGGTCAATCACTATGTGTTCATGATCTCATTTGTTGCTTCTTACT 228  
 Db 1801 CAATCCCTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860  
 QY 229 ACCTTGAACAGGTATATCCCTTATTCCTTACACCTTGGCTTACTTACATGATGGCCG 288  
 Db 1861 ACGTGGCAACATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920  
 QY 289 TTTACTGGTTTGTCAAGCTAGCATCTCACCGGCTTGGGTCATGCGTCAAGATGTG 348  
 Db 1921 TCTATGGGCTGTCAAGGCTGTGTCTTAAGTGTATCTGTGTATGATGATGATGATG 1980  
 QY 349 GTCAACATGCAATTTAGGACCTACAGTGTATGATGATGATGATGATGATGATGATG 408  
 Db 1981 GTCAACATGCAATTTAGGACCTACAGTGTATGATGATGATGATGATGATGATGATG 2040  
 QY 409 CGGCTTCCCTCACCGGATTTCTTCTTGAATTAATGACAGAAATCAACAGGCAACA 468  
 Db 2041 CTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100  
 QY 469 CAAATCACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528  
 Db 2101 CTGATCCCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160  
 QY 529 ATTCAAACTTTTAACATCAACCGGCGAGTGTCACTTGTGTTTGGTTGACTT 588  
 Db 2161 ACGGAAATACCTCAACACCTCTTGGAGCATGATGATGATGATGATGATGATGATG 2220  
 QY 589 TAGATTTCCGTATTAATCTTAACTAATCTGCGGCAAGAAATACCGGAGTTTGCA 648  
 Db 2221 TCGGATGCGCTTACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 2280  
 QY 649 ACCACTTGAATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
 Db 2281 GCCATTTCTTCCCAAGCTTCCATTAATGATGATGATGATGATGATGATGATGATGATG 2340



Qy	709	CCGATTTTCGGCTTCTCGCTGTATTTTATGCAATCAGCTCTTGTGACAGCAAAAGGGG	768
Db	2341	CTGATTCGGGTAATTTCTACCCGCTCTGTTTGGCTTTACCGTTACCGTCTCTCCACAAGGGA	2400
Qy	769	CAGCTTGGGTATCAACATGTACGCAATTCACAGTACTAGTGAAGCGTGTCTTCGTT	828
Db	2401	TGGCTCGATATCTGCTCTTAACGAGTACCGCTTCTGATATGTGATTCGTTCTCTGTTCT	2460
Qy	829	TGATCATAATTTTGACACACACCCATCTCTCACTCCCTCATTATGATTTCAACCGAATGA	888
Db	2461	TGATCATTACTTGGACAGACACTATCCCTCGTTCCTCACTACGATTCATCAGAGTGG	2520
Qy	889	ACTGGATTAAGGGCCCTTATCAACAATTCGATAGGATTTTGGGGTCTCGAATCGGGTT	948
Db	2511	ACTGGCTACGGGAGCTTTGGCTACCGTAGACAGACTACGGAATCTTGAACAAGGCT	2580
Qy	949	TCCAGACGTTACACACACTCAGCTCTTGACATCATTTGATCTCATACATTCGCATTATC	1008
Db	2581	TCCACAACTTATACAGACACACACGCGGTCACTCTGTTCTCGACAAATGCGGATTATA	2640
Qy	1009	ATGCAAGGAAGCAAGGATGCAATTCAGCCAGTGTGGCGAGTACTATAAATCCACA	1068
Db	2641	ACGCATATGAAGCTTACAAAGCGAATGAAGCCAAATTCGGAGAACATTAACCAAGTTCAGT	2700
Qy	1069	GGACTCCAAATTTTCAAAGCAATGTATAGAGGCTTAAGGATNGCATCTACATCGAGCCG	1128
Db	2701	GAAACCGCTGTATATGTGGCGATGTATAGGAGGCAAAAGATGTATCTATGTGAACCCG	2760
Qy	1129	ATGAGATAGCGAGACAAAGGTGTGTTCTGGTACACAAGATGTATCAAAAAGTG	1186
Db	2761	ACAGGAGGTGACAAAGAAAGGTGTGTACTGTATCAACAATAAGTATAGAGAGTATG	2818

## RESULT 15

ID AAC39457 standard; DNA; 1451 BP.

AC AAC39457;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24699.

KW Hybridisation assay; genetic mapping; gene expression control;

**KW** promoter; termination sequence; ss.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PN EP1033405-A2

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 09-MAR-1999; 99US-0123548P.

PR 25-MAR-1999; 99US-0126264P.

PR 01-APR-1999; 99US-0127462P.

PR 08-APR-1999; 99US-0128714P.

PR 19-APR-1999; 99US-0130077P.

PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130510P.
PR	23-APR-1999;	99US-0130510P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132407P.

PR	05-MAY-1999;	99US-01328454P
PR	05-MAY-1999;	99US-01328455P
PR	06-MAY-1999;	99US-01328456P
PR	06-MAY-1999;	99US-01328457P
PR	07-MAY-1999;	99US-01328633P
PR	11-MAY-1999;	99US-01342565P
PR	14-MAY-1999;	99US-01342189P
PR	14-MAY-1999;	99US-01342190P
PR	14-MAY-1999;	99US-01342212P
PR	14-MAY-1999;	99US-01343707P
PR	18-MAY-1999;	99US-01347689P
PR	19-MAY-1999;	99US-01349614P
PR	20-MAY-1999;	99US-01355124P
PR	21-MAY-1999;	99US-01355353P
PR	24-MAY-1999;	99US-01356299P
PR	25-MAY-1999;	99US-01360211P
PR	27-MAY-1999;	99US-01363392P
PR	28-MAY-1999;	99US-01367822P
PR	01-JUN-1999;	99US-01372282P
PR	03-JUN-1999;	99US-01375289P
PR	04-JUN-1999;	99US-01375502P
PR	07-JUN-1999;	99US-01377742P
PR	18-JUN-1999;	99US-01394573P
PR	16-JUN-1999;	99US-01394587P
PR	16-JUN-1999;	99US-01394588P
PR	17-JUN-1999;	99US-01394593P
PR	18-JUN-1999;	99US-01394607P
PR	18-JUN-1999;	99US-01394616P
PR	18-JUN-1999;	99US-01394632P
PR	18-JUN-1999;	99US-01394633P
PR	18-JUN-1999;	99US-01394750P
PR	18-JUN-1999;	99US-01397533P
PR	21-JUN-1999;	99US-01398177P
PR	22-JUN-1999;	99US-01398939P
PR	23-JUN-1999;	99US-01403534P
PR	23-JUN-1999;	99US-01403535P
PR	24-JUN-1999;	99US-01406359P
PR	28-JUN-1999;	99US-01408232P
PR	29-JUN-1999;	99US-01409591P
PR	30-JUN-1999;	99US-01412879P
PR	01-JUL-1999;	99US-01418442P
PR	01-JUL-1999;	99US-01421514P
PR	02-JUL-1999;	99US-01423055P
PR	06-JUL-1999;	99US-01423508P
PR	08-JUL-1999;	99US-01428033P
PR	09-JUL-1999;	99US-01429270P
PR	12-JUL-1999;	99US-01429772P
PR	13-JUL-1999;	99US-01435452P
PR	14-JUL-1999;	99US-01435624P
PR	15-JUL-1999;	99US-01440055P
PR	16-JUL-1999;	99US-01440859P
PR	16-JUL-1999;	99US-01440860P
PR	19-JUL-1999;	99US-01443325P
PR	19-JUL-1999;	99US-01443311P
PR	19-JUL-1999;	99US-01443312P
PR	19-JUL-1999;	99US-01443313P
PR	19-JUL-1999;	99US-01443334P
PR	19-JUL-1999;	99US-01443335P
PR	20-JUL-1999;	99US-01443522P
PR	20-JUL-1999;	99US-01446532P
PR	21-JUL-1999;	99US-01446842P
PR	21-JUL-1999;	99US-01446814P
PR	21-JUL-1999;	99US-01450066P
PR	21-JUL-1999;	99US-01450089P

[illegible]



```

Qy      889  ACTGATCAAAAGGCGCCTTATCAAAATCGATAGGATTTCGGTTCCTGATCGGTTT 948
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1015  ACTGGCTCAGGGGAGCTTTGGCTACCGTAGACAGAGCTAGSAACTTGAACAAGGTGT 1074
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      949  TCCACGAGCTTACACACACTCAGCTCTTGCAATCAATTGATCTCAATACATTCCACATTATC 1008
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1075  TCCACAACATTACAGACACACCTGGCTCATCACTGTTCTCGACAATGCCGATTATA 1134
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1009  ATGCAAGGAGGAGGAGGATGCAATCAAGCCAGTGTGGGCGAGTACTATATAATCGACA 1068
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1135  ACGCAATGGAAGCTTCAAAAGGCGATTAAGCCAAATTTCTGGAGACTATATACAGTTGATG 1194
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1069  GGAATCCAAATTTCAAAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCG 1128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1195  GAAACCCGTGTATGTGGCGATGTATAGGGAGGCAAAAGAGTGTATCTATGTAGAACCGG 1254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1129  ATGAGATAGCGAGCACAAAGGTGTGTTCTGTGTAACCAAGATGTAAATCAAAAAGGTG 1186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1255  ACAGGGAAAGGTGACAAAGAAAGGTGTACTGTACAACAATAAGTATAGAGATGATG 1312
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: June 23, 2004, 13:00:22  
 Job time : 430 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: June 23, 2004, 12:47:43 ; Search time 89 Seconds  
(without alignments)  
8012.493 Million cell updates/sec

Title: US-10-069-772-1  
Perfect score: 1285  
Sequence: 1 aaagctcactctctcgtga.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	718.6	55.9	1128	4	US-09-161-994A-1
2	715.8	55.7	1358	4	US-09-059-769-1
3	705.4	54.9	1312	4	US-09-059-769-3
4	699.8	54.5	1364	2	US-08-872-302-3
5	455.6	35.5	1231	1	US-08-314-596-44
6	455.6	35.5	1231	1	US-08-320-982-44
7	455.6	35.5	1231	3	US-08-819-037-44
8	455.6	35.5	1231	4	US-09-045-940-44
9	455.6	35.5	1372	4	US-09-133-962A-1
10	454.4	35.4	1476	2	US-08-872-302-1
11	454	35.3	2973	4	US-09-133-962A-15
12	432.4	33.6	1222	1	US-08-314-596-43
13	432.4	33.6	1222	1	US-08-320-982-43
14	432.4	33.6	1222	3	US-08-819-037-43
15	432.4	33.6	1222	4	US-09-045-940-43
16	432.4	33.6	1448	1	US-08-314-596-39
17	432.4	33.6	1448	1	US-08-320-982-39
18	432.4	33.6	1448	3	US-08-819-037-39
19	432.4	33.6	1448	4	US-09-045-940-39
20	432	33.6	1426	4	US-09-133-962A-3
21	431	33.5	1155	4	US-08-675-650B-5
22	431	33.5	1155	4	US-09-354-231B-9
23	431	33.5	1155	4	US-09-128-602B-9
24	431	33.4	1155	4	US-09-995-297-9
25	429.4	33.4	1155	2	US-08-675-650B-1
26	429.4	33.4	1155	2	US-08-675-650B-3
27	429.4	33.4	1155	4	US-09-354-231B-11

28	429.4	33.4	1155	4	US-09-128-602B-11	Sequence 11, Appl
29	429.4	33.4	1155	4	US-09-995-297-11	Sequence 11, Appl
30	427.8	33.3	1155	4	US-09-354-231B-13	Sequence 11, Appl
31	427.8	33.3	1155	4	US-09-128-602B-13	Sequence 13, Appl
32	427.8	33.3	1155	4	US-09-995-297-13	Sequence 13, Appl
33	426.2	33.2	1155	4	US-09-354-231B-15	Sequence 15, Appl
34	426.2	33.2	1155	4	US-09-354-231B-17	Sequence 15, Appl
35	426.2	33.2	1155	4	US-09-128-602B-15	Sequence 15, Appl
36	426.2	33.2	1155	4	US-09-128-602B-17	Sequence 15, Appl
37	426.2	33.2	1155	4	US-09-995-297-15	Sequence 15, Appl
38	426.2	33.2	1155	4	US-09-995-297-17	Sequence 17, Appl
39	425.2	33.1	1155	3	US-08-907-608-1	Sequence 1, Appl
40	425.2	33.1	1155	4	US-09-354-231B-1	Sequence 1, Appl
41	425.2	33.1	1155	4	US-09-128-602B-1	Sequence 1, Appl
42	425.2	33.1	1155	4	US-09-482-287-1	Sequence 1, Appl
43	425.2	33.1	1155	4	US-09-966-888-1	Sequence 1, Appl
44	425.2	33.1	1155	4	US-09-995-297-1	Sequence 1, Appl
45	424.6	33.0	1155	3	US-08-907-608-5	Sequence 5, Appl

## ALIGNMENTS

```

RESULT 1
US-09-161-994A-1
Sequence 1, Application US/09161994A
Patent No. 6333448
GENERAL INFORMATION:
APPLICANT: BAROR, Maureen
APPLICANT: BARAN, Antoni
APPLICANT: DAHLQVIST, Anders
APPLICANT: GUMMELSON, Per-Olov
APPLICANT: LEE, Michael
APPLICANT: SODAL, Staffan
APPLICANT: STENME, Sten
APPLICANT: LENMAN, Marit
TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAROR-1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1128
TYPE: DNA
ORGANISM: Crepis alpina
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(1125)
US-09-161-994A-1
Query Match 55.9%; Score 718.6; DB 4; Length 1128;
Best Local Similarity 77.4%; Pred. No. 3.8e-198;
Matches 871; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

```

```

QY 51 GGTGTCGATCGATTCATCTGAGGAAAAACATCTTGAACGTGCGCATGAT 110
DB 4 GTGTGCGATCGATTCATCTGAGGAAAAACATCTTGAACGTGCGCATGAT 63
QY 111 CCACCGTTACGTTAAGCATCTGAAGAGCATCTCTACCCATCTTGAACGATCT 170
DB 64 CCACCGTTACGTTAAGCATCTGAAGAGCATCTCTACCCATCTTGAACGATCT 123
QY 171 GTATCCGTCATCATATGATGTCATGATCTCATGTCATATGTCCTTACTAC 230
DB 124 GTATCCGTCATCATATGATGTCATGATCTCATGTCATATGTCCTTACTAC 183
QY 231 CTTCGCAACACGATATCTCTTATCTCAACCTGCTTACCTACGATGCGCGCTT 290
DB 184 CTTCGCAACACGATATCTCTTATCTCAACCTGCTTACCTACGATGCGCGCTT 243

```

OY	291	TACGAGTTTGTCAAGCTAGCATCTCAACCGGCTCGGTGCATCGGTCAAGATGTGT	350
Db	244	TACGTGTTCTGTCAAGCTAGCATCTCAACCGGCTTATGGGTCAATCGGTCAAGATGCGGT	303
OY	351	CACCATGCAATTTAAGGACTACCAAGTTGATGATGATGTTGATTCGTCGTCATTTG	410
Db	304	CACCATGCTCTCAGGAGACTACCAAGAGGGTTGACGACATGTGGGCTTATCTCCACATCG	363
OY	411	GCTGCTCCACCCCGGTATTTGCTCTTGAAATATATACCAAGGAATACCAAGCCAAACA	470
Db	364	TTTCTCATGACCCCGGTATTTCTCTGGAATATACGACACCGAATCCACCATATCCAAACA	423
OY	471	AATTCATCTCGATTAACGATGAAGTTTACATTCCTTAAACGTAAATCGAAGTCAAGATTTAT	530
Db	424	AATTCGCTTGACAAAGATGAAGTTTACATTCCTCCAAAGCAAGGCCAAAGTCGCGCTTAC	483
OY	531	TCCAACTCTTCTTAACAATCCACCCGGGGAGGTTCATCTTGGTGTTCGTGACTTTA	590
Db	484	TATTAAGTCTTCMAACACCCACCTGGGCGACTGGTATATGTTATCATCCTTCAACCTTA	543
OY	591	GGATTTCCGTTATACCTCTTAACTATATCTCGGGCAAGAAATACGGAGGTTTCCCAAC	650
Db	544	GGCTTCCCTCTATACCTCTTAAACAAATATTTCCGGCAAGAAATAGAAAGTTTCCCAAC	603
OY	651	CACTTTGATCCCATGAGTCCAAATTTTCAAACGATCGTGAACGCGTTCAAGTTTGCTATCC	710
Db	604	CATTTGACACCCCATGAGTCCGATTTTCAAAGGCGGTGACGGTTTCAAGTCTTGGCTATCG	663
OY	711	GATTTCCGCTTCTGCTGTATTTTATGCAATCAAGCTTCTGTGACGACAAAGGGGCA	770
Db	664	GATCTTGGCTCTTCTGCTGTCTTATCGAAGTTAACTTGGGTGACGACGAAAGGCGCC	723
OY	771	GCTTGGGTATTCACATGATGAGCAATTCGAGTACTAGTGTGTAAGCGGTCTTCTGTTTTG	830
Db	724	GCTTGGGTGACGATGATTTTACGGAATTCGAGTTTAAAGCGGTGTATCTTTTTCATATTC	783
OY	831	ATTCACATTTTGGACACCAACCATCTCTCACTCCCTCAATTATGATTCACACGAATGGAAC	890
Db	784	ATTCACATCTTGGACACCAACCATCTGTCTGCTCAATTATGATTCATCTGAATGGAAC	843
OY	891	TGGATCAAGGCGCTTATCAACAATGCATAGGGAATTCGGGTTCTCGAATCGGGTTTTTC	950
Db	844	TGGCTCAGAGGGGCTTTGTCAACATTCGATGAGGACTTTGGGTTCTGAAATGATGTGCTC	903
OY	951	CACGACGTTTACACACATCACTGCTCTTGATCATTTGATCTCATATATTCACATATATCAT	1010
Db	904	CATGATGTTTACACACATCACTGATGATCATCTGTTTTCATATTCACACATATATCAT	963
OY	1011	GCAAAGAGCAAGGAGTGCATATCAAGCAAGTGTGGGCGAGTACTATTAATTCAGACAG	1070
Db	964	GCGAAGAGGCAAGGAGTGCATATCAACACAGCTTGGGCGACTTTATTAAGATCATATGG	1022
OY	1071	ACTCCAAATTTTCAAGCAATGTATAGAGGCTAAGAGATGATCTAATCAATGAGCCGAT	1130
Db	1024	ACTCCAAATTTTCAAGCAATGTGAGAGAGGCAAGAGATGATCTTATCAATGAGCCGATA	1083
OY	1131	GAGATATGCGAGCAAGAGTGTGTTCTGATACCAAGATGTAA	1175
Db	1084	AAGGTAGAGAGTCCAAAGGTGTATATTTGTATCAATAATTTCTGA	1128

RESULT 2  
 US-09-059-769-1  
 ; Sequence 1, Application US/09059769  
 ; Patent No. 6329518  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green, Allan  
 ; APPLICANT: Singh, Surinder  
 ; APPLICANT: Lemman, Marc  
 ; APPLICANT: Styrene, Sen  
 ; TITLE OF INVENTION: Plant Pcty Acid Epoxigenase Genes and Useas  
 ; TITLE OF INVENTION: Therefor  
 ; NUMBER OF SEQUENCES: 20  
 ;

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Wimer and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feibert, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1358 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1151
US-09-059-769-1

Query Match 55.7%; Score 715.8; DB 4; Length 1358;
Best Local Similarity 78.2%; Pred. No. 2.7e-197;
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3

29 ATATATCAACAACATGGGTGCTGTGTGTGAGATGTCGATCCATCTGAGGAGAAAAACAT 88
17 ATCATTTATCAACATGGGTGCGGGGGTGC-----TGTCGAGCATCGAAAAATCGGT 70
89 CCTTGAACGTGTGCCATGCAATCC---ACGTTACAGTTAAGCGATCTGAAGAAAGCAT 145
71 CATGAAGAGTCTTCAGTTGATGATCCAGTAACCTTCTCACTGATGATTAATGAAGCAAGCAT 130
146 TCCATACCATGCTTTGAGCGATCTGTGATCCGGGATCATACTAGTATGTTTCATGATCT 205
131 CCGCTCCCATGTGCTTCAGAGATCTGTATCCGCTCATCTTAATGTTGTCAGATCT 190
206 CATTGTCGCATATCTTCTACTACTGACAAACAGATATCCCTTATCTCTACACC 265
191 CATATTGCCATACATCTTCTACTCTCTTGCCAAACATATATCCCTACTCTTCCATAG 250
266 TCTGAGCTTACCTAGCATGCGCCGTTTACTGAGTTTGTTCAGCTAGACATCTCCAGCCT 325
251 TCTAGACCTACTTACTGTGGCCCGGTTTACTGAGTTCTGTCAACCTAGCGCTCTACATG 310
326 CTGGGTATCTGGTACCAAAATGTGTCAACATGCAATTAGGCAATACCAAGTTGATGATGA 385
311 ATGATCTCTGGCCACGATATGTGTGACGATGCGCTTTAGCAATACATGATGGTTTGACGA 370

```

Qy 386 CATTGTTGATTCGCTGCTCATTGCGGCTCTCCCTGACCCCGATTCTCTTGGAATATAG 445  
 Db 371 CACTGTGGGCTTCATTCCTCCACTCATTTCTCTCCACCCCGATTCTCTTGGAATATAG 430  
 Qy 446 CCACAGATATACCAAGCCCAACCAATTAAGTCTGATATAGATGATTAATCTCTAA 505  
 Db 431 TCACCGGATATACCAAGTTCATTAAGTATGATGATGATGATGATGATGATGATGAT 490  
 Qy 506 ACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565  
 Db 491 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550  
 Qy 566 CACTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625  
 Db 551 GCTTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610  
 Qy 626 CAAGAAATACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 685  
 Db 611 CAAGAAATACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 Qy 686 TGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 745  
 Db 671 TGACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730  
 Qy 746 GCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 805  
 Db 731 AGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790  
 Qy 806 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 865  
 Db 791 AGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850  
 Qy 866 TCATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 925  
 Db 851 TCATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910  
 Qy 926 TTTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 985  
 Db 911 CTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970  
 Qy 986 GATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1045  
 Db 971 GTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030  
 Qy 1046 GGGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1105  
 Db 1031 GGGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1090  
 Qy 1106 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1165  
 Db 1091 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1144  
 Qy 1166 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1180  
 Db 1145 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1159

RESULT 3  
 ; US-09-059-769-3  
 ; Sequence 3, Application US/09059769  
 ; Patent No. 6329518  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green, Allan  
 ; APPLICANT: Singh, Surinder  
 ; APPLICANT: Lemman, Marit  
 ; APPLICANT: Styne, Sten  
 ; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
 ; TITLE OF INVENTION: Therefor  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSES: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder  
 STATE: Colorado  
 COUNTRY: US  
 ZIP: 80303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/059,769  
 FILING DATE: April 14, 1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: AU P06226  
 FILING DATE: 15-APR-1997  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/043706  
 FILING DATE: 16-APR-1997  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/050403  
 FILING DATE: 20-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Feider, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1312 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Crepis sp.  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 26..1147  
 US-09-059-769-3

Query Match 54.9%; Score 705.4; DB 4; Length 1312;  
 Best Local Similarity 78.6%; Pred. No. 2,7e-194;  
 Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;

Qy 77 GGAAGAAACATCTGTAAGCTGTCAGTCGATCC--ACCGTCAAGTTAAGCGATCT 133  
 Db 55 GGAAGAAAGCTGTAAGCTGTCAGTCGATCCGTAAGCTTCTCAGTGAATTT 114  
 Qy 134 GAAAGAAAGCAATCCCTCAATGCTTGAAGCAATCTGTCATCCGATCATCATATGT 193  
 Db 115 GAAAGAAAGCAATCCCTCAATGCTTGAAGCAATCTGTCATCCGATCATCATATGT 174  
 Qy 194 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253  
 Db 175 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 234  
 Qy 254 TATTCCTACACCTGCTGCTTACCTAGATGAGCCGCTTACGCTTTGTCAGCTAGAT 313  
 Db 235 TCTCCCTCATCTCTTACCTAGATGAGCCGCTTACGCTTTGTCAGCTAGAT 294  
 Qy 314 CTTCAAGGCTCTGCTGCTTACCTAGATGAGCCGCTTACGCTTTGTCAGCTAGAT 373  
 Db 295 CTTCAAGGCTCTGCTGCTTACCTAGATGAGCCGCTTACGCTTTGTCAGCTAGAT 354  
 Qy 374 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433  
 Db 355 ATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414

```

QY 434 TTGGAATATAGCCACAGGAATACACGCAACAAATTCACTCGATAAGT 493
Db 415 TTGGAATATAGCCACAGGAATACACGCAACAAATTCACTCGATAAGT 474
QY 494 TTACATTCCTAAAGTAAGTGAAGTCAAGATTATTCACAACTTCTTAACAATCCACC 553
Db 475 TTACATTCCTAAAGTAAGTGAAGTCAAGATTATTCACAACTTCTTAACAATCCACC 534
QY 554 CGGGGAGTGTTCACCTTGTGTTCGTTGATCTTGAAGTTCCTGTTAATCTTTCAC 613
Db 535 TGTGCACTGTGTGTTCGTTGATCTTGAAGTTCCTGTTAATCTTTCAC 594
QY 614 TAAATCTCGGCAAGAAATACGGAGTTTCCCAACACCTTGAATCCCAAGAGCCAT 673
Db 595 AAATATTCCTCGCAAGAAATACGGAGTTTCCCAACACCTTGAATCCCAAGAGCCAT 654
QY 674 TTTCAACATGATGTAACGCGTTCAAGTTTGTCTATCCGATTCGCTTCTGCTGATTT 733
Db 655 TTTCAACATGATGTAACGCGTTCAAGTTTGTCTATCCGATTCGCTTCTGCTGATTT 714
QY 734 TTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGGACCTTGGGTATCAATGTAGC 793
Db 715 TTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGGACCTTGGGTATCAATGTAGC 774
QY 794 AATTCAGTACTAGGTGAAGCGTCTTCTGTTTGAATCAATTTGCAACCAACCA 853
Db 775 AGTTCCGCTGTAGCGGTAATTAACCTTTTGTAGTGTACAGTTTCAACCAACCA 834
QY 854 TCTCTACTCCCTCATTTATGATTCACACGAATGAACTGATCAAAAGGCGCTTATCAAC 913
Db 835 TCAGTCGTGCGCTCATTTATGATTCACACGAATGAACTGATCAAAAGGCGCTTATCAAC 894
QY 914 AATGATNAGGAATTTGGGTTCTGTAATCGGGTTTTCACAGAGTTAACAACACTGACGT 973
Db 895 AATGATNAGGAATTTGGGTTCTGTAATCGGGTTTTCACAGAGTTAACAACACTGACGT 954
QY 974 CTTCGATCATTTGATCTCATCATTCACCATTAATCAAGAAAGAAAGGAATGCAAT 1033
Db 955 CATGATCATTTGATCTCATCATTCACCATTAATCAAGAAAGAAAGGAATGCAAT 1014
QY 1034 CAAGCAGTGTGGGCGAGTACTATTAATATGACAGAGCTCCAAATTTTCAAGCAATGTA 1093
Db 1015 CAAGCAGTGTGGGCGAGTACTATTAATATGACAGAGCTCCAAATTTTCAAGCAATGTA 1074
QY 1094 TAGAGAGGCTAAGGATGATCTATCATGAGCCGATGAGAGTACGCAAAAGGTGT 1153
Db 1075 GAGAGAGGCTAAGGATGATCTATCATGAGCC-----TGATAGCAGCTCAAAAGGTGT 1128
QY 1154 GTTCGTACCAACAAGATGTAATCAA 1180
Db 1129 TTATGTGATCATTAATGTGATCATTA 1155

```

```

RESULT 4
US-08-872-302-3
; Sequence 3, Application US/08872302
; Patent No. 5846784
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D
; TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
; TITLE OF INVENTION: Developing Seeds of Vernonia galamensis
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. duPont de Nemours and Co.
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,302
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Majorian, William R
; REGISTRATION NUMBER: P-41,173
; REFERENCE/DOCKET NUMBER: BB-1084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1364 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1254
; US-08-872-302-3

Query Match 54.5%; Score 699.8; DB 2; Length 1364;
Best Local Similarity 75.8%; Pred. No. 1.1e-192;
Matches 894; Conservative 0; Mismatches 277; Indels 8; Gaps 2;

QY 112 CACCGTTACAGTAAAGCATCTGAAGAAAGCATTCCTACCATTCGCTTTGAGCATCTG 171
Db 188 CACATTCCTGTTAAGGATTAAGAAAGCAATCCCTCGCATTTGCTTCAAGCATCTG 247
QY 172 TCATCCGCTCATTAATGATGTTGTTGATGATCTGATTTGCTGCTTCTTCACTACC 231
Db 248 CCATCCGTTCAATCGGTACCTGTTGATGATCTGATCTGATTAATTAATCAACGC 307
QY 232 TTGAAACAGTATATCCCTTATTCCTACACCTGCTGCTTACCTAGCATGGCCGCTT 291
Db 308 TCGCAACTCTTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 367
QY 292 ACTGTTTGTCAAGTACAGTACCTCAACCGGCTCTGGGTCATCGTCAAGATGTGTC 351
Db 368 ACTGTTTGTCAAGTACAGTACCTCAACCGGCTCTGGGTCATCGTCAAGATGTGTC 427
QY 352 ACATGATTTAGGAGTACCTCAACCGGCTCTGGGTCATCGTCAAGATGTGTC 411
Db 428 ATCATGTTATAGGAGTACCTCAACCGGCTCTGGGTCATCGTCAAGATGTGTC 487
QY 412 CTCCTCCACCGGCTATTTCTTCTGAAATATAGCAAGGAATCAACGCAACCAACAA 471
Db 488 TTCTTCTCACACCTTACTTCTTCTTCTGAAATATAGCAAGGAATCAACGCAACCAAC 547
QY 472 ATTCATCTGATACGATGAATTTTCAATCTCTTAACGTAAGTCAAGATGTAATTT--- 528
Db 548 ATTCATCTGATGAAGAGAGGTTTCAATCTCTTAACGTAAGTCAAGATGTAATTTACT 607
QY 529 ---ATTCGAATCTTTTCAATCAATCAACCGGCGAGTGTACTTGTGTGTGTGGA 585
Db 608 CCAATTTCAATTTCTTGAACAACACCCCTGTCTCAATCTTATTTGTGTTATCAATGTA 667
QY 586 CTTAGAATTTCCGTTTATCTCTTAACTAATATCTGGGCAAGAAATACGGAGGTTTG 645
Db 668 CTTGGGCTTCTTATTAATCTTCTTGAACAATATTTTGAAGCAAAATACCAAAAGTTTG 727
QY 646 CCAACCACTTGTATCCATGATGTCATTTTCAACGATGTCGAAGCGGTTCAAGTTTGC 705
Db 728 CCAACCACTTGTATCCATGATGTCATTTTCAACGATGTCGAAGCGGTTCAAGTTGCG 787
QY 706 TATCCGATTTGCTGCTTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGCAAGAAAG 765
Db 788 TATCGATGTTGCTGCTGCTGATTTTATGCAATCAAGCTTCTTGTAGCAAGAAAG 847
QY 766 GGGGAGCTTGGGTATCAACATGTAACGAATTCAGATCTAGTGTATGAGCGTTCTTGG 825

```





Qy 1069 GGAATCCATTTTCAAGCATGTATAGAGGCTAAGAGATGATCTACATCGAGCCG 1128  
 Db 1015 GAACACCGTGTATGTAGCCGATGTATAGAGGCAAGAGATGTATCTATGTAGAACCGG 1074  
 Qy 1129 ATGAGATAGGAGACAAAGAGTGTCTGTATACCAAGATGTATCAAAAGAGT 1186  
 Db 1075 ACAGGAGAGTGAACAGAAAGTGTGTACTGTATACCAATATAGTATAGACATGATG 1132

RESULT 6

US-08-320-982-44  
 ; Sequence 44, Application US/08320982  
 ; Patent No. 5601026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOMERVILLE, CHRIS  
 ; APPLICANT: VAN DE LOO, FRANK  
 ; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 ; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/320,982  
 ; FILING DATE: 11-OCT-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/314,596  
 ; FILING DATE: 26-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOKULIS, PAUL N.  
 ; REGISTRATION NUMBER: 16,773  
 ; REFERENCE/DOCKET NUMBER: 206905/1220  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3000  
 ; TELEFAX: 202-822-0944  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1231 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: CDNA  
 ; US-08-320-982-44

Query Match 35.5%; Score 455.6; DB 1; Length 1231;  
 Best Local Similarity 63.9%; Freq. No. 5.4e-122;  
 Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

Qy 109 ATCCACGCTTACGCTTGAAGCATGTATAGAGGCAATCCATTCCTTTGAGCAT 168  
 Db 55 AACCGCTTTCTCGGTGGAGATCTGAAGAAAGCATCCCGCGATTTTCAAGCCT 114  
 Qy 169 CTGTATCCGCTCATCATATATGTGTTCATGATCTGATTTGCTGCTATGTCTTACT 228  
 Db 115 CAATCCCTCGCTTCTTCTTCACTTATCACTGATCATATATAGCTTCATGCTTACT 174  
 Qy 229 ACCTTGAAACAGATATCTCTTATTTCTACACCTTGTGCTTACTACAGAGCCCG 288  
 Db 175 ACGTCCGACCAATTAATCTCTCTCCCTCCAGCTCTCTTAACTTGGCTGGCCAC 234  
 Qy 289 TTTACTGTTTTCATAGCATCTACCGGCTCTGGAGTCACTGGTACAGATGTG 348  
 Db 235 TCTATGGGCTGTCAAGGCTGTGTCTTAACTGTATCTGGGTCAATAGCCACAGATCG 294

Qy 349 GTCAACATGATTTAGGACCTACAGTTGATGATGAATTTGATTTGATTCGTCAT 408  
 Db 295 GTCAACAGATTTCAAGGACCTACCAATGGCTGATGACACAGTTGTCTTATCTTCA 354  
 Qy 409 CGGCTCTCCACCCCGATTTCTCTGAAAATATAGCCACAGAAATCAACCCCAACA 468  
 Db 355 CTTCTCTCTCTCTCTTCTTCTCTCTGAAATATGATGATGCGCGCTACCATTCGAACA 414  
 Qy 469 CAAATTCATCTGATTAACGATGAAGTTTACATTCCTTAAACGTAAGTCGAAGTCA 528  
 Db 415 CTGATCCCTCGAAGAGATGATGATTTTCCCAAGAGAAATCAGATTCAGATGTG 474  
 Qy 529 ATTCCAACTCTTAAATCAATCCACCGGCGAGTTCACCTTGTTGTTGTTGTTG 588  
 Db 475 ACGGAAATACCTTAACCAACCTCTTGAACGATCAATGATTAACGCTCAAGTTGTC 534  
 Qy 589 TAGGATTTCCGTTATACCTCTTAACTAATATCTGGGCAAGAAATACGGAGTTTGCA 648  
 Db 535 TCGGATGCGCTTGTACTTACCTTTAAGCTCTCTGCGACGCTATGACGGGTTGCTT 594  
 Qy 649 ACCACTTGTATCCCATGATGATCAATTTTCAAGATGTGAACGGCTTCAAGTTTCTAT 708  
 Db 595 GCATTTCTTCCCAAGGCTCCCATTAATGACCGAGAACGCTCCAGATATACCTCT 654  
 Qy 709 CCGATTTGCTCTCTCTGCTGTATTTATGCAATCAAGCTTCTGTAGCAAGAAAGGG 768  
 Db 655 CTGATGCGGATTTCTGACCGCTCTGTTTGTCTTACCGTTACGCTGCAAGAGGA 714  
 Qy 769 CAGCTGGGTAATCAAGATGACCAATTCAGACTAGGTGTAAGCGTGTCTTCTGTT 828  
 Db 715 TGGCTGTATGATGCTCTCTACGAGATACCGCTTGTATGTAAGCGTCTCTGCT 774  
 Qy 829 TGATCAATATTTGACACCAACCATCTCTCATCTCTTATGATTAACCGAATGGA 888  
 Db 775 TGATCACTTATTCACACACATCATCTCTGTTGCTCTCACTAGATTAATCAAGTGG 834  
 Qy 889 ACTGATCAAGGCGCTTATCAACATCGATAGGATTCGGGTCGTAAGGGGTT 948  
 Db 835 ACTGCTCAGGGGAGCTTTGCTACCGTACAGAGACTAGGAATCTTGAACAAAGGT 894  
 Qy 949 TCCACAGCTTACACACATCTGATCTTGCATTTGATCTCATATTCACATTTATC 1008  
 Db 895 TCCACATATTAACAGACACACATGCTATCATCTGTTTCCACATGCGCATTTATA 954  
 Qy 1009 ATGCAAGAGAGCAAGGATGCAATCAAGCCAGTGTGGCGATCTATTAATAATCGACA 1068  
 Db 955 ACGCAATGAGAGCTAACAAGCGATTAAGCCAAATTCGGAGACTATTAACAGTTGATG 1014  
 Qy 1069 GGAATCCATTTTCAAGCATGTATAGAGGCTAAGAGATGATCTACATCGAGCCG 1128  
 Db 1015 GAACACCGTGTATGTAGCCGATGTATAGAGGCAAGAGATGTATCTATGTAGAACCGG 1074  
 Qy 1129 ATGAGATAGGAGACAAAGAGTGTCTGTATACCAAGATGTATCAAAAGAGT 1186  
 Db 1075 ACAGGAGAGTGAACAGAAAGTGTGTACTGTATACCAATATAGTATAGACATGATG 1132

RESULT 7

US-08-819-037-44  
 ; Sequence 44, Application US/08819037  
 ; Patent No. 6028248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOMERVILLE, CHRIS  
 ; APPLICANT: VAN DE LOO, FRANK  
 ; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 ; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.

COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/819,037  
 FILING DATE: 19-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,982  
 FILING DATE: 11-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/314,596  
 FILING DATE: 26-SEP-1994  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1231 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-819-037-44

Query Match 35.5%; Score 455.6; DB 3; Length 1231;  
 Best Local Similarity 63.9%; Pred. No. 5.4e-122;  
 Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

109 ATCCACCGCTTACGTTAAGCATCTGAAGAAAGCATTCCTACCCATTCTTTGAGCGAT 168  
 55 AACCGCTTTCGCGTGGAGATCTGAAGAAAGCATCCCGCGATTGTTCAAAACGCT 114  
 169 CTGTCATCCGCTCATCATCTATGTTGTCATGATCTGTTGCTTCTTCTTACT 228  
 115 CAATCCCTCGCTCTTCTCTCACTTATCAGTACATCATATTAACCTCATGCTTCTACT 174  
 229 ACCTTGCAACAGCATATATCCCTCTTATCTTACACCTCTGCTGCTTACCTAGATGCGCG 288  
 175 ACGTGGCAACATTAATCTCTCTCTCTCCCTCAAGCTCTCTCTTACTTGGCTTGGCCAC 234  
 289 TTATCTGTTTGTCAAGCTAGATCTCACCGGCTCTGGGTCATCCGTCACGATGTG 348  
 235 TCTATGGGCGCTGTCAGAGCTGTGTCCTAATCGGATCTGGGTCAATACCCACGATGCG 294  
 349 GTCAACATGATTTAGGACATCAACGATTGATGATGATGATGATGATGATGATGATGAT 408  
 295 GTCAACAGCATTCAGCATCAACATGCTGATGATGATGATGATGATGATGATGATGAT 354  
 409 CGGCTCTCTCAACCCGCTATTTCTTGGAAATATAGCCACAGAAATGACAGCGCACCA 468  
 355 CTTCTCTCTCTGCTCTTACTTCTCTGGAAGTATAGTCATGCGCGTCAACATTCACACA 414  
 469 CAATTCATCTGATTAAGATGATTTTCAATCTTAAAGTAAAGTAAAGTAAAGTAAAGT 528  
 415 CTGATCCCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
 529 ATTCAAACTTTTAAATCAATCAACCCGCGAGTGTCACTTGTGTTGTTGTTGATTT 588  
 475 ACGGAATATACCTCAACACCTCTTGGACCATCATATATATACCTTCAAGTTTGTCC 534  
 589 TAGGATTTCCGTTATCTTAACTAATATCTGGGGAAGAAATAGGAGGATTTGCA 648  
 535 TCGGATGCGCTTGTACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 594  
 649 ACCACTTGTATCCATGATGATTTTCAAGATGATGATGATGATGATGATGATGATGAT 708  
 595 GCGATTTCTTCCCAAGCTCCCATCTACATGATGATGATGATGATGATGATGATGATGAT 654  
 709 CCGATTTCCGCTTCTGCTGATATTTTATGATGATGATGATGATGATGATGATGATGAT 768  
 655 CTGATGGGGATTTCTAGCCGCTGTGTTTGGCTTTTACCGTTACGCTGCTGACAAAGGA 714

769 CAGCTGGGATATCAACATGATAGCAATTCAGTACTAGTAAAGCTGTTCTGTTT 828  
 715 TGGCTGATATATGCTCTTACAGAGTACCGCTTCTGATAGTAAAGCTGTTCTGCT 774  
 829 TGATCATATTTTGAACCAACCATCTTCACTCTCTCATTTATGATTTCAACCAATGGA 888  
 775 TGATCATATTTTGAACCAACCATCTTCACTCTCTCATTTATGATTTCAACCAATGGA 834  
 889 ACTGATCAAGGGGCTTATCAACATGATAGGATTTGGGTTCTGATGAGGTTT 948  
 835 ACTGCTCAAGGGGCTTATCAACATGATAGGATTTGGGTTCTGATGAGGTTT 894  
 949 TCCACAGCTTACACACTCAGCTTTCATCATTTGATCTCATATTCACATTCATATC 1008  
 895 TCCACATATTCACACACTCAGCTTTCATCATTTGATCTCATATTCACATTCATATC 954  
 1009 ATGCAAGAGAGCAAGGATGATCAATCAAGCATGTTGGGCGAGTACTATTAATGACA 1068  
 955 ACGCAATGAGAGTCAAAAGGCGATTAAGCCATTTCTGGAGACTATTAACAGTTGATG 1014  
 1069 GACTCCATTTTCAAGCATATGATAGAGGCTAAGGATGATCAATTCAGGCGCG 1128  
 1015 GAACACCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074  
 1129 ATGAGATAGGAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186  
 1075 ACAGGAGAGTGAAGAGAGAGTGTGTACTGTGTAACAAATATGATATGACATGATG 1132

RESULT 8  
 US-09-045-940-44  
 ; Sequence 44, Application US/09045940  
 ; Patent No. 6433250  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOMERVILLE, CHRIS  
 ; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 ; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Microsoft Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/045,940  
 ; FILING DATE: 23-MAR-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/320,982  
 ; FILING DATE: 11-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/314,596  
 ; FILING DATE: 26-SEP-1994  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1231 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-045-940-44

Query Match 35.5%; Score 455.6; DB 4; Length 1231;  
 Best Local Similarity 63.9%; Pred. No. 5.4e-122;

Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

```

Oy 109 ATCCACGGTTCACGTTAAGCATGGAAGAAAGCATCTTACCATTTGTTGAGCGAT 168
Db 55 AACCGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCGATTTGTTCAACGCT 114
Oy 169 CTGTATCCGGTCACTACTATATGTTTCAATGATCTCATTTGGCTTATCTTACT 228
Db 115 CAATCCCGCTCTTCTCTACCTTATCAGTACATATATAGCCCTCAGTCTTACT 174
Oy 229 ACCTTGAAACAGCATATCCCTTATCTTACACCTCGGCTTACCTAGCAGGCGCG 288
Db 175 AGGTGCCCAATTAATCTCTCTCTCCCTCAGCCCTCTCTTACTTGGCTTGGCAC 234
Oy 289 TTTACTGTTTGTCAAGCTAGCATCTTACCGGCTCTGGTCAATCCGTCAGCATGTG 348
Db 235 TCTATGGGCGCTGAAGGCTGTGTCTTACCTGATCTGGGTCTATACCCAGCATGCG 294
Oy 349 GTCAACATGATTTAGGACCTACCAAGTGTATGATGACATTTGGATTGCTCCATT 408
Db 295 GTCAACAGCATTTAGGACCTACCAATGGCTGATGACACAGTTGGTCTTATCTTCAAT 354
Oy 409 CGGCTCTCTCAACCCCGTATTTCTTGAATATAGCAGCAAGAAATACAGCCGACA 468
Db 355 CTTCTCTCTGCTCTTACTTCTCTGAAATATGATGATGCGGTCACCATTTCAACA 414
Oy 469 CAATTCACGATTAAGCATGATTTTCACTTCTTAAAGTAACTGAAAGGTCAAGATT 528
Db 415 CTGATCTCTCGAAGAAATGATGATTTGTCCCAAGAAATACAGCATCAAGTGT 474
Oy 529 ATTCCAACTTCTTAAATCAATCAACCCGCGAGTGTCACTTGGTGTTCGTTGACTT 588
Db 475 ACGGAAATATCTCAACAACCTCTTGGACGATGATGTTAACCTTCAAGTTGTTC 534
Oy 589 TAGATTTCCGTATATCTTAACTATATCTCGGGAAGAAATACGAGGTTTGCA 648
Db 535 TCGGTGCGCTTGTACTTACCTTAAAGTCTTGGGACACCGTATACGCGTTGCTT 594
Oy 649 ACCACTTGTATCCATGATGATCAATTTTCAAGATCTGAAAGCGCTTCAAGTTTGTAT 708
Db 595 GGCATTTCTTCCCAAGCTCCCATCTACATGACGGAAGCGCTCAGATATATCTCT 654
Oy 709 CCGATTTGCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTACAGCAAAAGGG 768
Db 655 CTGATGCGGTATCTTACCGCTGTGTGTCTTACCGTTACCGCTGACAGGGA 714
Oy 769 CAGCTTGGGTATCAACATGATGCAATTTCAAGTACTAGTGTAAAGGTTCTTCTGTT 828
Db 715 TGCGCTCATGATCTGCTCTACGAGTACCGCTTCTGATAGTATGATGCTTCTGCT 774
Oy 829 TGATCATATTTGGACCAACCATCTCTCACTCCCTCATTTATGATTTCAACGATGGA 888
Db 775 TGATCATTTACTTGGACCACTATCCCTGTTGCTCACTAGATTTCACTAGAGTGG 834
Oy 889 ACTGATCAAAAGCGCTTATCAACATGATGAGGATTTGGGTTCTGTAATCGGTTT 948
Db 835 ACTGCTCAGGAGACTTGTGCTTACCGTACGAGACGATCAGGAACTTGTGAACAAGGTGT 894
Oy 949 TCCACGAGTTTACACACTGATGCTTGCATCATTTGATCTCAATCAATTCACATATC 1008
Db 895 TCCACAACTTACACACACACGAGGCTCATCACTGTTCTCGAATAGCCGCAATTA 954
Oy 1009 ATGCAAAAGCAAGGATGCAATCAAGCCAGTGTGGGCGAGTACTATAAATCGACA 1068
Db 955 ACGCATGAGAGCTTCAAAAGGAGTAAAGCCATTTCTGGAGACATTTACAGTTGATG 1014
Oy 1069 GAATCTCAATTTTCAAGCAATGTATAGAGGCTAAGAGATGATCTTACATGAGCCG 1128
Db 1015 GAACACCGTGTATGATGATGATAGGAGGCAAGAGAGTATCTATGTAAGACGG 1074
Oy 1129 ATGAGATAGAGAGCAAAAGTGTCTGTATACCAAGATGTATCAAAAGAGT 1186
Db 1075 ACAAGGAGGTGACAAAGAGGTGTACTGTATCAACAAATTAAGTATGAGCATGATG 1132

```

RESULT 9  
US-09-133-962A-1  
Sequence 1, Application US/09133962A  
Patent No. 6372865  
GENERAL INFORMATION:  
APPLICANT: JONATHAN EDWARD LIGHTNER  
JOHN JOSEPH OKULEY  
TITLE OF INVENTION: GENES FOR MICROSOMAL FATY ACID  
DELTA-12 DESATURASES AND RELATED  
ENZYMES FROM PLANTS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/133,962A  
FILING DATE: 14-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 07/977,339  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHRISTENBURY, LYNNIE M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1043-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302)992-5481  
TELEFAX: (302)773-0164  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1372 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
IMMEDIATE SOURCE:  
CLONE: p92103  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..1244  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-133-962A-1

Query Match 35.5%; Score 455.6; DB 4; Length 1372;  
Best Local Similarity 63.9%; Freq. No. 5.7e-122;  
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

```

Oy 109 ATCCACGGTTCACGTTAAGCATGGAAGAAAGCATCTTACCATTTGTTGAGCGAT 168
Db 175 AACCGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCGATTTGTTCAACGCT 234
Oy 169 CTGTATCCGGTCACTACTATATGTTTCAATGATCTCATTTGGCTTATCTTACT 228
Db 235 TCTATGGGCGCTGAAGGCTGTGTCTTACCTGATCTGGGTCTATACCCAGCATGCG 294
Oy 349 GTCAACATGATTTAGGACCTACCAAGTGTATGATGACATTTGGATTGCTCCATT 288
Db 295 GTCAACAGCATTTAGGACCTACCAATGGCTGATGACACAGTTGGTCTTATCTTCAAT 234
Oy 409 CGGCTCTCTCAACCCCGTATTTCTTGAATATAGCAGCAAGAAATACAGCCGACA 288
Db 355 CTTCTCTCTGCTCTTACTTCTCTGAAATATGATGATGCGGTCACCATTTCAACA 294
Oy 469 CAATTCACGATTAAGCATGATTTTCACTTCTTAAAGTAACTGAAAGGTCAAGATT 228
Db 415 CTGATCTCTCGAAGAAATGATGATTTGTCCCAAGAAATACAGCATCAAGTGT 294
Oy 529 ATTCCAACTTCTTAAATCAATCAACCCGCGAGTGTCACTTGGTGTTCGTTGACTT 288
Db 475 ACGGAAATATCTCAACAACCTCTTGGACGATGATGTTAACCTTCAAGTTGTTC 234
Oy 589 TAGATTTCCGTATATCTTAACTATATCTCGGGAAGAAATACGAGGTTTGCA 228
Db 535 TCGGTGCGCTTGTACTTACCTTAAAGTCTTGGGACACCGTATACGCGTTGCTT 294
Oy 649 ACCACTTGTATCCATGATGATCAATTTTCAAGATCTGAAAGCGCTTCAAGTTTGTAT 288
Db 595 GGCATTTCTTCCCAAGCTCCCATCTACATGACGGAAGCGCTCAGATATATCTCT 234
Oy 709 CCGATTTGCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTACAGCAAAAGGG 288
Db 655 CTGATGCGGTATCTTACCGCTGTGTGTCTTACCGTTACCGCTGACAGGGA 234
Oy 769 CAGCTTGGGTATCAACATGATGCAATTTCAAGTACTAGTGTAAAGGTTCTTCTGTT 288
Db 715 TGCGCTCATGATCTGCTCTACGAGTACCGCTTCTGATAGTATGATGCTTCTGCT 234
Oy 829 TGATCATATTTGGACCAACCATCTCTCACTCCCTCATTTATGATTTCAACGATGGA 288
Db 775 TGATCATTTACTTGGACCACTATCCCTGTTGCTCACTAGATTTCACTAGAGTGG 234
Oy 889 ACTGATCAAAAGCGCTTATCAACATGATGAGGATTTGGGTTCTGTAATCGGTTT 288
Db 835 ACTGCTCAGGAGACTTGTGCTTACCGTACGAGACGATCAGGAACTTGTGAACAAGGTGT 234
Oy 949 TCCACGAGTTTACACACTGATGCTTGCATCATTTGATCTCAATCAATTCACATATC 288
Db 895 TCCACAACTTACACACACACGAGGCTCATCACTGTTCTCGAATAGCCGCAATTA 234
Oy 1009 ATGCAAAAGCAAGGATGCAATCAAGCCAGTGTGGGCGAGTACTATAAATCGACA 288
Db 955 ACGCATGAGAGCTTCAAAAGGAGTAAAGCCATTTCTGGAGACATTTACAGTTGATG 234
Oy 1069 GAATCTCAATTTTCAAGCAATGTATAGAGGCTAAGAGATGATCTTACATGAGCCG 288
Db 1015 GAACACCGTGTATGATGATGATAGGAGGCAAGAGAGTATCTATGTAAGACGG 234
Oy 1129 ATGAGATAGAGAGCAAAAGTGTCTGTATACCAAGATGTATCAAAAGAGT 288
Db 1075 ACAAGGAGGTGACAAAGAGGTGTACTGTATCAACAAATTAAGTATGAGCATGATG 234

```



QY 649 ACCACTTGTATCCATGATGCCAATTTTCAAGATGTAAGCGCTTCAAGTTTGTCTAT 708  
 Db 753 GCCACTTTTCTCTTAAGAGCCCTAATATACAGGAAGTGAAGGTCTCCAAATATGCTTT 812  
 QY 709 CCGATTTCGCTCTTCTGCTGATTTATGCAATCAAGCTTCTTTAGCAGAAAGGG 768  
 Db 813 CGGATTTTGGATGATGATCAACATGCTTCATCTTATCGTGTGCTTACGAAAGGTG 872  
 QY 769 CAGCTTGGTATATCAACATGTAACGAATTTCAAGTACTAGTGTAGCGGTCTTCTGTT 828  
 Db 873 TGGCTTGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 932  
 QY 829 TGATCAATATTTTGGACCAACCCATCTCTCACTCCCTCATATGATTTCAACCGAATGA 888  
 Db 933 CGATACGTAACCTTCAACACACTCACTCCCTTATGCCCCCATATGATGCTCAGAGTGG 992  
 QY 889 ACTGATCAAAAGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATG 948  
 Db 993 ACTGCTAAGGCGGCAATGCAACGCTGCAACCTGATGATGATGATGATGATGATGATG 1052  
 QY 949 TCCACGAGTTATACACATGCTGCTTGTATGATGATGATGATGATGATGATGATGATG 1008  
 Db 1053 TCCATATATCAATCAATATCAACGCTGCTGATGATGATGATGATGATGATGATGATG 1112  
 QY 1009 ATGCAAGGAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1068  
 Db 1113 ACGCAATGAGGCAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1172  
 QY 1069 GACTCTCAATTTTCAAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1128  
 Db 1173 GACTCCCTTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1232  
 QY 1129 ATGAGATAGGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1172  
 Db 1233 ATGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1276

RESULT 11  
 US-09-133-962A-15  
 ; Sequence 15, Application US/09133962A  
 ; Patent No. 6372965  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JONATHAN EDWARD LIGHTNER  
 ; JOHN JOSEPH OKULEY  
 ; TITLE OF INVENTION: GENES FOR MICROSMAL FATTY ACID  
 ; DELTA-12 DESATURASES AND RELATED  
 ; ENZYMES FROM PLANTS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
 ; STREET: 1007 MARKET STREET  
 ; CITY: WILMINGTON  
 ; STATE: DELAWARE  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 19898  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: DISKETTE, 3.50 INCH  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
 ; SOFTWARE: MICROSOFT WORD VERSION 7.0A  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/133,962A  
 ; FILING DATE: 14-Aug-1998  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 07/977,339  
 ; FILING DATE: 17-NOV-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CHRISTENBURY, LYNN M.  
 ; REGISTRATION NUMBER: 30,971  
 ; REFERENCE/DOCKET NUMBER: BB-1043-D  
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-5481  
 ; TELEFAX: (302) 773-0164  
 ; TELEX: 835420  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2973 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Arabidopsis thaliana  
 ; IMMEDIATE SOURCE:  
 ; CLONE: PAGE2-6  
 ; FEATURE:  
 ; NAME/KEY: exon  
 ; LOCATION: 433..520  
 ; FEATURE:  
 ; NAME/KEY: intron  
 ; LOCATION: 521..1654  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-09-133-962A-15

Query Match 35.3%; Score 454; DB 4; Length 2973;  
 Best Local Similarity 63.8%; Pred. No. 2.5e-121;  
 Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;

QY 109 ATCCACGTTACAGTTAAGCATCTGAAGAAAGGATTCCTACCATTCCTTAGCGAT 168  
 Db 1741 AACCGCTTTTTCGGTGGGAATCTGAAGAAAGCATCCCGCATTTGTTCAACGCT 1800  
 QY 169 CTGTATCCGGTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 228  
 Db 1801 CAATCCCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860  
 QY 229 ACCTTGCAACAGATATATCCCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 288  
 Db 1861 ACGTCCAGCAATATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920  
 QY 289 TTTACTGTTTGTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 348  
 Db 1921 TCTATTTGGCTGTGCAAGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980  
 QY 349 GTCCACCATGATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 408  
 Db 1981 GTCCACCATGATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
 QY 409 CGGCTCTCTGACCCCGTATTTCTTGGAAATATGACAGAGATGACAGATGACAGATGAC 468  
 Db 2041 CTTCTCTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100  
 QY 469 CAATTTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
 Db 2101 CTGATATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
 QY 529 ATTCAAACTTCTTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588  
 Db 2161 ACGGAAATATCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220  
 QY 589 TAGATTTTCGTTATATCTTAACTAATATCTGCGGCAAGAAATACGGAAGTTTGC 648  
 Db 2221 TGGGTGCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280  
 QY 649 ACCACTTGTATCCATGATGCCAATTTTCAAGATGTAAGCGCTTCAAGTTTGTCTAT 708  
 Db 2281 GCCATTTCTTCCCAACGCTCCCATCTCAATGACCGGAAGCGCTTCAAGATATACCTCT 2340  
 QY 709 CCGATTTGCTCTTCTGCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATG 768  
 Db 2341 CTGATGCGGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400

Oy	769	CAGCTTGGGGATCAACAACTGTAACGCAATTCACAGTACTAGGTGTAAGACGGTCTTCGTT	828
Db	2401	TGGCTTCGATGATCTGCCTCTTAGGAGTACCGCTTCTGTAATGTAATGCGTTCTCGTGT	2466
Oy	829	TGATCACAATTTGGACCAACCCACTCTCTCACTCCCTCATTTATGATTCAACCGAATGGA	888
Db	2461	TGATCACTTACTTGCAGACACATCACTCCCTCGTGGCTCCTACATGATTCATCAGAGTGGG	2522
Oy	889	ACTGGAATCAAAAGGCCCTTATCAACAATCGATAGGATTTGGGGTTCCTGAATCGGGTTT	948
Db	2521	ACTGGCTCAGGGGACCTTTGGGTACCGTAGACAGACATCAACGAATCTTGAACAAGGTGT	2580
Oy	949	TCCAGAGCGTTACACACACTCAGTCTTGGCATCTTGTATCTTCANACATTCACATTTATC	1008
Db	2581	TCACAAACATTTACAGACACACACGTTGGCTCATCACTGTTCTTCGACAATGCCGCAATTAA	2644
Oy	1009	ATGCAAAGGAAGCAAGGATGCAATCAAGCCAGTGTGGCGAGTACTTAATAATCGACA	1068
Db	2641	AACGAATGGAAGCTACAAAGGGATTAAGCCAAATCTGGGAAACATTTATACAGTTGANTG	2700
Oy	1069	GAATCTCCAATTTCAAAGCATGTATTAGAGGGCTTAAGGAATGCATCTACATCGAGCCCG	1122
Db	2701	GAACCACTGTGTATGTGGCGAATGTATAGGAGGCAAAAGAGTGTATCTATGTAGAACCGG	2760
Oy	1129	ATGAGAGTAGCGAGACAAGGTGTGTTCTGGTACCAAGAATGTATCAAAAAGGTG	1186
Db	2761	ACAGGGAAGGTGACAGAAAGGTGTGTACTGTGTACACATATAGTTATAGAGGATATG	2818

RESULT 12  
US-08-314-596-43

; Patent No. 5668292  
; GENERAL INFORMATI

APPLICANT: SOMERVILLE, CHRIS  
APPLICANT: VAN DE LOO, FRANK  
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.  
STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON  
STATE: D.C.

STATE: D.C.  
COUNTRY: U.S.A

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS 3.31

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.25

```

```

; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/0

FILING DATE: 26-SEP-1994

CLASSIFICATION: 435

NAME: KOKULIS, PAUL N.  
AGENCY/AGENCY INFORMATION:

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 20

TELECOMMUNICATION INFORMATION ;  
TELEPHONE 203 651 2005

TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 43:

**SEQUENCE CHARACTERISTICS:**

LENGTH: 1222 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA ;

US-08-314-596-43

23 68  
Over Match

Query Macchi	55.6%
Best Local Similarity	61.3%

**References**

Matches 716; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

QY	109	ATCCAGCGTTACAGTTAAGCATCTGAAGAAAGGAAATTCACCACTAGCTTTAGCGAT	168
Db	55	AGCCCTCTTTCACACTGTGTGACCTCAAGAGGCACTCCACCCATGTCTTGAACGT	114
QY	169	CTGTATCCGGGATCATACTATATGTTTGTCAATGATCTCATGTTGGCTATGTCTTACT	228
Db	115	CTTTTGTGGCTCATCTCTCTATGTGGCTATGATGTGTGCTTAAGTTTCTTTTCTACT	174
QY	229	ACCTTGAACAACGATATATCCCTCTTATTCCTACACTCTGGCTTACCTAGATGGCCG	288
Db	175	CGATGGCCACCAACTTCTCCCTTACATCTCTTCCGCTCTGATGTGCTTGGCTGG	234
QY	289	TTTATCTGTTTGTGAAGCTAGCATCTTCACCGGCTCTGGGTATCTGGTACGAATGTG	348
Db	235	TTTACTGGCTCTTCCAGAGCTGCATCTTCACCTGGTCTTGGGTCAATCGCCCATGAAATG	294
QY	349	GTACACATGCAATTATGGGACTACCAAGTTGATGACATGTTGGATTCGTCCTCANT	408
Db	295	GCCATCATGCTTTTATGTATGATACAGCTGGCTGATGACATGTGTGGCTTAATGTTCATT	354
QY	409	CGGCTCTCCGTGACCCCGTATTTCTCTTGGAAATATAGCCACAGGAATGACACGCAACA	468
Db	355	CTGCACCTTCTGGTTCATATTTTTCATGGAATAATAGCAATCGCGCCACCATTTCAACA	414
QY	469	CAATTCACCTGATATACGATGAAGTTTACATTTCTTAAAGTATGCAAGGTCAAGATT	528
Db	415	TAGGATCTCTGAGAGACACGAAGTGTCTGTCCCAAAATCAAAGTCGAAAAATTCATG	474
QY	529	ATTCGAACTTCTTACATCAACCCGGGCGAGTTCACTTGGTGTGGTGTGACTT	588
Db	475	ATTCGATGACTCAACACACCGCGAGTCAAGTTTACACTGTCTGCGACGCTCTCC	534
QY	589	TAGATTTCCGTTATACCTCTTAACTAATATCTCGGCGAAGAAATACGGAGGTTTGCCA	648
Db	535	TTGGTGGCTTTTATACTTAGCTTTCATATGTCTCTGTGATAGACTTAACATTCGCTT	594
QY	649	ACCACTTTGATCCCATGATGATCAATTTTCAAAGATCTGAAACGCTTCAAGTTTGTAT	708
Db	595	GCCATTTATGATCCCATATGACCCTAATTTTCCGAAAGAAAGGCTTCAGATTTCATTTG	654
QY	709	CGAATTTGGCTTCTCGCTGATTTTATGCAATCAACTTCTGTACACAGAAAGGG	768
Db	655	CTGACCTCGGAATCTTTGCCAACACGTTTGTCTTATCACGCTACAAATGCGAAAAAGT	714
QY	769	CAGCTTGGGTATCAACATGTAACGCAATTCAGTACTGTAGTGAACGNGTCTTCTGTT	828
Db	715	TGGCTTGGTAAATGGATCTATATGAGGGTGCATTTGCTTATTTACTGTTTCTTGTTA	774
QY	829	TGATCACATATTTGACACCAACCCATCTCTCACTCCCTCATTAATGATTTCAACCGAATGA	888
Db	775	TGATCACATCTTGGAGACACTCACCGGATTTCCACGGTATGGCTCATTCGAAATGG	834
QY	889	ACTGATCAAAAGGCGCTTATCAACATTCGATAGGGAATTTGGGGTTCCTGAATCGGTTT	948
Db	835	ATTGGCTCCGGGAGCATGTGTGATGCTGATAGGATTAAGGGGTGTTGAATAAAGTAT	894
QY	949	TCCAGAGCTTACACACTCAACGCTTGCACATTTGATCTCANTCAATTCACATTTATC	1008
Db	895	TCCATTAATGTGACACACTATGATGCTCATCACTTTTGTCTACAGTGCACATTAAC	954
QY	1009	ATGCAAAAGAAAGCAGGATGCAATTCAGCCAGTGTGGGCGAGTACTATTAATTCGACA	1068
Db	955	ATGCATAGGAAGCCCTAAAGCANTCAAGCTTATATAGGGTGAAGTATTAACGGTATGATG	1014
QY	1069	GGACTTCAATTTTCAAAGCAATGATATAGAGGCTTAAGGAATGCATCTACATCGAGCCG	1128
Db	1015	GTACCCCATTTTTCAGAGCATTTGTGAGGGGAGCGAAAGAGTGTGTTGTCTGACGACG	1074
QY	1129	ATGAGGATAGGAGACACAAAGGTGTGTTCTGTATCCCAATGATGTAATCAAAAAGTGTTA	1188
Db	1075	ATGAAGAAGCTCTTACACAGAGCGGTTTCTGTATCCGGAACAGATTTAAAAAAAGTGTCA	1134

Qy 1189 TGTCAATGCAATGTGATGCTTAATTAAGTTGTTAA-----ACTTTCTATTCCGTGTAAT 1242  
 Db 1135 TGTAGCCCTGTTCTTTTAAGAGAAGAAATTAAGAACAGAGAAATGTGTGTAGTGAAT 1194  
 Qy 1243 AAATTATCATTAAGAGAAAAAAA 1270  
 Db 1195 GTGTTCTTAATAAGAGGCAAAAAAAA 1222

RESULT 13

US-08-320-982-43  
 ; Sequence 43, Application US/08320982  
 ; Patent No. 5801026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOMERVILLE, CHRIS  
 ; APPLICANT: VAN DE LOO, FRANK  
 ; TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 ; TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/320,982  
 ; FILING DATE: 11-OCT-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/314,596  
 ; FILING DATE: 26-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOKULIS, PAUL N.  
 ; REGISTRATION NUMBER: 16,773  
 ; REFERENCE/DOCKET NUMBER: 206905/1220  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3000  
 ; TELEFAX: 202-822-0944  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1222 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-320-982-43

Query Match

33.6%; Score 432.4; DB 1; Length 1222;  
 Best local similarity 61.3%; Pred. No. 2.8e-115;  
 Matches 716; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

Qy 109 ATCCACCTTCAACCTTGAAGCATCTGAAGAAAGCATTCCTACCCATTCCTTTGAGCAT 168  
 Db 55 AGCCCTCTTCAACCTTGAAGCATCTGAAGAAAGCATTCCTACCCATTCCTTTGAGCAT 114  
 Qy 169 CTGTATCCGGTATCATATGTTGTTCAATGATCTCATTTGTTGCTTATGCTTCTACT 228  
 Db 115 CTTTGTGCGCTATCTCCATATGTTGCTATGATGTCGTAAAGTTTCTTTTCTACT 174  
 Qy 229 ACCTTGCAAGACGATATTCCTTATCTTACACCTCTGCTTACCTAGAGGCGCG 288  
 Db 175 CGATGCGCACCAACTTCTTCCCTTACATCTCTTCCGCTCTCGATGTCGCTTGCGTGG 234  
 Qy 289 TTTACTGTTTTGTCAAGTACCTCACCGGCTCTGGGTCAATGGTACGAAATGTG 348  
 ||||||| ||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 235 TTTACTGCTCTTCCAGGCTGATTCATCTGCTCTTTGGGTGATGCGCATGAATGTG 294  
 Qy 349 GTCAACATGATTTAGGACTACAGATTGATTAATGATTTGATTTGCTGCTCCATT 408  
 Db 295 GCCATCATGCTTTAGTATGATGATGATGCTGCTGATGATGATTTGCTTATTTGCTCAT 354  
 Qy 409 CGGCTTCCCAACCCCGATTTCTTGTGAATATATAGCAAGAAATCAGGACGCAACA 468  
 Db 355 CTGACCTTGTGTTCTATTTTCAATGAATAATATAGCATGCGCCGACCATCTTAACA 414  
 Qy 469 CAAATTCATGATAGATGATGATTTTACATTCCTTAAACGTATGATGAAAGTCAAGATT 528  
 Db 415 TAGGATCTCTGACGAGAGAGATGTTGTCGCCGAATCAAAATCGAAATTTTCATGCT 474  
 Qy 529 ATTCGAACTTTTACATTCACATCCCGGCGAGTGTTCATTTGTTGCTTACTT 588  
 Db 475 ATTCGAACTTTTACATTCACATCCCGGCGAGTGTTCATTTGTTGCTTACTT 534  
 Qy 589 TAGGATTTCCGTATTTACTCTTAACTAATATCTGGGCAAGAAATPAGGAGTTTGCA 648  
 Db 535 TTGCTGCGCTTATTTACTTACTTCAATGCTCTGTAACCTTACGATGCTTGTGCTT 594  
 Qy 649 ACCACTTTGATCCCATGATGATGATTTTCAACGATGATGATGATGATGATTTGCTAT 708  
 Db 595 GCCATTTATGATTCCTATGCGCCAAATTTTCCGAAAGAGAGCTTCAATTTACATG 654  
 Qy 709 CCGATTTGATGCTTCTGCTGATTTTATGATCAATCAATCTTGTAGACAGCAAAAGGG 768  
 Db 655 CTGACCTCGAATCTTTGCCACAAAGTTTGCTTTATCAGGCTTACATGCAAAAGGGT 714  
 Qy 769 CAGTTGGGTATATCAATGATGATGATTTTCAAGATGATGATGATGATGATTTGCTT 828  
 Db 715 TGGCTGGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774  
 Qy 829 TGATCACAATTTTGCACACACCATCTCTCACTCCCTCATTAATGATTTCAACGATGA 888  
 Db 775 TGATCACAATTTTGCACACACCATCTCTCACTCCCTCATTAATGATTTCAACGATGA 834  
 Qy 889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGAT 948  
 Db 835 ATTGCTCCGGGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894  
 Qy 949 TCCACAGCTTACACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008  
 Db 895 TCCATTAATTTGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 954  
 Qy 1009 ATGCAAGAGAGCAAGGATCAATCAAGCAGTGTGGGAGTATGATTAATAATCGACA 1068  
 Db 955 ATGCAATGAGGCGCATTAACATCAAGCCTTAATATGATGATTAACCGGATATGATG 1014  
 Qy 1069 GGAATCCATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1128  
 Db 1015 GTACCCCATTTTACAGGCAATTTGAGAGGAGGCAAGAGATGATGATGATGATGATGAT 1074  
 Qy 1129 ATGAGATGAGGAGCAAGAGTGTGTTCTGTATCAACAAATGATTAATCAAAAGGTCTA 1188  
 Db 1075 ATGAGAGGCTCTTACACAGGCTTTCTGTATCAACAAATGATTAATCAAAAGGTCTA 1134  
 Qy 1189 TGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242  
 Db 1135 TGTAGCCGTTCTTTAAGAGAAATTAAGAAAGAAATGTGTGTAGTGAAT 1194  
 Qy 1243 AAATTATCATTAAGAGAAAAAAA 1270  
 Db 1195 GTGTTCTTAATAAGAGGCAAAAAAAA 1222

RESULT 14

US-08-819-037-43  
 ; Sequence 43, Application US/08819037  
 ; Patent No. 6028248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOMERVILLE, CHRIS



APPLICANT: VAN DE LOO, FRANK  
 TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/819,037  
 FILING DATE: 19-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/320,982  
 FILING DATE: 11-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/314,596  
 FILING DATE: 26-SEP-1994  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1222 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-819-037-43

Query Match 33.6%; Score 432.4; DB 3; Length 1222;  
 Best Local Similarity 61.3%; Pred.No. 2.8e-115;  
 Matches 716; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

109 ATCCAGCGTTCAGCTTAAGCATCTGAAGAAAGGATCCCACTTCCTTTGAGCAT 168  
 55 AGCCCTCTTTCACCTTGCTGACCTCAAGAGGACATCCCACTTCCTTTGAGCAT 114  
 169 CTGTCATCCGCTCATCTACTATGTGTCATGATCTCATGTTGCTTCTTACT 228  
 115 CTTTGGCGCTCATCTCTCATGTTGCTTGAATGCTGTTAAGTTTCTTTTACT 174  
 229 ACCTTGCAACACGCTATATCTCTTATCTCTACACCTCTGCTTACCTAGCATGCGCG 288  
 175 CGATCGCACCACTTCTTCCCTTACATCTCTTCCGCTCTCGATGCTGCTGCG 234  
 289 TTTACTGTTTTCAGCTGATCTCTCTACCGGCTCTGCTGATCGGTACGAATGTG 348  
 235 TTTACTGCTCTTCCAGGCTGATCTCTCACTGCTCTTGGGCTATCGGCATGAATGTG 294  
 349 GTCAACGATTTAGGACATCAACGATGATGATGATGATGATGATGATGATGATGATGAT 408  
 295 GCATCATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354  
 409 CGGCTCTCTACCCCGTATTTCTTGGAAATATAGCAGAGAAATACCAACGCAACA 468  
 355 CTGCACTTCTGCTTCATATTTTTCATGAAATATAGCAGAGAAATACCAACGCAACA 414  
 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
 415 TAGATCTCTGACGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
 529 ATTCAAACTTCTTAAACATCAACGAGGAGATGATGATGATGATGATGATGATGATGATGAT 588  
 475 ATTCTAGTACTCAACACCCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 534  
 589 TAGATTTCCGTTATACCTCTTAAATATCTGCGGCAAGAAATACGAGGAGGTTTGCCA 648

535 TTGCGCGCTTATATCTTACCTTCAATGCTCTGATGACCTTACGATGCTTTGCTT 594  
 649 ACCACTTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
 595 GCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654  
 709 CGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768  
 655 CTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714  
 769 CAGCTTGGATATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
 715 TGCGTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774  
 829 TGATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 888  
 775 TGATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834  
 889 ACTGATCAAAAGGCGCTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 948  
 835 ATTGCTCCGGGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894  
 949 TCCAGACGTTTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008  
 895 TCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954  
 1009 ATGCAAGGAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068  
 955 ATGCAAGGAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014  
 1069 GCACTCAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128  
 1015 GTACCCATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074  
 1129 ATGAGATGAGGACACAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188  
 1075 ATGAGAGAGCTCTTACCAAGGCTTGTGATCGGACCAAGATATTAAGGATGATGATGATGAT 1134  
 1189 TGTCAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242  
 1135 TGTAGCTGTTTCTTAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194  
 1243 AAATATCATTAAGCAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270  
 1195 GTGTTCTAATTAAGAGCAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222

RESULT 15  
 US-09-045-940-43  
 Sequence 43, Application US/09045940  
 Patent No. 643350  
 GENERAL INFORMATION:  
 APPLICANT: SOMERVILLE, CHRIS  
 TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO  
 TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/045,940  
 FILING DATE: 23-MAR-1998  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/320,982  
FILING DATE: 11-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/314,596  
FILING DATE: 26-SEP-1994  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1222 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-045-940-43

Query Match 33.6%; Score 432.4; DB 4; Length 1222;  
Best Local Similarity 61.3%; Pred. No. 2.8e-115;  
Matches 716; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

QY 109 ATCCACCGTTACGTTAAGCATCTGAAGAAAGCATTCCTACCCATTGCTTTGAGCAT 168  
DB 55 AGCTCCCTTTCACCTTGSTGACCTCAAGAGGCAATCCACCCATTGCTTTGAGCAT 114  
QY 169 CTGTCATCCGGTCACTCATCTATGTTGTTCAATGTCATTTGCTTATGCTTCTACT 228  
DB 115 CTTTTGCGCTCATCTCTCATGTTGCTTAAGTCTGCTTAAGTTTCTTTTCTACT 174  
QY 229 ACCTTGCAACACGATATATCCCTTATTCCTAACCTCTGCTTACCTAGCATGGCCCG 288  
DB 175 CGATCGCACCACTCTTCCCTTAACATCTTTCGCGCTCTCGATATGCTTGGCTGG 234  
QY 289 TTTACTGCTTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTCACTGGTCAAGATGTG 348  
DB 235 TTTACTGCTCTTCCAGGCTGCAATCTCAGTGTCTTTGGTCACTGGCATGATGTG 294  
QY 349 GTCAACATGATTAAGGAGTACCAAGTATGATGATGATGATGATGATGATGATGATGAT 408  
DB 295 GCCATCATCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354  
QY 409 CGGCTCTCCACCCCGTATTTCTTTGAAATATAGCCACAGAAATCACCAAGCCCAACA 468  
DB 355 CTGACCTCTGCTTCATATTTTTCATAGAAATATAGCCATCGCCGACCATTTCTAACA 414  
QY 469 CAATTCATCTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
DB 415 TAGATCTCTGAGGAGACCAAGTGTCTCCGAAATCAAAAGTCGAAATTTTCATGAT 474  
QY 529 ATTCAAACTTCTTAACATCAACCCGCGAGTGTCACTTGTGTTGCTTGAAT 588  
DB 475 ATTCTAAGTACTCAAAACACCGGAGTCAAGTTTTCACACTTGTCTGCAAGCTCTCC 534  
QY 589 TAGATTTCCGTTATACCTCTTAATTAATCTCGGCGAAGAAATACGGAAGTTTGCA 648  
DB 535 TTGGCTGGCTTTTATTAAGTCTTAATGTCCTGTAACCTTAAGATCGCTTGTCTT 594  
QY 649 ACCACTTTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
DB 595 GCCATTTAATGATCCATGAGCCCAATATTTTCGAAAGAAAGGCTTCAATTTACATYG 654  
QY 709 CCGATTTGCTCTGCTGCTGATTTTATGCAATCAAGCTTCTGTAGCAGAAAGGGG 768  
DB 655 CTGACCTCGAATCTTTTCCACAGCTTTGCTTTTATCAGGCTACAAATGCGAAGGGGT 714  
QY 769 CAGCTTGGGTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
DB 715 TGGCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774  
QY 829 TGATCAATATTTGACACCAACCATCTCTCACTCTCATATGATTAACCAAGATGA 888  
DB 775 TGATCAATATTTGACACCAACCATCTCTCACTCTCATATGATTAACCAAGATGA 834  
QY 889 ACTGATGAAGGGGCTTATCAATCATGATGATGATGATGATGATGATGATGATGATGAT 948

DB 835 ATTGGCTCCGGGAGCAATGTGATCTGTGATAGATTAATGGGGTGTGTAATAAGTAT 894  
QY 949 TCCACGAGTTTACACACTACCTCTTGATCATTTGATCTCATATTTCACTTATC 1008  
DB 895 TCCATTAACATTTGACACACTATGATCTCATCTCTTTGCTTACAGTGCACATTAAC 954  
QY 1009 ATGCAAGGAAGCAAGGATGATCAAGCCAGTGTGGGAGGATGATTAATAATCGACA 1068  
DB 955 ATGCAATGAGGCCACTTAAGCAATCAAGCTTATATGAGTATTAACCGGTATGATG 1014  
QY 1069 GGACTCAATTTTCAAGCAATGATATAGAGGCTTAAGATGATCATATCGAGCCG 1128  
DB 1015 GTACCCATTTTACAGGCAATGATGAGGAGGCAAGAGATGCTTGTGCTGACAGCCAG 1074  
QY 1129 ATGAGATGAGGACACAAAGGTGTCTTGTGTGTCACAGATGATTAACAAAAGCTGA 1188  
DB 1075 ATGAGAGAGCTCTTACACAAAGGCTTTTCTGTACCGAACAAGATTAATAAAGTGA 1134  
QY 1189 TGTCAATGCAATTTGATGCTTAATTAAGTTGTTA-----ACTTGTATCCGATAT 1242  
DB 1135 TGTAGCTGTTTCTTTAAGAGAGTAAATTAAGACCAAGAGATGTGTGTATGAT 1194  
QY 1243 AAATATCATTAAGAGAAAAA 1270  
DB 1195 GTGTTCTAATAAGAGCAAAAAA 1222

Search completed: June 23, 2004, 14:45:08  
Job time : 93 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 14:00:28 ; Search time 454 Seconds  
(without alignments)  
12966.299 Million cell updates/sec

Title: US-10-069-772-1

Perfect score: 1285  
Sequence: 1 aaaagctcactctctctgta.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA: \*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715.8	55.7	1358	9 US-09-981-124-1	Sequence 1, Appl1
2	705.4	54.9	1309	9 US-09-981-124-3	Sequence 3, Appl1
3	681	53.0	1199	9 US-09-981-124-19	Sequence 19, Appl1
4	484.4	37.7	1566	13 US-10-425-114-14778	Sequence 14778, A
5	484.4	37.7	2931	13 US-10-424-599-123945	Sequence 123945, A
6	484.4	37.7	6220	15 US-10-465-800-3	Sequence 3, Appl1
7	484.4	37.7	6220	15 US-10-176-149-3	Sequence 3, Appl1
8	481.2	37.4	1457	13 US-10-425-114-12782	Sequence 5, Appl1
9	445.8	34.7	1422	9 US-09-837-751-5	Sequence 3, Appl1
10	444.8	34.6	1411	9 US-09-852-399-3	Sequence 3, Appl1
11	436.8	34.0	1411	9 US-09-837-751-3	Sequence 5, Appl1
12	434.2	33.8	1155	16 US-10-330-775-5	Sequence 9, Appl1
13	431	33.5	1155	9 US-09-995-297-9	Sequence 9, Appl1
14	431	33.5	1155	10 US-09-771-904-9	Sequence 9, Appl1

15	431	33.5	1155	17 US-10-715-100-9	Sequence 9, Appl1
16	429.4	33.4	1155	9 US-09-995-297-11	Sequence 11, Appl1
17	429.4	33.4	1155	10 US-09-771-904-11	Sequence 11, Appl1
18	429.4	33.4	1155	17 US-10-715-100-11	Sequence 11, Appl1
19	427.8	33.3	1155	9 US-09-995-297-13	Sequence 13, Appl1
20	427.8	33.3	1155	10 US-09-771-904-13	Sequence 13, Appl1
21	427.8	33.3	1155	17 US-10-715-100-13	Sequence 13, Appl1
22	426.8	33.2	1164	15 US-10-185-578-1	Sequence 15, Appl1
23	426.2	33.2	1155	9 US-09-995-297-15	Sequence 15, Appl1
24	426.2	33.2	1155	9 US-09-995-297-17	Sequence 15, Appl1
25	426.2	33.2	1155	10 US-09-771-904-15	Sequence 15, Appl1
26	426.2	33.2	1155	10 US-10-435-521-1	Sequence 15, Appl1
27	426.2	33.2	1155	17 US-10-715-100-15	Sequence 15, Appl1
28	426.2	33.2	1155	17 US-10-715-100-17	Sequence 17, Appl1
29	425.2	33.1	1155	9 US-09-995-297-1	Sequence 1, Appl1
30	425.2	33.1	1155	10 US-09-771-904-1	Sequence 1, Appl1
31	425.2	33.1	1155	16 US-10-435-521-1	Sequence 1, Appl1
32	425.2	33.1	1155	17 US-10-715-100-1	Sequence 1, Appl1
33	424.6	33.0	1155	9 US-09-995-297-5	Sequence 5, Appl1
34	424.6	33.0	1155	10 US-09-771-904-5	Sequence 5, Appl1
35	424.6	33.0	1155	16 US-10-435-521-5	Sequence 5, Appl1
36	424.6	33.0	1155	17 US-10-715-100-5	Sequence 5, Appl1
37	424.6	33.0	1155	16 US-10-330-775-3	Sequence 3, Appl1
38	423	32.9	1155	9 US-09-995-297-7	Sequence 7, Appl1
39	423	32.9	1155	10 US-09-771-904-7	Sequence 7, Appl1
40	423	32.9	1155	16 US-10-435-521-3	Sequence 3, Appl1
41	423	32.9	1155	17 US-10-715-100-7	Sequence 3, Appl1
42	422	32.8	1155	9 US-09-995-297-3	Sequence 3, Appl1
43	422	32.8	1155	10 US-09-771-904-3	Sequence 3, Appl1
44	422	32.8	1155	17 US-10-715-100-3	Sequence 3, Appl1
45	411	32.0	1357	17 US-10-419-865-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-981-124-1  
Sequence 1, Application US/09981124  
Patent No. US20020166144A1  
GENERAL INFORMATION:  
APPLICANT: Green, Allan  
APPLICANT: Singh, Surinder  
APPLICANT: Lemhan, Marit  
APPLICANT: Skymne, Sten  
TITLE OR INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
FILE REFERENCE: 26-98A  
CURRENT APPLICATION NUMBER: US/09/981.124  
CURRENT FILING DATE: 2001-10-17  
PRIOR APPLICATION NUMBER: US 09/059769  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/043706  
PRIOR FILING DATE: 1997-04-16  
PRIOR APPLICATION NUMBER: AU P06223  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: AU P06226  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: US 60/050403  
PRIOR FILING DATE: 1997-06-20  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1358  
TYPE: DNA  
ORGANISM: Crepis palaestina  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (30)..(1151)  
OTHER INFORMATION:  
US-09-981-124-1  
Query Match 55.7%; Score 715.8; DB 9; Length 1358;

Best Local Similarity 78.2%; Pred. No. 2,5e-184;  
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;

```

Qy 29 ATATATCAACAACATGGGTGCTGTGTGCGATGTCGATCCATCTGAGGGAAGAAACAT 88
Db 17 ATCATTTATCAACATGGGTGCGGGGTG-----TGTGTGACATCGGAAATTCGCT 70
Qy 89 CCTTGAACGTGTGCCAGTCGATCC--ACCGTTCAGTTAAGCGATCTGAAAGAACGAT 145
Db 71 CATGAACGTGTCTCATGTGATCCAGTAACCTTCTCATGTAGTGAATTGAAGCAAGCAAT 130
Qy 146 TCCATACCATGCTTTGAGCATCTGTCATCCGGTCATCATATATGTTTTCATGATCT 205
Db 131 CCTCCCATGCTTCCAGAGATCTGATATCCGCTCATCTTACTATATGTTTCAAGATCT 190
Qy 206 CATTTGTCCTATGCTTCTTACTACTCTGCAAAACAGTATATCCCTTTATTCCTACACC 265
Db 191 CATTTATGCTCAATCTTCTTCTCTGTCACCAACAGATATCTCTACTCTTCTCTACGAT 250
Qy 266 TCTGGCTTACCTAGCATGGCCGTTTACTGTGTTTGTCAAGCTAGCATCTCACCGGCT 325
Db 251 TCTAGCCTTACTAGCTTGGCCGCTTACTGTGTCTGATCAAGCTAGCGTCTCACGCGCT 310
Qy 326 CTGGGTATCGGTACGAGATGTGTACACAGCATTTGAGCACTACAGTATGATGATGA 385
Db 311 ATGATATCTCGCCACGATGTGTGACACATGCTTTGACAACTACATGATGTTGACGA 370
Qy 386 CATTTGATGATTCGTGCTCATTCGGCTCTCTCCACCCCGATTTCTTGGAAATATAG 445
Db 371 CACTGTGGCTTCAATCTCTCACTATTTCTCTCAACCCCGATTTCTTGGAAATATAG 430
Qy 446 CCACAGGATACCAACGCCAACAAATTAATCTAGATAGATGAATTAATCTCTTAA 505
Db 431 TCACCGGATACCAATCTCAACACAAAGTTGATGATGATGAATTAATCTCTTAA 490
Qy 506 ACGTAAGTCGAAGGTCAGATTTATTCGAACTCTTAAACATCCACCGGCGGAGTGT 565
Db 491 AAGCAAGTCGAAGTCGCGGATCTATTAACCTTAAACCAACCACTGATCGCGTGT 550
Qy 566 CACTTGTGCTTGTGCTGATCTTATGATTTCCGTTATCTCTTAAATATCTCCGG 625
Db 551 GGTTTTATTTATCAATGTTTCAACCTAGATTTCTTTATATCTCTTGAACAAATATTCGG 610
Qy 626 CAAGAAATACGAGAGGTTTGCACACCACTTGTATCCATGATGATCAATTTTCAAGATCG 685
Db 611 CAAGAAATACGAGAGGTTTGCACACCACTTGTATCCATGATGATCAATTTTCAAGAAAG 670
Qy 686 TGAAGCGCTTCAAGTTTGTCTATCCGATTTGCGTCTTCTGATATTTATGCAATCAA 745
Db 671 TGACGCGTTTGAAGCTTCTTTCGATCTTGTCTTTCCTGCTTATGGAATTTAA 730
Qy 746 GCTTCTTGTAGCAGCAAAAGGGGAGCTTGGGTATCAACATGTAACGATTTCCAGTACT 805
Db 731 AGTTGCTGTACAAATTAAGAGAGCTGTGGTGAAGCGATGATGATGATTTCCGATTT 790
Qy 806 AGGTGTAAAGCGTGTCTTCTGTTTGTATCAATTTTGGACACACCACTCTCTCACTCC 865
Db 791 AGGGGTATTTACTTTTTCGATGTGATCACTTCTTGGACACACCACTCACTGCTGCC 850
Qy 866 TCAATTATGATTAACCCGAATGGAATGGAATGGAAGGCGCTTATCAACAAATCGATGAGGA 925
Db 851 TCATTATGATTAACCTGATGGAATGGAATGGAAGGCGCTTGTACGAATCGATGAGGA 910
Qy 926 TTTGCGGTTCTGATCGGGTTTTCACAGATTTACACACTCACTCACTGATCATTT 985
Db 911 CTTTGGATCTCTGATTAAGTGTTCATGATGATGATGATGATGATGATGATGATGAT 970
Qy 986 GATCTCATACATTCACATTAATCATGCAAGAAAGCAAGGATGATCAAGCAAGTGT 1045
Db 971 GTTTTCAATACATTCACACTATCATGCAAGAAAGGAGGATGATCAAGCAAGTGT 1030
Qy 1046 GGGGAGATCATTAATAATGACAGGATCTCAATTTTCAAGCATGATTAAGAGGCTTA 1105

```

```

Db 1031 GGGGAGCTTTATATGATCGACAGACTCCATTTTAAAGCAATGTGAGAGAGGCGAG 1090
Qy 1106 GGAATGATCTTACATCGAGCCCGATGAGATGAGGACACAAAGTGTGTTCTGATCCA 1165
Db 1091 GGAGTGATGATCATCGAGCC-----TGATGCAAGGTCAAAAGTGTATTTGATATCA 1144
Qy 1166 CAAGATGTAATCAA 1180
Db 1145 TAAATGTGATCATTA 1159

```

RESULT 2  
US-09-981-124-3  
Sequence 3, Application US/09981124  
Patent No. US2002016144A1  
GENERAL INFORMATION:  
APPLICANT: Green, Allan  
APPLICANT: Singh, Surinder  
APPLICANT: Lemman, Marit  
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
FILE REFERENCE: 26-98A  
CURRENT APPLICATION NUMBER: US/09/981,124  
PRIOR FILING DATE: 2001-10-17  
PRIOR APPLICATION NUMBER: US 09/059769  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: US 60/043706  
PRIOR FILING DATE: 1997-04-16  
PRIOR APPLICATION NUMBER: AU P06223  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: AU P06226  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: US 60/050403  
PRIOR FILING DATE: 1997-06-20  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 1309  
TYPE: DNA  
ORGANISM: *Crepis sp.*  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (937)..(937)  
OTHER INFORMATION: N is any nucleotide residue  
NAME/KEY: CDS  
LOCATION: (126)..(1147)  
OTHER INFORMATION:  
NAME/KEY: misc.feature  
LOCATION: (901)..(901)  
OTHER INFORMATION: N is any nucleotide residue  
US-09-981-124-3

Query Match 54.9%; Score 705.4; DB 9; Length 1309;  
Best Local Similarity 78.6%; Pred. No. 1.7e-181;  
Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;

```

Qy 77 GGGAAAAAATCCTTGAACGTGTGACATGATCC--ACCGTTCAGTTAAGCGATCT 133
Db 52 GGAAGAGCGGTATGAGAGCTGTCTGATGATGATGATGATGATGATGATGATGAT 111
Qy 134 GAAGAAAGCAATTCCTTCAACCTTGTGAGCATGTGTCAATCCGTCATCATATGT 193
Db 112 GAAGCAAGCAATTCCTTCAACCTTGTGAGCATGTGTCAATCCGTCATCATATGT 171
Qy 194 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
Db 172 TGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
Qy 254 TATTCCTACACCTGTGCTTACCTAGCATGGCCGTTTACTGTTTGTCAAGTATGAT 313
Db 232 TCTCTCTATCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 291

```

QY 314 CCTCAGCGGCGCTCTGGGTCATTCGGTCAAGAAATGAGTACCATGATTTAGAGCATAC 373  
 Db 292 CCTCACTGGGTTATGATATCTCGGCGCAATGATGATCAACATGCTATAGCAACTAC 351  
 QY 374 GTTATGATGACATTTGTGATTTGATGCTCCATTCGGCTCTCTCAACCCGTAATTTCTC 433  
 Db 352 ATGGGTTACGACACTGTGGGCTTCATCATCTATTCTTCGACACCCGTAATTTCTC 411  
 QY 434 TTGGAATATATGCCACAGGAATCACACGCCAACACAAATTCACCTCGATTAAGATGAGT 493  
 Db 412 TTGGAAATACAGTCACCGGAATCACCATTCCAACCAAGTTGATGATTAACGATGAGT 471  
 QY 494 TTACATTCCTAAAGTATGAGTGAAGTCAAGTATTAATCCAACTTTCAATCAATCCACC 553  
 Db 472 TTACATTCGAAAGCAAGTCAAACTCAAGGATATCATTAATCTTTAAACCAACCCACC 531  
 QY 554 CGGGGAGTGTTCACCTTGATGTTCCGTTGACTTTAGAGATTCGGTATACCTTTAAC 613  
 Db 532 TGGTGCATCTGTGGTTTGTGTTATCATGTTCAACCTTAGATTTCTTTATACCTTTGAC 591  
 QY 614 TAAATCTCGGGCAAGAAATACCGGAGGTTTGCACACCACTTGAATCCATGATCCAT 673  
 Db 592 AAATATTTCCGGCAAGAAATACGATAGGTTTGCACACCACTTGCACCCCATGAGTCCAT 651  
 QY 674 TTTCAACGATGTGAACCGCTTCAAGTTTGTGATTCGATTTCCGATCTTCTCGCTGATTT 733  
 Db 652 TTTCAAAACGATGACGGGTTTCAAGTCTTCTTCCGATCTTGTCTTCTGCTGATTT 711  
 QY 734 TTATGATCATCAAGCTTCTTGTAGCAGCAAAAGGGGACCTTGGGATCAACATGATAGC 793  
 Db 712 TTATGATATTAAGTGTGCTGTAGCAAAATAAAGAGCTGCTTGGTGGCGGTGATGTATGG 771  
 QY 794 AATTCAGTACTAGGTGTGAAGCGGTGTTCTTGTTGATCAATATTTGACACACACCA 853  
 Db 772 AGTTCGGGTCTAGGCGTATTTTACCTTTTCGATGTGATCAAGTCTTACACACACCA 831  
 QY 854 TCTCTCACTCCCTCATTTATGATTCACCGAATGGAATCGATCAAAAGCGCTTATCAAC 913  
 Db 832 TCAGTCGTGCGCTCATATGATTCAACTGAATGGAACGATCAAGAGGGCTTTGTCTAGC 891  
 QY 914 AATCGATAGGGAATTCGGGTTCCGGAATCGAGTTTTCACAGACGTTACACACCTCAGCT 973  
 Db 892 AATGATATGNACTTTGGGTTCTGGAATAGTGTTCATGATGTMACACACCTCAGCT 951  
 QY 974 CTTGATCATTTGATCTCATATTCATTCACATTTATCATGCAAAAGGACAAAGGATGCAAT 1033  
 Db 952 CATGATCATTTGTTTTCATATTCATTCACACATATCATGCAAAAGGACAAAGGATGCAAT 1011  
 QY 1034 CAAGCAGTGTGGGCGAGTACTATAAATGACACAGACTCCAAATTTTCAAGCAATGTA 1093  
 Db 1012 CAACCCGACTTGGGCGACTTTTATATGATGATGAGTCAATTTTAAAGCAATGTG 1071  
 QY 1094 TAGAGAGCTTAAGAAATGATCTCATTCGAGACCCGATGAGATGACGACCAAAAGGTGT 1153  
 Db 1072 GAGAGAGGCGAGGAAATGATCATGATGAGCC-----TGATGACAGCTCAAAAGGTGT 1125  
 QY 1154 GTTCTGTACCACAAGATGATCAAA 1180  
 Db 1126 TTATTTGATCATTAATTTGTGATCATTA 1152  
 RESULT 3  
 US-09-981-124-19  
 : Sequence 19, Application US/09981124  
 : Patent No. US2002016614A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Green, Allan  
 : APPLICANT: Singh, Surinder  
 : APPLICANT: Lemman, Marc  
 : APPLICANT: Steyne, Sten  
 : TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MO  
 : FILE REFERENCE: 26-98A

QY	107	CGATCCACGGTTCACGTTAAGGACATCTAAGAAAGCGATTCCTACCCATGCTTGAGCG	166
DB	115	CAAACACCATTTCTCTGGCTGATCTTTAGAAAGCCATACCAACCCACTGTTCCAAAG	174
QY	167	ATCTGTCACTCCGGTCACTAATAATGTTGTCATGATCTCATTTGTGCTATGTCCTTA	226
DB	175	ATCCCTCCGTTCACTTAATAAGTGGTTCATGATCTCGTACGCTAAGCTTACGTTTAA	234
QY	227	CTACTTGGAAACACGTAATATCCCTTATTCTTACACCTCTGGCTTAC--CTAGCATG	283
DB	235	CTATCTCCGCAACATACATACATCCCTCTTCCCTCCCTCTTGGCTTAAATTAAGCTTG	294
QY	284	GCCGTTTACGTGTTTGTCAAGTAGATCCTCAACGGGCGCTCGGGTCATGGGTCAACGA	343
DB	295	GCCCTTACGTGTTCTGTCAAGGAGATCCTCAACGGGCTGTGGTCAATCGTATCA	354
QY	344	ATGTGTCAACATGATTTAGACGACTACAGTGTGATGATGATGATGATGATGATGATG	403
DB	355	ATGTGTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	414
QY	404	CAATTGGCTCTCTCAACCCCGTATTTCTTGGAAATATAGCCACAGAAATCACACGC	463
DB	415	TCAGTCTGCACTTCAACCCCTTATTTCTTGGAAATATAGCTACCGTAATCACATGCG	474
QY	464	CAACCAAAATTCATCTGATTAACGATGAAGTTTACTTCTTAAGATAAGTGAAGTCA	523
DB	475	CAACCAAAATTCATCTGATTAACGATGAAGTTTACTTCTTAAGATAAGTGAAGTCA	534
QY	524	GATTATTTCAAACTTTTAAACAATCAACCGGAGGATGTTTCACTTTGTTGTTGCT	583
DB	535	GATTATTTCAAAATTCCTTAACAACCCCTCTGCTGCTGCTTTTCACTTTGCTTTCA	594
QY	584	GACTTAAAGATTTCCGTTTAACTCTTAACTAATATCTCGGCAAGAAATACGGAAGTT	643
DB	595	GATCGTGGGTTTCTCTTAACTCTTAACTAATATCTCGGCAAGAAATACGGAAGTT	654
QY	644	TGCCAACCACTTTGATCCCATGAAGTCCAAATTTTCAAGATGTTGAAGCGGTTCAAGTTT	703
DB	655	TGCCAACCACTTTGATCCCATGAAGTCCCAATTTTCAAGATGTTGAAGCGGTTCAAGTTT	714
QY	704	GCTATCCGATTTGGGTTCTTCTGCTGATTTTAAATCAAGCTTTCTTGATGACAA	763
DB	715	GCTTTCTGATTTTGTCTCATAGCAAGTTGCTTACGTTGTTGTCAAGCTGTAAGTCTTA	774
QY	764	AGGGGACGCTTGGGTAATCAATGTACGAATTCAGTAAGTGTAAAGCTTCTT	823



LENGTH: 2931  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_8292C.1  
US-10-424-599-123945

Query Match 37.7%; Score 484.4; DB 13; Length 2931;  
Best Local Similarity 65.8%; Pred. No. 5.2e-121;  
Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

```
QY 109 ATCCACCGTCAAGTTAGCGATCTGAGAGAAAGCAATTCACCACTGCTTGAGCGAT 168
DB 1631 AACCTCCATTTAGTCTAGCCAAATCAAGAGGTATCTCACCCTCACTGTTCCAGCGTT 1572
QY 169 CTGTCATCCGGTCAATCATATATGTTGTTGTCATGATCTCATTTTGTGCTTACT 228
DB 1571 CTGTTTCCGTCATCTCTCTATGTTGTTAGACCTCAACATAGCTTCTGCTTAT 1512
QY 229 ACCCTGCAAAACAGTATATCCCTTATCTTACACCTGCTTACCTAGCATGAGCCCG 288
DB 1511 ATGTTGCCACCATTAATCTTCCAGCTCTCTCCAGCCCTCTCTTTCTTGGCATGCGCA 1452
QY 289 TTTACTGTTTGTCAAGTACATCTTCAACCGGCTCTGGGTCAATCGGTCAAGATGTG 348
DB 1451 TCTACTGGGCTGTCCAAAGGTTGCATCTTACTGAGTTGGGTCAATGGCCATGAGTGTG 1392
QY 349 GTACACATGSCATTTAGCGCATACAGTTGATGATGACATTTGGATTCGCTCCAT 408
DB 1391 GGCACATGATCATAGTACATACAGTTGCTGATGATATTTGGCTTGTCTTCCACT 1332
QY 409 CGGCTCTCTCAACCCCGTATTTCTCTGGAATATATAGCAGATCCACAGCCACA 468
DB 1331 CCGGCTCTCTAGTCCCATATCTTTATGGAATATAGCCATGCGGTACACCTCCACA 1272
QY 469 CAATTTCACTCGATTAACGATGAAGTTTACATCTTAAACGTAAGTGAAGTCAAGATT 528
DB 1271 CTGTTCTCTGAGGGGATGAGTATTTGTGCCAAAGAGATCTGATCAAGTGT 1212
QY 529 ATTCAAACCTCTTAAACATCCACCGGCGAGTGTCACTTGTGTTGCGTTGACT 588
DB 1211 ACTTAATAATCTTAAACATCTCTCAGGAGAGTCTCACTTCTGTCACCCCTCACAC 1152
QY 589 TAGGATTTCCGTTATACCTCTTAACATAATCTCGGCGCAAGAAATACGGAGATTTGCCA 648
DB 1151 TTGTTGGCCCTTGTACTTGGTTAAATGTTCTGGAAGCCCTTAATGATATTTGCTT 1092
QY 649 ACCACTTTGATCCATGATGATCAATTTTCAACGATCGTGAAGCGTTCAAGTTTGTAT 708
DB 1091 GCCACTATGACCCATATGATGATCCCACTTACTGATCGTGAAGCACTTCAAAATATATAT 1032
QY 709 CGGATTTGGTCTTCTGCTGATTTTATGCAATCAAGTTTGTAGACAGAAAGGG 768
DB 1031 CAGATGCAAGAGTACTTGAAGTATGATGAGCTTTTCCGTTCCCATGGAAGAAAGAC 972
QY 769 CAGTTGGGTATCAACATGATGCAATTCAGTACTAGTATGAGTATGAGTCTTCTGTT 828
DB 971 TTGCTGGGTGGTGTGTTATGAGATTCATCTCTAGTGTCAATGATTTTGGTGT 912
QY 829 TGATCAATTTTGGACACACACCATCTCTCACTCTCATTTATGATTTCAACGAGATGGA 888
DB 911 TGATTAACATTTCTGAGACATCTCACCCCTGATGCCACATTAACCTCTCTGAGTGGG 852
QY 889 ACTGATGAAGAGCGCTTATCAACAATCGATGAGGATTTGGGGTTCCTGAATCGGGTTT 948
DB 851 ACTGTTAGAGAGACCTTTAGCAACAGTGAATGAGATTAATGAAATCTTGAACAGGTCT 792
QY 949 TCACAGAGTATACACACTCACTCTGTCATCTTTGATCTCATATTCACATTTATTC 1008
DB 791 TCATTAATATTAACACACTCACTCACTGATGACATCTTGTCTCCACATTCACATTTATTC 732
QY 1009 ATGCAAGAAAGCAAGGATGATCAAGCCAGTGTGGCGAGTACTATTAATTCACA 1068
```

```
DB 731 ATGCAATGAGGCTCAAAAGGCATTAACCACTTTTGGAGATTAATCGTTGATG 672
QY 1069 GGACTCCATTTTCAAGCAATGTATAGAGGCTAAGAAATGATCATATCGAGCCG 1128
DB 671 AGACTCCATTTTGTCAAGCAATGTATAGAGGCTAAGAAATGATTAATGATGAGCCAG 612
QY 1129 ATGAGATAGCGAGCAAAAGGTGTCTGTGTACCAAGATGTAATCA 1178
DB 611 ATCAAGATACGAGAGCAAAAGGTGATTTTGGTACACATTAATGATGTA 562
```

RESULT 6  
US-10-465-800-3  
Sequence 3, Application US/10465800  
Publication No. US20040029283A1  
GENERAL INFORMATION:  
APPLICANT: Filialetti, Joanne  
TITLE OF INVENTION: Intron Double Stranded RNA Constructs and Uses thereof  
FILE REFERENCE: 16517.266  
CURRENT APPLICATION NUMBER: US/10/465,800  
CURRENT FILING DATE: 2003-06-20  
PRIOR APPLICATION NUMBER: US 60/390,186  
PRIOR FILING DATE: 2002-06-21  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 6220  
TYPE: DNA  
ORGANISM: Glycine max  
US-10-465-800-3

Query Match 37.7%; Score 484.4; DB 13; Length 6220;  
Best Local Similarity 65.8%; Pred. No. 8.1e-121;  
Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

```
QY 109 ATCCACCGTCAAGTTAGCGATCTGAGAGAAAGCAATTCACCACTGCTTGAGCGAT 168
DB 4816 AACCTCCATTTAGTCTAGCCAAATCAAGAGGTATCTCACCCTCACTGTTCCAGCGTT 4875
QY 169 CTGTCATCCGGTCAATCATATATGTTGTTGTCATGATCTCATTTGTCCTTACT 228
DB 4876 CTGTTTCCGTCATCTCTCTATGTTGTTTACGACTCAACATAGCTTCTGCTCTAT 4935
QY 229 ACCCTGCAAAACAGTATATCCCTTATCTTACACCTGCTTACCTAGCATGAGCCCG 288
DB 4936 ATGTTGCCACCATTAATCTTCAACCTCTTCCAGCCCTCTCTTTCTTGGATGCGCA 4995
QY 289 TTTACTGTTTGTCAAGTACATCTTCAACCGGCTCTGGGTCAATCGGTCAAGATGTG 348
DB 4996 TCTACTGGGCTGTCCAAAGTGTGATCTTACTGAGGTTGGGTCAATGCCATGAGTGTG 5055
QY 349 GTACACATGATTTAGCGCATCAACGATGATGATGATGATGATGATGATGATGATGAT 408
DB 5056 GCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5115
QY 409 CGGCTCTCTCAACCCCGTATTTCTTGGAAATATAGCAGAAATGACACAGCCACA 468
DB 5116 CCGGCTCTCTAGTCCATATCTTCAATGAAATATAGCAGAAATGACACATCTCAACA 5175
QY 469 CAATTTCACTCGATTAACGATGAAGTTTACATCTCTTAAACGTAAGTGAAGTCAAGATT 528
DB 5176 CTGTTCTCTTGAAGGGGATTAAGTATTTGCGCAAGAGCAAGATCGGTATCAAGTGT 5235
QY 529 ATTCAAACCTTTTAAACATCAACCCGGGCGAGTGTCACTTTGTGTTGTTGCTTCACTT 588
DB 5236 ACTTAATAATCTTAAACATCTCTCAGGCAAGATGCTTCACTTGTCTCAACCTCAAC 5295
QY 589 TAGGATTTCCGTTATACCTCTTAATAATATCTGGGCAAGAAATACGGAGGTTTGGCA 648
DB 5296 TTGTTGGCCCTTGTACTTGGCTTAAATGTTTCTGGAAGCCCTTAATGATGATTTGCTT 5355
QY 649 ACCACTTGAATCCATGATGATCAATTTTCAACGATCGTGAAGCGCTTCAAGTTTGTCTAT 708
```

Db 5356 GCCACTATGACCCATATGATGCTCCATTACTGATGCTGAAAGCACTTCAATATATATAT 5415  
 Qy 709 CGGATTTGCGTCTTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGACAGAAAGGGG 768  
 Db 5416 CAGATGCAAGGAGTACTTGCAAGTATGCTATGGCTTTTCGCTCTTCATGCGAAAGAGAC 5475  
 Qy 769 CAGCTTGGGTAATCAACATGTAAGCAATTTCCAGTACTAGGTGTAAGCGTGTCTTCGTTT 828  
 Db 5476 TTGCTGGGTGGTGTGTGTTATGAGAGTTCATGCTGTGATGATGATTTTGTGGTGT 5535  
 Qy 829 TGATCAATATTTTGGACCAACCCATCTCTGCACTCCCTCATATGATTTCAACCGAATGGA 888  
 Db 5536 TGATTAATTTCTTGGACATTAATCTGACCTCGATTCGCAATTAACCTTCTGTAGTGG 5595  
 Qy 889 ACTGGATCAAAAGCGCCCTTATCAACATGATGAGGATTTGGGTTCTGTAATCGGGTGT 948  
 Db 5596 ACTGGTTGAGAGCACTTTAGCAACAGTGAATAGATTAATGAAATCCGTAACAGGTCT 5655  
 Qy 949 TCCAGAGCTTACACACTGCTCTTGCATCTTATGATCTCATACATTCGACATTTATC 1008  
 Db 5656 TCCAAATTAATTAACAGACTCAATGAGCAATCACTTGTCTCCAAATGCGACATTTATC 5715  
 Qy 1009 ATGCAAGGAAGCAAGGAGTGAATCAAGCCAGTGTGGCGAGTACTATAAATGACA 1068  
 Db 5716 ATGCAATGAGGCTTCAAAAGGCAATTAACCCATTTGGAGAGTATTAAGGTTGATG 5775  
 Qy 1069 GGAATCCAAATTTTCAAGCAATGATTAAGAGGCTTAAGGAATGATCTACATCGAGCCG 1128  
 Db 5776 AGACTCCATTTGTCAAGCAATGTGAGAGGCAAGAGATGTTATTAATGAGAGCCAG 5835  
 Qy 1129 ATGAGATTAAGGAGCAAAAGGTGTCTGTGTACCACAAGATGTAATCA 1178  
 Db 5836 ATCAAGATACGAGAGCAAAAGGTGTATTTGTGTACCACAAGATGTTGTA 5885

RESULT 7

US-10-176-149-3  
 ; Sequence 3, Application US/10176149  
 ; Publication No. US20030172399A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fillat, Joanne, J.  
 ; TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of F  
 ; FILE REFERENCE: 16518.056  
 ; CURRENT APPLICATION NUMBER: US/10/176.149  
 ; PRIOR FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/151.224  
 ; PRIOR FILING DATE: 1999-08-26  
 ; PRIOR APPLICATION NUMBER: US 60/172.128  
 ; PRIOR FILING DATE: 1999-12-17  
 ; PRIOR APPLICATION NUMBER: US 09/638.508  
 ; PRIOR FILING DATE: 2000-08-11  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 6220  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 US-10-176-149-3

Query Match 37 7%; Score 484.4; DB 15; Length 6220;  
 Best Local Similarity 65.8%; Pred. No. 8.1e-121;  
 Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

Qy 109 ATCCACCGTTCAGTTAAGCGATGAGAAAGCAATTCCTTACCCATTGCTTTGAGCGAT 168  
 Db 4816 AACCTCCATTTAGTCTCAGCCAAATCAAGAGGTATTCACCTCACTGTTTCCAGCGTT 4875  
 Qy 169 CTGTATCCGCTCATATAGTATGTTGTTCATGATCTCAATGTTGCTTATGCTTCTACT 228  
 Db 4876 CTGTTTCCGCTCATCTTCTATGTTGTTTACAGCTCAACATACCTTTCGCTCTATTT 4935  
 Qy 229 ACCTTGCAAAACGATATCCCTTATTTCTTACACCTTGTGCTTAACCTAGCATGCCCCG 288

Db 4936 ATGTGCAACCCATTAATCTTCAACCTCTTCCAGCCCTCTCTCTTTCTTGGACATGCCCCA 4995  
 Qy 289 TTTACTGGTTTGTGACGTAAGCAATCCATCCAGCCCTCTGAGTATCGGTACAGATGTC 348  
 Db 4996 TCTACTGGCTGTGCAAGGTGTGATTCCTTACTGAGATTTGGGTATTTGCCATGATGTG 5055  
 Qy 349 GTCAACATGATTTAGGCACTACAGATTTGATGATGATTTGATTTGGATTTGCTCTCAT 408  
 Db 5056 GCCACATGCAATGATGATCACTACAGATTTGATGATTTGATTTGGCTTGTCTTCACT 5115  
 Qy 409 CGGCTTCCCAACCCGATTTCTTGGAAATATPAGCAAGGAATACCAAGCCAGCA 468  
 Db 5116 CCGGCTCTCTAGTCCATCTTTTCAATGAAATACAGCCATCGCGTCACTTCCATCA 5175  
 Qy 469 CAATTCAGTCAATACAGTAAGTTTACATTTCTTAAACGTAACTGAAAGGTCAAGATTT 528  
 Db 5176 CTGGTTCTCTTGAAGGGGATGAAGATTTTGCCAAAGCAAGTCTGTATCAAGTGT 5235  
 Qy 529 ATTCGAACTTTTAAATCAATCAACCCGAGAGTGTCACTTTGGTGTGTTGATTT 588  
 Db 5236 ACTCTAAATACCTTAACATCTCCAGGCAAGTCTCACTCTGTGTCAACCTCAAC 5295  
 Qy 589 TAGGATTTCCGTTTAACTCTTAATATCTGCGGCAAGAAATPACGGAGTTTGCA 648  
 Db 5296 TTGGTTGCGCTTGTACTTGGCTTTAAATGTTTCTGAAAGCCCTTATGATGATTTGCTT 5355  
 Qy 649 ACCACTTGTATCCATGATGATCCAAATTTTCAACGATGGAACGGCTTCAAGTTTGCTAT 708  
 Db 5356 GCCACTATGACCCATTAAGTGTCCATTTACTGTATGCGAAGCACTTCAATATATATAT 5415  
 Qy 709 CCGATTTGCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTAGACAGCAAAAGGGG 768  
 Db 5416 CAGATGCAAGAGTCTTGCATATGATGATGAGCTTTTCCGCTTGTCCATGCGCAAAAGGAC 5475  
 Qy 769 CAGCTGGGTAATCAACATGATGCAATTCAGTACTAGGTGTAAGCGTGTCTTCTGTT 828  
 Db 5476 TTGCTGGGTGGTGTGTGTTATGAGATTTCCATTTCTTATGATGATTTTGGTGT 5535  
 Qy 829 TGATCAATATTTGACACCAACCCATCTGCTCTCTCATTAATGATTAACCGAATGGA 888  
 Db 5536 TGATTAATTTCTTGAAGATCACTCAACCTGATTTGCCATTAACCTTCTGTAGTGG 5595  
 Qy 889 ACTGATTAAGGCGCTTATCAACATCAATGATGATTTGGGTCTGTAATGCGGTTT 948  
 Db 5596 ACTGTTGAGAGGCTTTACCAACAGTGAATGATTAAGATCTTGAACAAGGTCT 5655  
 Qy 949 TCCAGAGCTTACACACTGACGCTTGCATCTTATGATCTCAATCAATTCACATTTATC 1008  
 Db 5656 TCCATTAATTAATTAACAGACTCAATGAGCAATCACTTGTCTCCAAATGCGACATTTATC 5715  
 Qy 1009 ATGCAAGGAAGCAAGGAGTCAATCAAGCCAGTGTGGCGAGTACTATAAATGACA 1068  
 Db 5716 ATGCAATGAGGCTTCAAAAGGCAATTAACCCATTTGGAGAGTATTAAGGTTGATG 5775  
 Qy 1069 GGAATCCAAATTTTCAAGCAATGATTAAGAGGCTTAAGGAATGATCTACATCGAGCCG 1128  
 Db 5776 AGACTCCATTTGTCAAGCAATGTGAGAGGCAAGAGATGTTATTAATGAGAGCCAG 5835  
 Qy 1129 ATGAGATTAAGGAGCAAAAGGTGTCTGTGTACCACAAGATGTAATCA 1178  
 Db 5836 ATCAAGATACGAGAGCAAAAGGTGTATTTGTGTACCACAAGATGTTGTA 5885

RESULT 8

US-10-425-114-12782  
 ; Sequence 12782, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.



APPLICANT: Tabaska, Jack E  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(533)3B  
 CURRENT APPLICATION NUMBER: US/10/425,114  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 73128  
 SEQ ID NO: 12782  
 LENGTH: 1457  
 TYPE: DNA  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: 701211444\_FLI  
 US-10-425-114-12782

Query Match 37.4%; Score 481.2; DB 13; Length 1457;  
 Best Local Similarity 65.6%; Pred. No. 2,66-120; Indels 0; Gaps 0;  
 Matches 702; Conservative 0; Mismatches 368;

109 ATCCACCGTTACGTTAAGCATGAGAAAGCGATTCACCCATTGCTTGAAGCAT 168  
 112 AACCCCATTTAGTCTGACGCAAAAGAGTATTCACCTGCTTCCAGCGTT 171  
 169 CTGTGATCCGTCATCATCTATGTTGTTCAATGATCTCAATGTTGCTTACT 228  
 172 CTGTTTCCGTCATCTCTATGTTGTTACGACCTCAATAGCTTCTGCTTACT 231  
 229 ACCTTGAAACGATATCCCTTATCTTCTACACCTTGGCTTACTAGACGCGC 288  
 232 ATGTGCAACCATTAATCTTCAACCTCTCCAGCCCTCTCTTCTTGGATGCGAA 291  
 289 TTTACTGTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTCATCGGTCAAGATG 348  
 292 TCTACTGGGCTGTCAAGGTTGATCTTACTGAGGTTGGGTCATTCCTCAATG 351  
 349 GTCAACATGATTTAGGACATCAAGTTGATGATGATGATGATGATGATGATG 408  
 352 GCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411  
 409 CGGCTCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468  
 412 CGGCTCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471  
 469 CAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
 472 CTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531  
 529 ATTCCAAATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCTTACT 588  
 532 ACTCTAAATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCTTACT 591  
 589 TAGATTTCCGTTATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCT 648  
 592 TTGCTTCCGTTATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCT 651  
 649 ACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
 652 GCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711  
 709 CCGATTTCCGTTATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCT 768  
 712 CAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771  
 769 CAGCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
 772 TTGCTTCCGTTATCTTAAATCAATCAACCGGCGAGTGTCTTGTGTTGCT 831  
 829 TGATCAATTTTGAACACACCATCTCTGATCCCTCATATGATCAACCAATGA 888  
 832 TGATCAATTTTGAACACACCATCTCTGATCCCTCATATGATCAACCAATGA 891  
 889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATG 948

992 ACTGATGAGGAGGCTTTAGCAACAGTGAATGATGATGATGATGATGATGAT 951  
 949 TCCACAGCTTACACACACTGATGATGATGATGATGATGATGATGATGATGAT 1008  
 952 TCCATATATATACAGACTGATGATGATGATGATGATGATGATGATGATGAT 1011  
 1009 ATGCAAGAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1068  
 1012 ATGCAATGAGAGCTTAAAGGCAATTAATGATGATGATGATGATGATGATG 1071  
 1069 GAGCTCCAAATTTTAAAGCAATGATGATGATGATGATGATGATGATGATGAT 1128  
 1072 AGACTCCATTTTGAAGCAATGATGATGATGATGATGATGATGATGATGAT 1131  
 1129 ATGAGATGAGAGCAACAAAGTGTGTTCTGATCAACCAATGATGATGAT 1178  
 1132 ATCAAGTACAGAGCAAGAGTGTGTTCTGATCAACCAATGATGATGATGAT 1181

RESULT 9  
 US-09-837-751-5  
 Sequence 5, Application US/09837751  
 Patent No. US20020104124A1  
 GENERAL INFORMATION:  
 APPLICANT: Green, Allan  
 APPLICANT: Singh, Surinder  
 APPLICANT: Liu, Qing  
 TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
 FILE REFERENCE: 45-00  
 CURRENT APPLICATION NUMBER: US/09/837,751  
 CURRENT FILING DATE: 2001-04-18  
 PRIOR APPLICATION NUMBER: US 60/198,124  
 NUMBER OF SEQ ID NOS: 35  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 1422  
 TYPE: DNA  
 ORGANISM: Gossypium sp.  
 NAME/KEY: CDS  
 LOCATION: (98) .. (1246)  
 US-09-837-751-5

Query Match 34.7%; Score 445.8; DB 9; Length 1422;  
 Best Local Similarity 63.5%; Pred. No. 1,1e-110;  
 Matches 681; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

109 ATCCACGTTACGTTAAGCATGAGAAAGCGATTCACCCATTGCTTGAAGCAT 168  
 180 AGCCACCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 239  
 169 CTGTATCCGTCATCATCTATGTTGTTCAATGATGATGATGATGATGATGAT 228  
 240 CCGTTTAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 299  
 229 ACCTTGAAACGATATCCCTTATCTTAAATCAATCAACCGGCGAGTGTCT 288  
 300 ATGTGCGACCAATTAATCTTCTCAACCTCTCTCAAGGCTCTCTCAACG 359  
 289 TTTACTGTTTGTCAAGCTAGCATGATGATGATGATGATGATGATGATGATGAT 348  
 360 TTTATTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
 349 GTCAACATGATTTAGGACATCAAGTGTGATGATGATGATGATGATGATGAT 408  
 420 GCAACATGATTTAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 479  
 409 CGGCTCTCTCAACCGGATTTCTTGTGAAATATGACACAGAAATCAACGCA 468  
 480 CTCTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539

QY 469 CAATTCCTGATACGATGAAGTTTCAATTCCTTAAACGTAAGTCGAAGTCGAAGTTT 528  
Db 540 CCGGTTCCCTCGAAGGATGAAGTTCGTTCCCAAGAAAATCTGGTTTAAGATGAT 599  
QY 529 ATTCGAATCTTAAAGATCAACCGGCGGATGTCATCTTGGTTGGTGAAGTT 588  
Db 600 GGGCCAAACATTCACACATTCACCGGATCGGTTCTGTCAATCAACATTCACATTCACC 659  
QY 589 TAGGATTTCCGTTATACCTTTAACTAAATATCTCGGCGAAGAAATACGAGGATTCGCA 648  
Db 660 TTGGTTGGCCGCTTAACTAGCTTTCAAGTTGCGGCGGCGCTTACAGACAGGTTGCTT 719  
QY 649 ACCACTTGAATCCATGATGTCATTTTCAAGATGTCGAAGCGCTTCAAGTTTGCAT 708  
Db 720 GCCACTATGACCTTACCGCCCATATTTTCCGAGCGGGAACGACTCCAAATCTATATCT 779  
QY 709 CGGATTTGGTCTTCTGCTGATTTTATGCAATGAAGCTTCTGATACAGCAAAAGGAG 768  
Db 780 CTGACGCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839  
QY 769 CAGCTTGGGTAATCAACATGTAAGCAATTCAGTACTAGTGTAAAGCGTGTCTTCTGTT 828  
Db 840 TAGGTTGGGTAATGATGCTTAAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899  
QY 829 TGATCAATATTTGCAACACACCATCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 888  
Db 900 TGATCAATATTTGCAACACACCATCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 959  
QY 889 ACTGATGAAGGCGCTTATCAACATGTAAGGATTTGGGATTCGCTGCTGCTGCTGCT 948  
Db 960 ACTGATGAAGGCGCTTATCAACATGTAAGGATTTGGGATTTGGAATTTAAACAGGTT 1019  
QY 949 TCACGAGGTTAACAACACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008  
Db 1020 TCACGAGGTTAACAACACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
QY 1009 ATGCAAGGAGCAAGGATGCAATCAACGATGTTGGGCGAGTACTTAATAATGCA 1068  
Db 1080 ATGCAAGGAGCAAGGATGCAATCAACGATGTTGGGCGAGTACTTAATAATGCA 1139  
QY 1069 GAGCTCCATTTTCAACGATGTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAG 1128  
Db 1140 GAGCTCCATTTTCAACGATGTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAG 1199  
QY 1129 ATGAGATGAGGAGCAAGGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1181  
Db 1200 ATGAGATGAGGAGCAAGGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252

RESULT 10  
US-09-852-399-3

; Sequence 3, Application US/09852399  
; Patent No. US20020045232A1

; GENERAL INFORMATION:

; APPLICANT: Qiu, Xiao

; TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND  
; FILE OF INVENTION: LINOENIC ACIDS IN PLANTS

; FILE REFERENCE: BNZ-002

; CURRENT APPLICATION NUMBER: US/09/852,399

; PRIOR FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: USSN 60/203,027

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 3

; LENGTH: 1411

; TYPE: DNA

; ORGANISM: Calendula officinalis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (89)...(1237)

; US-09-852-399-3

Query Match 34.6%; Score 444.8; DB 9; Length 1411;  
Best Local Similarity 63.4%; Pred. No. 2,1e-110;  
Matches 680; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

QY 109 ATCCACGCTTACCTTAAAGCATGGAAGAGGATTCCTTACCATTTGCTTGAAGCAT 168  
Db 174 AACCCCATTTACAGTTGGAAGCATGGAAGAGGATTCCTTACCATTTGCTTGAAGCAT 233  
QY 169 CTGTATCCGCTATCAT 228  
Db 234 CGGTAATATGTTAT 293  
QY 229 ACCTTGCAAGAGAT 288  
Db 294 ACATTTGCAAGAT 353  
QY 289 TTTATGCTTTTGTCAAGCTAGCATCTTACCGGCTCTGAGTATGCTGCTGCTGCTGCT 348  
Db 354 TTTATGCTTTTGTCAAGCTAGCATCTTACCGGCTCTGAGTATGCTGCTGCTGCTGCT 413  
QY 349 GTCAACATGCAATTTAGGCACTACAGTATGATGATGATGATGATGATGATGATGATG 408  
Db 414 GCATCATGCTTTTATGAGGACCAACCAATGCTGATGATGATGATGATGATGATGATGAT 473  
QY 409 CGGCTTCTTACCCCGATTTTCTTGAATATATATATATATATATATATATATATATAT 468  
Db 474 CGTTCTTACCTGCTGCTTCTTGAATATATATATATATATATATATATATATATATAT 533  
QY 469 CAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
Db 534 CGGCTTCTTACCTGCTTCTTGAATATATATATATATATATATATATATATATATAT 593  
QY 529 ATTCGAACCTTCTTACCATTCACCGGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCT 588  
Db 594 CCGGCTTCTTACCATTCACCGGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653  
QY 589 TAGGATTTCCGTTATATCTTAACTATATATATATATATATATATATATATATATAT 648  
Db 654 TCGGTTGCTTCTTATATCTTAACTATATATATATATATATATATATATATATATAT 713  
QY 649 ACCACTTGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
Db 714 GCATTTTGAACCCGATATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 773  
QY 709 CCGATTTGCTTCTTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGG 768  
Db 774 CCGAGCGGAGATCTTACGCTGATGCTTGTGATCTTCTGCACTGCAATGACCAAGGGC 833  
QY 769 CAGCTTGGGTAATCAACATGTAAGCAATTCAGTACTAGTGTAAAGCGTGTCTTCTG 828  
Db 834 TCACGTTGGGCTTAACTATGTAAGCGTGGCCGCTTAACTGCTGATCAACGCTTCTG 893  
QY 829 TGATCAATATTTGACACACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888  
Db 894 TGATCAATATTTGACACACACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953  
QY 889 ACTGATGAAGGCGCTTATCAACATGTAAGGATTTGGGATTCGCTGATGCGGTTT 948  
Db 954 ATGCTTGAAGGCGGCTTCAACACATGTAAGGATTTGGGATTCGCTGATGCGGTTT 1013  
QY 949 TCACGAGGTTAACAACACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008  
Db 1014 TCACGAGGTTAACAACACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073  
QY 1009 ATGCAAGGAGCAAGGATGCAATCAACGATGTTGGGCGAGTACTTAATAATGCA 1068  
Db 1074 ATGCAAGGAGCAAGGATGCAATCAACGATGTTGGGCGAGTACTTAATAATGCA 1133  
QY 1069 GAGCTCCATTTTCAACGATGTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAG 1128  
Db 1134 GAGCTCCATTTTCAACGATGTAAGGATGTAAGGATGTAAGGATGTAAGGATGTAAG 1193  
QY 1129 ATGAGATGAGGAGCAAGGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1180

Db 1194 ATGAGAGTGAGTAAGATGCTGTTTATGTGATCGTAATTAAGATTGAAGAA 1245

RESULT 11  
US-09-837-751-3

; Sequence 3, Application US/09837751  
; Patent No. US20020104124A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Gossypium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (79) ..(1233)  
US-09-837-751-3

Query Match 34.0%; Score 436.8; DB 9; Length 1411;  
Best Local Similarity 64.0%; Pred. No. 3.2e-108;  
Matches 660; Conservative 0; Mismatches 372; Indels 0; Gaps 0;

Qy 109 ATCCACCGTTCACGTTAGCGATCTGAAGAAAGCATTCACCATGCTTTGAGCAT 168  
Db 158 AGCCCTCGTTACGTCGTCGATCAAGCAAGCCATCCGCCATGTTTCCGCGCT 217  
Qy 169 CTGTCATCCGCTCATCATATATGTTTCAATGATCTGATGTTGCTTCTACT 228  
Db 218 CCGCTCTCGATCCCTCCCTCAAGTCGTCATGATGCTTACCTCTTTTACT 277  
Qy 229 ACCTTGCAACAGTATATCCCTTATTCCTACACCTCTGCTTACCTAGCAGCCG 288  
Db 278 ACATTCGCAACATATATTTCACTTTCACCAACACCTTTCCTACATGCTTGCGCTG 337  
Qy 289 TTTACTGTTTGTCAACTGATCTCTCAACCGGCTCTGGTCTATCGGTACCAATGTG 348  
Db 338 TCTATGGGTTCTCCAAAGTTGCACTCCACCGGTTGGTCAATCCACACGAGTGG 397  
Qy 349 GTCAACATGATTAAGCACTACCAAGTATGATGATGATGATGATGATGATGATG 408  
Db 398 GTCAACAGCTTTTCAAGACTCAACATGATGATGATGATGATGATGATGATGAT 457  
Qy 409 CGGCTCTCCGACCCCGTATTTCTTGGAAATATAGCAGCAAGATCAACGCGCA 468  
Db 458 CCGGCTCTTATAGTCCCGTACTTCTGTTGAAATATAGTCAACGCGCTCAACCTG 517  
Qy 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
Db 518 CCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 577  
Qy 529 ATTCCAAATCTTTAAACATCAACCGGCGAGTGTCACTTTGGTGTGGTGAAT 588  
Db 578 TTGGGAATATTAACATCAACCGGCTGAGTTCTTCTTGTATGATGATGATGAT 637  
Qy 589 TAGAATTCCTGTTATCTTAACTAATATCTGGGAGAGAAATCGGAGGTTTGA 648  
Db 638 TTGGTGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697  
Qy 649 ACCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
Db 698 CCGCACTAATACCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 757

Qy 709 CCGATTCGGTCTCTCTGCTGATTTTATGCAATCAAGCTTCTGTACGACCAAGGG 768  
Db 758 CCGATTCGGTCTCTCTGCTGATTTTATGCAATCAAGCTTCTGTACGACCAAGGG 817  
Qy 769 CAGCTTGGGTAATCAACATGATGCAATTCAGTACTAGTGTAGCTGTTCTGCTT 828  
Db 818 TGGCTTGGCTTTTATGCACTTATGAGGGGCTCTTACTTATGTGATGATGATGAT 877  
Qy 829 TGATCAATATTTGACACAGCCCATCTCTGACCTCCCTCATATGATGATGATGAT 888  
Db 878 TGATCACTTACTTGTACATATCTCTCTGATGATGATGATGATGATGATGATGAT 937  
Qy 889 ACTGATCAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGAT 948  
Db 938 ATTGGTTGCGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 997  
Qy 949 TCCAGACGTTACACACGTCAGCTCTTGTATGATGATGATGATGATGATGATGAT 1008  
Db 998 TCCATATCATCACCGATACGATGATGATGATGATGATGATGATGATGATGATGAT 1057  
Qy 1009 ATGCAAGAGAGCAAGGATGATCAAGCGATGTTGGGAGTACTATATAATGACA 1068  
Db 1058 ATGCAATGAGGCGCATTAAGCAATCAACCAATATCTGGCAATATATCTTTGACG 1117  
Qy 1069 GCACTCCATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1128  
Db 1118 GCAACCGATTTTACAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1177  
Qy 1129 ATGAGATAGCG 1140  
Db 1178 ACGTTGGTGTG 1189

RESULT 12  
US-10-330-775-5  
; Sequence 5, Application US/10330775  
; Publication No. US20030221217A1  
; GENERAL INFORMATION:  
; APPLICANT: Saskatchewan Wheat Pool  
; TITLE OF INVENTION: PLANT PBD2 CODING SEQUENCE BALANCING FOR FATTY ACID PROFILING IN  
; FILE REFERENCE: 4810-64260  
; CURRENT APPLICATION NUMBER: US/10/330,775  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: CA 2,382,767  
; PRIOR FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Brassica juncea  
US-10-330-775-5

Query Match 33.8%; Score 434.2; DB 16; Length 1155;  
Best Local Similarity 63.5%; Pred. No. 1.5e-107;  
Matches 680; Conservative 0; Mismatches 388; Indels 3; Gaps 1;

Qy 111 CCACGTTACGTTAAGGATCTGAAGAAAGCATTCCTACCATTCCTTGAAGCATCT 170  
Db 85 CCGCTCTTCAAGAGAGAGGATCAAGAAAGCATTCACCGCATGTTTCAAGCGCTCC 144  
Qy 171 GTCAATCCGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230  
Db 145 ATCCCTGCTCTCTCTTACCTATCTGGAACATCAATGATGATGATGATGATGAT 204  
Qy 231 CTTCGAACAGTATATCCCTTATTCCTAACAACCTGCTGCTTACATGATGATGAT 290  
Db 205 GTGCGACACATATCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264  
Qy 291 TACTGTTTGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 350  
Db 265 TACTGGGCTGCGCAAGGCTGCTCTTACCGGCGCTTGGGTATGATGATGATGATGAT 324



```

Db      925 TTCCAAATATACGACGACGCGGCGATCATCTGTTCTCGACCATGCCGATTAT 984
Qy      1008 CATGCAAGAAGCAAGGAGTATGATCAAGCAGTGTGGGAGTACTATTAATATGAC 1067
Db      985 CATGCAAGTGAAGTACGAGGCGATTAAGCCGATCTGGGAGATATATCATGTTCAAT 1044
Qy      1068 AGGACTCCAAATTTTCAAGCAATGTATAGAGGCTAAGATGATCTACATCGAGCC 1127
Db      1045 GGGAGCGCGGTGTAAAGCGCATGTGAGGGAGCGGAGAGTGTATCTATGTGGAACG 1104
Qy      1128 GATGAGATACGAGCAAAAGGTGTGTTGTTGTTCCCAAGATATATCA 1178
Db      1105 GACAGGCAAGGTGAGAGAAAGTGTGTGTGTGTAACAATTAAGTTATGA 1155

```

```

RESULT 14
US-09-771-904-9
; Sequence 9, Application US/09771904
; Publication No. US20030131379A1
; GENERAL INFORMATION:
; APPLICANT: Debonite, Lorin R.
; APPLICANT: Fan, Zhegong
; APPLICANT: Miso, Guo-Hua
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-771-904-9

```

```

Query Match      33.5%; Score 431; DB 10; Length 1155;
Best Local Similarity 63.3%; Pred. No. 1.1e-106;
Matches 678; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

Qy      111 CCACGCTTACGATTAAGGATCTGTAAGAAAGGATTTCTACCCATTTGAGGATCT 170
Db      85 CCGCCCTTACCTGTGCGAAGACTCAAGAAAGCAATCCACGCACTGTTCAAGGCTCG 144
Qy      171 GTCATCCGGTATCATATATGTTGATGATCATGTTGCTTATGCTTCTACTAC 230
Db      145 ATCCCTGGCTTTCTCTACCTCATCTGGGACATCATAGCCTCTGCTTCTACTAC 204
Qy      231 CTTCGAACAGTATATCTCTTATTTCTACACCTCTGGCTTACATGAGCCGCTT 290
Db      205 GTCCGACACGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264
Qy      291 TACTGTTTTCAGAGTACGATCTCTCAACGCGCTCTGGCTCATCGGATCAAGATGAGT 350
Db      265 TACTGGGCTCTCCAGGCGTGGCTCTTACCGGCTCTGGCTCTTACCGGAGTGGCG 324
Qy      351 CACCATGATTTAGCGATACAGTGAATGATGATGATGATGATGATGATGATGATGAT 410
Db      325 CACCAAGCTTCAAGGATCAAGTGGCTGAGCAGCAGTGGCTGATCTTCCACTCC 384
Qy      411 GCTTCTCTCAACCCGATTTTCTTTGAAATATAGCCAGAGATCAACGCCACACA 470
Db      385 TTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
Qy      471 AATTCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
Db      445 GGTCTCTCTGAGAGAGAGAGTGTGTCTCCCAAGAAAGTCAAGATCAAGGAGTAC 504
Qy      531 TCCAACTTCTTAACAATCCACCGGCGAGTGTTCATCTTGTGTGTTGCTGATCTTGA 590

```

```

Db      505 GGCAAGTACTCAACAACCTTTGGAGCAGCAGCGATGATTAACGTTCACTCTCTC 564
Qy      591 GGATTTCCGTTATATCTTATCTATATATCTCGGCA---AGAAATACGGAAGTTTCC 647
Db      565 GGTGGCCCTTGTGATTAAGCTTCAACGCTCTGGGGAACCTTACGAGGGCGGCTTGCT 624
Qy      648 AACCATTTGATCCCATGATGATCAATTTTCAAGCATGTAAGCGGCTCAAGTTTGTGA 707
Db      625 TGCCATTTCAACCCCAAGCTTCCATCTACACAGACGATGAGGCTCTCAATATACATC 684
Qy      708 TCCGATTTGCTCTCTCTGCTGTATTTTATGCAATCAAGCTTCTTGTAGCAGCAAGGG 767
Db      685 TCCGAGCTGATCTCTGCGCTGCTGCTACGCTCTACCGCTACGCTGCTGTCCAGGA 744
Qy      768 GCAGTTGGGTATATCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 827
Db      745 GTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
Qy      828 TTGATCAATATTTGACACCAACCATCTCTCACTCCCTCATTTATGATTAACCGAATG 887
Db      805 TTGATCACTTACTTGACAGACAGCATCTTCTCTGCTCACTATGATCTGATGATG 864
Qy      888 AACTGATCAAGGCGCTTATCAACAATGATGATGATGATGATGATGATGATGATGAT 947
Db      865 GATTGTTGAGGAGGAGCTTTGGCACCCTTGACAGAGCTACGGAATCTTGAACAAGTC 924
Qy      948 TTCCACACGCTTACACACATCATGCTTGTGATCATTTGATCTCATATTCACATTTAT 1007
Db      925 TTCCAAATATACGAGCAGCAGCGATGATGATGATGATGATGATGATGATGATGAT 984
Qy      1008 CATGCAAGAAGCAAGGAGTATGATCAAGCAGTGTGGGAGTACTATTAATATGAC 1067
Db      985 CATGCAAGTGAAGTACGAGGCGATTAAGCCGATCTGGGAGATATATCATGTTCAAT 1044
Qy      1068 AGGACTCCAAATTTTCAAGCAATGTATAGAGGCTAAGATGATCTACATCGAGCC 1127
Db      1045 GGGAGCGCGGTGTAAAGCGCATGTGAGGGAGCGGAGAGTGTATCTATGTGGAACG 1104
Qy      1128 GATGAGATACGAGCAAAAGGTGTGTTGTTGTTCCCAAGATATATCA 1178
Db      1105 GACAGGCAAGGTGAGAGAAAGTGTGTGTGTGTAACAATTAAGTTATGA 1155

```

```

RESULT 15
US-10-715-100-9
; Sequence 9, Application US/10715100
; Publication No. US20040083503A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharna
; APPLICANT: Fan, Zhegong
; APPLICANT: Debonite, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/10/715,100
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/995,297
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-10-715-100-9
Query Match      33.5%; Score 431; DB 17; Length 1155;

```

Best Local Similarity 63.3%; Pred. No. 1.1e-106; Matches 678; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

```
OY 111 CCACGGTTCACGTTAAGCATCTGAAGAAGGATTTCTTACCCATTCGTTGAGGACCT 170
Db 85 CCGCCCTTCACTGTCGGAAGACTCAAGAAAGCAATCCACCGCATGTTTCAAAAGCTCG 144
OY 171 GTCATCGGTCATCACTATGTTGTTCAATGATCTCATTTGCTTACTATGCTTACTAC 230
Db 145 ATCCCTCGCTCTTCTCTTACTCATCTGAGCATATCATATAGCCTCTGCTTACTATAC 204
OY 231 CTGGAACAGGTATATCCCTTATTCCTTACACCTGCTTACTAGCAATGGCCGTT 290
Db 205 GTGCGACACCTTACTTCCCTCTCTCCCTCAACCTCTCTCTACTTGGCCGCTCTC 264
OY 291 TACTGTTTTCAGTACGATGATCTTCAACCGGCTCTGAGTCATCGTCAAGATGTGT 350
Db 265 TACTGGGCTGCGACAGGCTGCGCTCTTAACCGGCTCTGAGTCATGCCACGAGTGGC 324
OY 351 CACCATGATTTAGGACTACCACTTGAATGATGATGATTTGATGCTGCTCATTTG 410
Db 325 CACCAAGCCTTCAGGACTACCACTGAGCTGAGACACCGTGGCTCATCTTCCACTCC 384
OY 411 GCTGCTCAACCCGATTTCTCTGAAATATAGCCACAGAAATCACCAAGCAACA 470
Db 385 TTCTCTCTGCTCTTACTTCTCTGAAATGATGATGATGATGATGATGATGATGAT 444
OY 471 AATTCATCGATTAACGATGAAGTTTACATCTCTAAACGTAAGTCGAAGTCGAATTTAT 530
Db 445 GGCTCCCTCGAGAGAGAGAGAGTGTTCCTCCCAAGAAAGTCAAGATCAAGTGTAC 504
OY 531 TCCAACTCTTAAATCAATCCACCGGAGAGTGTTCATTTGGTGTTCGTTGACTTTA 590
Db 505 GGCAGATCTCAACACCTTTGGAGACACCGATGATTTAAAGTTCAAGTTCACTCTC 564
OY 591 GGATTTGCTTATCTTACTTAAATATCTGAGGCA---AGAAATACGGAGGTTTGGC 647
Db 565 GGCTGGCTTTGATTTAGCTTCAAGCTCTGGGAGACCTTACGACGGCGCTTCGT 624
OY 648 AACCACTTGAATCCCATGATGATCAATTTTCAACGATGTAACGGCTTCAAGTTTGCTA 707
Db 625 TGGCATTTCAACCCCAAGGCTCCCATCTCAACGACGAGGCTCTCAAGATATACATC 684
OY 708 TCCGATTTGCTTCTGCTGTATTTATGCAATCAAGCTTCTGTAGCAGCAAAAGG 767
Db 685 TCCGAGCTGAGCATCTGCGCTCTGCTCAAGCTCTCAAGCTGCTGTCCAAAGA 744
OY 768 GCAGCTTGGGTATCAATGATGAGCAATTCAGTACTAGTGAAGGCTTCTTCTGT 827
Db 745 GTTGCTCGATGCTGTGCTTCTACGAGATTCCTTCTGATTTGTCAAGGGTCTTATGTT 804
OY 828 TTGATCAATATTTGACACACACCATCTCTCACTCCCTCATTTATGATTTCAACGATGG 887
Db 805 TTGATCACTTACTTCAAGACACGATCCTTCCGCTCACTATGACTCGTGAAGTGG 864
OY 888 AACTGATCAAAAGCGCTTATCAACAATCGATGAGGATTTGGGTTCTCTGATCGGTT 947
Db 865 GATTGTTGAGGGGAGCTTTGGCCACCGTTCAGAGACTACGGAATCTTGAACAAAGTTC 924
OY 948 TTCCAGAGCTTACACACTGAGCTTGTGATCTTGTGATCTCATATTCACATTTAT 1007
Db 925 TTCCAAATATACAGGACACGAGCTGGGCACTCTGTTTTCGACCAATGCCCATTTAT 984
OY 1008 CATGCAAGAGCAAGGATGCAATCAAGCCAGTGTGGCGAGTACTATAAATCGAC 1067
Db 985 CATGAGTAGAAGCTACGAAAGCGATTAAGCCGATACGAGAGATATATCATGTTGAT 1044
OY 1068 AGGATCTCAATTTTCAAGCAATGATATAGAGGCTAAGAAATGATCTACATGAGCCC 1127
Db 1045 GGGAGCGCGGTGTTAAGCGATGAGGAGGCGAAGGATGTATCTATGTGAAACCG 1104
OY 1128 GATGAGATAGGAGCAAAAGGTGTTCTGTACCAAGATGTAATCA 1178
```

Db 1105 GACAGGCAAGTGAGAAAGAGTGTGTTCTGTATCAACATATAGTTATGA 1155

Search completed: June 23, 2004, 15:51:15  
Job time : 457 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:52:13 ; Search time 3580 Seconds

(without alignments)  
15557.486 Million cell updates/sec

Title: US-10-069-772-1

Perfect score: 1285  
Sequence: 1 aaagctcactctctcgtga.....aaaaaaaaaaaaaaaaaa 1285Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_ey.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_ats.\*  
28: em\_un.\*  
29: em\_vl.\*  
30: em\_hcg\_hum.\*  
31: em\_hcg\_inv.\*  
32: em\_hcg\_mus.\*  
33: em\_hcg\_other.\*  
34: em\_hcg\_pln.\*  
35: em\_hcg\_rod.\*  
36: em\_hcg\_mam.\*  
37: em\_hcg\_vtc.\*  
38: em\_gy.\*  
39: em\_hcg\_hum.\*  
40: em\_hcg\_mus.\*  
41: em\_hcg\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1285	100.0	1285	6 AX089471	AX089471 Sequence
2	1152	89.6	1152	8 COF245938	AD245938 Calendula
3	871	67.8	1419	8 AY165773	AY165773 Helianthu
4	750.4	58.4	979	8 AY166776	AY166776 Rudbeckia
5	738	57.4	979	8 AY166777	AY166777 Dimorphot
6	728.6	56.7	1435	8 CAY16285	Y16285 Crepis alpi
7	715.8	55.7	1358	6 AR367437	AR367437 Sequence
8	715.8	55.7	1358	6 AX031160	AX031160 Sequence
9	715.8	55.7	1358	6 BD061164	BD061164 Plant fat
10	715.8	55.7	1358	6 CPY16283	CPY16283 Sequence
11	705.4	54.9	1312	6 AR367438	AR367438 Sequence
12	705.4	54.9	1312	6 AX031162	AX031162 Sequence
13	705.4	54.9	1312	6 BD061165	BD061165 Plant fat
14	699.8	54.5	1364	6 AR064128	AR064128 Sequence
15	694.8	54.1	979	8 AY166778	AY166778 Helichrys
16	673	52.4	1406	8 AY462108	AY462108 Stokesia
17	496.4	38.6	110900	8 AP006377	AP006377 Lotus cor
18	495.4	38.6	1291	8 AF074324	AF074324 Borago of
19	487.6	37.9	1516	8 AF525534	AF525534 Vernicia
20	486.6	37.9	1259	8 AF251844	AF251844 Helianthu
21	481.6	37.3	1507	8 AF188264	AF188264 Vernonia
22	478.8	37.3	1452	8 AF083163	AF083163 Olea euro
23	478.4	37.2	1475	8 AF188263	AF188263 Vernonia
24	476.4	37.1	1556	8 SOYMO6DA	LA3921 Glycine max
25	474.4	36.9	1466	8 AF192486	AF192486 Sesamum i
26	473.8	36.9	1219	8 AF071892	AF071892 Prunus ar
27	467.4	36.4	1344	8 HAN292275	AR292275 Helianthu
28	467.4	36.4	1345	8 AF251843	AF251843 Helianthu
29	465.6	36.2	1447	8 PCU86072	U86072 Petroselinu
30	462	36.0	1356	8 CPY16284	Y16284 Crepis pala
31	461.8	35.9	1472	8 SCD120LDS	X92847 S. commerson
32	455.6	35.5	1231	6 AR037150	AR037150 Sequence
33	455.6	35.5	1231	6 T65761	T65761 Sequence 44
34	455.6	35.5	1372	6 AR207486	AR207486 Sequence
35	455.6	35.5	1372	6 ATHD12AAB	L26296 Arabidopsis
36	455.6	35.5	1451	8 AY039572	AY039572 Arabidops
37	455.6	35.5	1451	8 AP002063	AP002063 Arabidops
38	455.6	35.5	85657	8 AC069473	AC069473 Arabidops
39	454.4	35.4	1476	6 AR064127	AR064127 Sequence
40	454	35.3	1152	8 AY142057	AY142057 Arabidops
41	454	35.3	2973	6 AR207494	AR207494 Sequence
42	453.6	35.3	1451	8 AY084545	AY084545 Arabidops
43	453.4	35.3	1580	6 BD171810	BD171810 Gene part
44	451.2	35.1	1627	8 AB094415	AB094415 Spinacia
45	449	34.9	1300	8 AY178445	AY178445 Trichosan

## ALIGNMENTS

RESULT 1  
AX089471  
LOCUS AX089471 1285 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 1 from Patent WO0116362.  
ACCESSION AX089471  
VERSION AX089471.1 GI:13443732  
SOURCE  
ORGANISM  
Calendula officinalis  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Calenduleae; Calendula.  
REFERENCE  
1 Feussner, I., Hornung, E., Fritzsche, K., Peltzsch, N. and Renz, A.

TITLE Fatty acid desaturase gene from plants  
JOURNAL Patent: WO 0116362-A 1 08-MAR-2001;  
BASF AKTIENGESELLSCHAFT (DE)  
FEATURES  
source 1. 1285  
/organism="Calendula officinalis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:41496"  
42. 1175  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC34898.1"  
/db\_xref="gi:13443733"  
/translation="MGAGRMSDSEGNIIIEVPVDPPTLSLKKAIPTHCERSY  
IRSSYYVVDLIVAVFYLANVYIPLIPLAYLAMYFCOASILTGAVIGHEC  
GHAHSPYDOLIDIVGFVLSALITPYSMKXSHRNHNANSLDNDVYIPKRSKY  
KIYKLNLPGRVPTLVPLTLGPRILYLNISGKKYGRANHPDPSPIENDERY  
QVLSDFGLAVFAIKLVAKGAWYINNTALPVLSVSPFVLITLHTHSLPH  
YDSTEMWIKALSTIDRDFGLNRFVDFVTHVHLHLISYIPHYAKKARDAIKPV  
LGEYKIDRTPIFKMYREAKECIYIEPDEDSHKGVFWYHMKM"

## ORIGIN

Query Match 100.0%; Score 1285; DB 6; Length 1285;  
Beech Local Similarity 100.0%; Pred. No. 0;  
Matches 1285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AAAAGCTACTTCTCTGTGAGGGTAATATATCAACAACATGGGTGTCGCGA 60
DB 1 AAAAGCTACTTCTCTGTGAGGGTAATATATCAACAACATGGGTGTCGCGA 60
QY 61 TGTGGATTCATCTGAGGAAAAAATCTCTTGAACGTGTGCAATCCACCTTCA 120
DB 61 TGTGGATTCATCTGAGGAAAAAATCTCTTGAACGTGTGCAATCCACCTTCA 120
QY 121 CGTTAAGGATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTGATCCGGT 180
DB 121 CGTTAAGGATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTGATCCGGT 180
QY 181 CATCATATCTATGTTGTCATGATCTCATGTTGCTTACTTACTTACCTTGCAACA 240
DB 181 CATCATATCTATGTTGTCATGATCTCATGTTGCTTACTTACTTACCTTGCAACA 240
QY 241 CGTATATCTCTTATTCCTACACCTCTGCGCTTACCTAGCATGCGCGTTTACTG 300
DB 241 CGTATATCTCTTATTCCTACACCTCTGCGCTTACCTAGCATGCGCGTTTACTG 300
QY 301 GTCAAGTACGATCTCTACCGCGCTCTGAGTCATGTCGATGATGATGATGATGAT 360
DB 301 GTCAAGTACGATCTCTACCGCGCTCTGAGTCATGTCGATGATGATGATGATGAT 360
QY 361 TTAGGACATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 TTAGGACATACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 CCCCGTATTTCTCTTGAAGATATAGCCACAGGAATCACCGCAACAATTCATCTG 480
DB 421 CCCCGTATTTCTCTTGAAGATATAGCCACAGGAATCACCGCAACAATTCATCTG 480
QY 481 ATTAAGATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 540
DB 481 ATTAAGATGAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 540
QY 541 TTAAACATCCACCGCGGAGTGTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 TTAAACATCCACCGCGGAGTGTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 TATACCTCTTAATATATCTCGGCAAGAAATAGGAGGTTTGCCAAACATTTGATC 660
DB 601 TATACCTCTTAATATATCTCGGCAAGAAATAGGAGGTTTGCCAAACATTTGATC 660
QY 661 CCAAGAGTCCAAATTTTCAACATCGTGAACGGTTTCAAGTTTGTATCCGATTTCCGTC 720
DB 661 CCAAGAGTCCAAATTTTCAACATCGTGAACGGTTTCAAGTTTGTATCCGATTTCCGTC 720

```

```

DB 661 CCAAGAGTCCAAATTTTCAACATCGTGAACGGTTTCAAGTTTGTATCCGATTTCCGTC 720
QY 721 TTTCGCTGTAATTTTATGCAATCAAGCTCTTGTAGCAGCAAAAGGGCAGCTGGTAA 780
DB 721 TTTCGCTGTAATTTTATGCAATCAAGCTCTTGTAGCAGCAAAAGGGCAGCTGGTAA 780
QY 781 TCACATGTATAGCAATTCCTACTAGGTGTAAACCGTCTTCTGTTTGTATCATATT 840
DB 781 TCACATGTATAGCAATTCCTACTAGGTGTAAACCGTCTTCTGTTTGTATCATATT 840
QY 841 TGACACACACCATCTCTCATCTCCCTCATTTATGATTCACCGAATGAAATGATCAAA 900
DB 841 TGACACACACCATCTCTCATCTCCCTCATTTATGATTCACCGAATGAAATGATCAAA 900
QY 901 GCGCCTTATCAACAATGAGGATTTGGGCTTCTGAAATCGGAGTTTCCACGATTA 960
DB 901 GCGCCTTATCAACAATGAGGATTTGGGCTTCTGAAATCGGAGTTTCCACGATTA 960
QY 961 CACACACTCAGCTCTTGATCATTTGATCTCATATCATTCATTCATTTATTCGCAAGAG 1020
DB 961 CACACACTCAGCTCTTGATCATTTGATCTCATATCATTCATTCATTCATTCGCAAGAG 1020
QY 1021 CAAGGATGCAATCAAGCAGTGTGGGCGAGTACTATTAATGACAGACTCCAAATTT 1080
DB 1021 CAAGGATGCAATCAAGCAGTGTGGGCGAGTACTATTAATGACAGACTCCAAATTT 1080
QY 1081 TCAAAGCAATGTATAGAGGCTTAAGAAATCATCTACATGAGCCCGATGAGATAGCG 1140
DB 1081 TCAAAGCAATGTATAGAGGCTTAAGAAATCATCTACATGAGCCCGATGAGATAGCG 1140
QY 1141 AGCACAAGGTGTGTCTGTGATCCACAAAGATGTATCAAAAAGGTGTATGTCAAT 1200
DB 1141 AGCACAAGGTGTGTCTGTGATCCACAAAGATGTATCAAAAAGGTGTATGTCAAT 1200
QY 1201 TGTATGCTTAATTAAGTGTAACTTCTATTCGTTAATTAATTAATTAAGAGAA 1260
DB 1201 TGTATGCTTAATTAAGTGTAACTTCTATTCGTTAATTAATTAATTAAGAGAA 1260
QY 1261 AAAAAAAAAAAAAAAAAAAAAA 1285
DB 1261 AAAAAAAAAAAAAAAAAAAAAA 1285

RESULT 2
COR245938 1152 bp mRNA linear PLN 22-DEC-1999
LOCUS Calendula officinalis partial mRNA for (8,11)-linoleoyl desaturase
DEFINITION (des8.11 gene).
ACCESSION AJ245938
VERSION AJ245938.1 GI:6634079
KEYWORDS (8,11)-linoleoyl desaturase; des8.11 gene.
SOURCE Calendula officinalis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Calendula.
REFERENCE 1
Fritsche, K., Hornung, E., Peitzsch, N., Renz, A. and Feussner, I.,
Isolation and characterization of a calendic acid producing
(8,11)-linoleoyl desaturase
FEBS Lett. 462 (3), 249-253 (1999)
MEDLINE 20086417
PUBMED 10622705
REFERENCE 2 (bases 1 to 1152)
Feussner, I.,
Direct Submission
Submitted (02-SEP-1999) Feussner I., Hormonforschung, Institut fuer
Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, GERMANY
FEATURES
source 1. 1152
/organism="Calendula officinalis"
/mol_type="mRNA"

```



```

/db_xref="taxon:41496"
/clone="pcode8.11"
/tissue_type="developing seed"
/tissue_lib="developing seed"
1. .1152
/gene="dees8.11"
1. .>1131
/gene="dees8.11"
/function="production of calendic acid"
/codon_start=1
/evidence=experimental
/product="8,11)-linoleyl desaturase"
/protein_id="CAB64256.1"
/db_xref="GI:6634080"
/db_xref="GOA:Q9SCG2"
/db_xref="SPTREMBL:Q9SCG2"
/translation="MGAGRMSDPSBGNILERVVDPPETLSLKKALPHPCERSV
IRSSYVVDLIIVAVFYFLANTYIPLIPFLATLAMPVYFCAASILTGAVI
GHNC
GHAHFSYQLIDIVGVFLHSALTPYFSWKSHRNHANTNSLDNEVYLPKRSKY
KYSKLNPNPGRVFLVFLRGLPFLYLNISGKXGRFANFDPSPFNDREY
QVLSDFGLAVFAIKLIVAKGAAMVINYAIPLGVSVFVLYLHTHTLSLPH
YDSTEMWIKALSTIDRDFGLNRVFDVHTVHLISYIPIHYAKKARDAIKPV
LGEYKXIDRPIRFAMRYREAKECIYIBDESEHKVFWYHKM"

```

ORIGIN

Query Match 89.6%; Score 1152; DB 8; Length 1152;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-292;  
 Matches 1152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 42 ATGGGTGCTGGTGGATGTCGATTCATCTGAGGAAAAAACATCTGGAACGTGTG 101
DB 1 ATGGGTGCTGGTGGATGTCGATTCATCTGAGGAAAAAACATCTGGAACGTGTG 60
QY 102 CCAATCGATCCACCGTTCAGCTTAAGCGATCTGAAGAAAGCATTCCTACCATTCGCTT 161
DB 61 CCAATCGATCCACCGTTCAGCTTAAGCGATCTGAAGAAAGCATTCCTACCATTCGCTT 120
QY 162 GAGGATCTGTCATCCGGTCACTACTATGTTGTCATGATTCATTCATTCCTATGTC 221
DB 121 GAGGATCTGTCATCCGGTCACTACTATGTTGTCATGATTCATTCATTCCTATGTC 180
QY 222 TTCTACTACTCTGCAAAACGATATCCCTTATTCCTACCACTCTGGCTTACCTAGCA 281
DB 181 TTCTACTACTCTGCAAAACGATATCCCTTATTCCTACCACTCTGGCTTACCTAGCA 240
QY 282 TGCGCCGTTTACCTGTTTGTCAAGCTAGCATCCCTACCCGCTCTGGGTATCGGTAC 341
DB 241 TGCGCCGTTTACCTGTTTGTCAAGCTAGCATCCCTACCCGCTCTGGGTATCGGTAC 300
QY 342 GAATGTGTCACATGATTTAGGCACTACAGTTGATTTAGACATTTGATTCGTCG 401
DB 301 GAATGTGTCACATGATTTAGGCACTACAGTTGATTTAGACATTTGATTCGTCG 360
QY 402 CTCGATTCGGCTCTCTACCCCGGTATTCCTTGAATAATAGCCACAGGAATCACCAC 461
DB 361 CTCGATTCGGCTCTCTACCCCGGTATTCCTTGAATAATAGCCACAGGAATCACCAC 420
QY 462 GCCAACCAATTCATCTGATTAAGATGAAGTTTCAATCTTAACGTAAGTCCAGATC 521
DB 421 GCCAACCAATTCATCTGATTAAGATGAAGTTTCAATCTTAACGTAAGTCCAGATC 480
QY 522 AAGATTATTCGAATCTTCAATCAATCCACCGGCGAGGTTCATCTTGGTGTTCGG 581
DB 481 AAGATTATTCGAATCTTCAATCAATCCACCGGCGAGGTTCATCTTGGTGTTCGG 540
QY 582 TTGACTTTAGGATTCGGTATTAACCTCTTAATATATCTCGGCAAGAAATACGGAGG 641
DB 541 TTGACTTTAGGATTCGGTATTAACCTCTTAATATATCTCGGCAAGAAATACGGAGG 600
QY 642 TTGGCCAAACATTTGATCCATGAGTCGAATTTTCAACGATCGTGAACGGCTTCAAGTT 701
DB 601 TTGGCCAAACATTTGATCCATGAGTCGAATTTTCAACGATCGTGAACGGCTTCAAGTT 660

```

```

QY 702 TTGCTATCCGATTTGCGGCTCTCGCTGATATTTTATAGCAATCAAGCTTCTTGACAGCA 761
DB 661 TTGCTATCCGATTTGCGGCTCTCGCTGATATTTTATAGCAATCAAGCTTCTTGACAGCA 720
QY 762 AAAGGGCAGCTTGGTATATCAATGATGATGCAATTCAGTACGATGATGATGATGATG 821
DB 721 AAAGGGCAGCTTGGTATATCAATGATGATGCAATTCAGTACGATGATGATGATGATG 780
QY 822 TTGCTTTGATCATATTTTGACACACACCATCTCTACCTCCCTCATTTATATTCAC 881
DB 781 TTGCTTTGATCATATTTTGACACACACCATCTCTACCTCCCTCATTTATATTCAC 840
QY 882 GAATGAATCTGATCAAAAGCGCTTATCAACATTCATGATGATGATGATGATGATG 941
DB 841 GAATGAATCTGATCAAAAGCGCTTATCAACATTCATGATGATGATGATGATGATG 900
QY 942 CGGCTTTTCCAGCGATTAACACACATCAAGCTCTGATCAATTTGATCTCATATTC 1001
DB 901 CGGCTTTTCCAGCGATTAACACACATCAAGCTCTGATCAATTTGATCTCATATTC 960
QY 1002 CATTATCATGCAAAAGAAAGCAAGGATGATCAAGCAGTGTGGCGAGTACTATTA 1061
DB 961 CATTATCATGCAAAAGAAAGCAAGGATGATCAAGCAGTGTGGCGAGTACTATTA 1020
QY 1062 ATGACACAGACTCCATTTTCAAGCATGTATAGAGCTTAAGAAATGATCTTACATC 1121
DB 1021 ATGACACAGACTCCATTTTCAAGCATGTATAGAGCTTAAGAAATGATCTTACATC 1080
QY 1122 GAGCCGATGAGATTAACGACACAAAGTGTGTTCTGATCCACAGATGATTA 1181
DB 1081 GAGCCGATGAGATTAACGACACAAAGTGTGTTCTGATCCACAGATGATTA 1140
QY 1182 AGGTGATGTCA 1193
DB 1141 AGGTGATGTCA 1152

```

RESULT 3  
 AY166773 1419 bp mRNA linear PLN 02-JUN-2003  
 LOCUS  
 DEFINITION Helianthus annuus delta12-fatty acid acetylase mRNA, complete cds.  
 ACCESSION AY166773  
 VERSION AY166773.1 GI:31322134  
 KEYWORDS  
 SOURCE  
 ORGANISM Helianthus annuus (common sunflower)  
 Helianthus annuus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Helianthus.  
 REFERENCE 1 (bases 1 to 1419)  
 Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.  
 Fungal responsive fatty acid acetylases occur widely in  
 evolutionarily distant plant families  
 Plant J. 34 (5), 671-683 (2003)  
 REFERENCE 2 (bases 1 to 1419)  
 Cahoon, E.B.  
 Direct Submission  
 Submitted (18-OCT-2002) Crop Genetics, DuPont, Bldg. 402  
 Experimental Station, Wilmington, DE 19880-0402, USA  
 JOURNAL  
 TITLE  
 AUTHORS  
 JOURNAL  
 FEATURES  
 source  
 1. .1419  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4232"  
 69. .1202  
 /codon\_start=1  
 /product="delta12-fatty acid acetylase"  
 /protein\_id="AA038032.1"  
 /db\_xref="GI:31322135"  
 /translation="MGAGRMSDPSBGNILERVVDPPETLSLKKALPHPCERSV  
 IRSSYVVDLIIVAVFYFLANTYIPLIPFLATLAMPVYFCAASILTGAVI  
 GHNC"

CDS

```

1. .1202
/codon_start=1
/product="delta12-fatty acid acetylase"
/protein_id="AA038032.1"
/db_xref="GI:31322135"
/translation="MGAGRMSDPSBGNILERVVDPPETLSLKKALPHPCERSV
IRSSYVVDLIIVAVFYFLANTYIPLIPFLATLAMPVYFCAASILTGAVI
GHNC"

```

## ORIGIN

GHHAYSDYQIDIDIVGVLSALTYPTFSWKSHRNHNANTSLDNDEVITPKKAKY  
 AVVSKLNNPGRVFTLVRLJLGFPLYLNLNISKGRANHPDLSPJTERER  
 QVNSIDIGILAVLAKLIVKAGAWTCWYLIPLVIGVNFPLIYLTHLTHLSLPH  
 YDSTEMMIRGALSTIDRDFGLNRPVDFDVTHTVHLHLISYIHYNAKEARDAIKPV  
 LGEFYKIDRTPIFFAMREAKECIYIBDEDESEHKGYTHWMKM"

Query Match 67.8%; Score 871; DB 8; Length 1419;  
 Best Local Similarity 82.1%; Pred. No. 4.3e-218;  
 Matches 1015; Conservative 0; Mismatches 220; Indels 2; Gaps 1;

10 CTTCTCTGAGGGGAAATATATATCAACAATGGGCTGCTGCTGGATGTCGATC 69  
 37 CTCATCTCTGAGGTATCAACATCCACCAATGAGGAGCGGAGATGTCAGCC 96  
 70 CATCTGAGGAGAAAAAATCTTGAACGTGTGCCAGTGCATCCACCTTCAAGTAAAGC 129  
 97 CATCTGAGGAGAAAAAATCTTGAACGTGTGCCAGTGCATCCACCTTCAAGTAAAGC 156  
 130 ATCTGAAGAAAGCATTCCTACCCATTCCTTGAAGCATCTGTCAATCCGATCATCACT 189  
 157 ATCTGAAGAAAGCATTCCTACCCATTCCTTGAAGCATCTGTCAATCCGATCATCACT 216  
 190 ATCTGATTCATGATCTCATTTGCTTATGCTTCTTACTTACCTTGCAAAACGATATCC 249  
 217 ATCTGATTCATGATCTCATTTGCTTATGCTTCTTACTTCTTCCGCAACATATATCC 276  
 250 CTTCTTATCTCAACCTCTGGCTTACCTAGACATGGCCGGTTTACCTGCTTGTGTAAGTA 309  
 277 CTTCTTATCTCAACCTCTGGCTTACCTAGACATGGCCGGTTTACCTGCTTGTGTAAGTA 336  
 310 GCATCTCAACCCGCTCTGGGTCATCGGTCAAGATGCTGTCACCATCATTTAGCGACT 369  
 337 GCATCTCAACCCGCTCTGGGTCATCGGTCAAGATGCTGTCACCATCATTTAGCGACT 396  
 370 ACCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429  
 397 ACCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456  
 430 TCTCTGGAATATATGACAGAGATGACAGAGATGACAGAGATGACAGAGATGACAGAGATG 489  
 457 TCTCTGGAATATATGACAGAGATGACAGAGATGACAGAGATGACAGAGATGACAGAGATG 516  
 490 AAGTTTACATTCCTTAAAGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 549  
 517 AAGTTTACATTCCTTAAAGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 576  
 550 CACCGGCGGAGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 609  
 577 CACCGGCGGAGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 636  
 610 TAACTATATATCTCGGGGCAAGAAATACGGGAGGTTTGCACACATTTGATCCCATGAGTC 669  
 637 TGACTATATATCTCGGGGCAAGAAATACGGGAGGTTTGCACACATTTGATCCCATGAGTC 696  
 670 CAATTTTCAAGATCTGTAACGCTTCAAGTTTGTCTATCCGATTTCCGCTCTTCTGCTG 729  
 697 CGATTTTCAAGATCTGTAACGCTTCAAGTTTGTCTATCCGATTTTCCGCTCTTCTGCTG 756  
 730 TATTTTATGATATCAAGCTTCTTGTAGACAGAAAGGGGAGCTTGGTATCAACATGT 789  
 757 TTTTGTATGAACTAACTACTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816  
 790 AAGCAATTCAGATCTAGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849  
 817 ATTTATATTCGGGTCTAGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 876  
 850 CCAATCTCTCACTCCCTCATTTATGATTAACGAGATGAGATGAGATGAGATGAGATGAGAT 909  
 877 CCAATCTCTCTTACTTATGATTAACGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 936  
 910 CAACATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 969

Db 937 CGACAATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 996  
 Qy 970 AAGCTTTCATCATTTGATCTCATATATTCATATTCATATGACAGAGAGAGATG 1029  
 Db 997 AAGCTTTCATCATTTGATCTCATATATTCATATTCATATGACAGAGAGAGATG 1056  
 Qy 1030 CAATCAAGCCAGTCTTGGGAGAGATCTATTAATTCAGAGAGATCTCCATTTTCAAGCA 1089  
 Db 1057 CAATCAAGCCAGTCTTGGGAGAGATCTATTAATTCAGAGAGATCTCCATTTTCAAGCA 1116  
 Qy 1090 TGTATGAGAGAGGCTAAGAGATGATCTATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1149  
 Db 1117 TGTGAGAGAGAGGCTAAGAGATGATCTATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1176  
 Qy 1150 GTGTGTTCTGTATCACAGATGATTAATCAAAAGGTATGATCAATGATGATGATGAT 1209  
 Db 1177 GCATATATGATGATCAATTAATGATATTC--AGTATATGAGAGAGATGATGATGATGAT 1234  
 Qy 1210 AATTAAGTTGTTAACTTCTATTCGCTGATTAAT 1246  
 Db 1235 AAGTATTTGATATTCCTATATTAATGAGGATGATGAT 1271

RESULT 4  
 AY166776 979 bp DNA linear PLN 02-JUN-2003  
 LOCUS  
 DEFINITION Rudbeckia hirta delta12-fatty acid acetylase gene, partial cds.  
 ACCESSION AY166776  
 VERSION AY166776.1 GI:31322140  
 KEYWORDS  
 ORGANISM Rudbeckia hirta  
 SOURCE Rudbeckia hirta  
 CAUTION: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asterales; Asteraceae; Asteroidae;  
 Heliantheae; Rudbeckia.  
 REFERENCE  
 1 (bases 1 to 979)  
 Cahoon, E.B., Schurr, J.A., Huffman, E.A. and Minto, R.E.  
 Fungal responsive fatty acid acetylases occur widely in  
 evolutionarily distant plant families  
 Plant J. 34 (5): 671-683 (2003)  
 2 (bases 1 to 979)  
 Cahoon, E.B.  
 Direct Submission  
 Submitted (19-OCT-2002) Crop Genetics, Dupont, Bldg. 402  
 Experimental Station, Wilmington, DE 19880-0402, USA

FEATURES  
 source  
 1..979  
 /organism="Rudbeckia hirta"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:52239"  
 <1..>979  
 /product="delta12-fatty acid acetylase"  
 <1..>979  
 /codon\_start=1  
 /product="delta12-fatty acid acetylase"  
 /protein\_id="AA038035.1"  
 /db\_xref="GI:31322141"  
 /translation="KATPCHERSVIRSSYVVVHDLIVAVPEVLYANTYPIPLPTM  
 AYLMPIYWCASITLGLVITGEGCHNAFSDYQILDVVGFTLHLPYRYSWKY  
 SHRNHNANTSLDNDEVITPKKAKVAAYSKLXPKRPFVRLFLPLTLN  
 ISGKGRFANHPDLPSPIFTDRERVVLSIDGLAFYAIKLVAAKGFANVTSWY  
 LIPVGMFPEVLTLYLHHTLSLPHDSTEMNIGALSTIDRDFGLNRPVDFDVT  
 THVLHHLISYIHYNAKEARDAIKPVLEFYKIDRTPIFFAMREAKEXY"

## ORIGIN

Query Match 58.4%; Score 750.4; DB 8; Length 979;  
 Best Local Similarity 85.3%; Pred. No. 2.3e-186;  
 Matches 835; Conservative 0; Mismatches 144; Indels 0; Gaps 0;  
 Qy 138 AAGGCAATCCCGCCCATGTCTTGAAGAGATCGGTATCATCTACTATCTTCTT 197  
 Db 1 AAGGCAATCCCGCCCATGTCTTGAAGAGATCGGTATCATCTACTATCTTCTT 60

KEYWORDS	SOURCE	ORANISM	REFERENCE	TITLE	AUTHORS	FEATURES	source
Dimorphochea sinuata (African daisy)	Dimorphochea sinuata	Dimorphochea sinuata	Dimorphochea sinuata	Dimorphochea sinuata	Dimorphochea sinuata	Dimorphochea sinuata	Dimorphochea sinuata
Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.	Euarietia, Vitridiellidae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenulaceae; Dimorphochea.
1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)	1 (bases 1 to 979)
Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.	Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.
Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families	Fungal responsive fatty acid acetyltransferases occur widely in evolutionarily distant plant families
Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)	Plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)	2 (bases 1 to 979)
Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers
1..979	1..979	1..979	1..979	1..979	1..979	1..979	1..979
/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"	/organism="Dimorphochea sinuata"
/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"	/mol_type="genomic DNA"
/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"	/db_xref="taxon:112408"
<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979
/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"
<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979	<1..>979
/codon_start=1	/codon_start=1	/codon_start=1	/codon_start=1	/codon_start=1	/codon_start=1	/codon_start=1	/codon_start=1
/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"	/product="delta12-fatty acid acetyltransferase"
/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"	/protein_id="AA038036.1"
/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"	/db_xref="GI:31322143"
/translation="KKAIIPHCERSLRSYVYVHDLVAVYFPLANTYIPLLPAPLAVYAVYVWCCASILGLWVIGHECGHAFSCQWIGDVFILSLPTPYFSWVYSHSHANTSLDNDVYIPKRSKYRANSKIANNPGRFTYVFLTLGFLYLLITVNSKRYERFANHPDWSPIFTEKERIQVAVSDISGLVCAALVLAAKATATWCKYGVAVGVHAFVPLIYVHHTLSLPEVDSWMIKALSTIDRDFGLNRVHDVYVHTVHLHLISYIPHYHAKERADAIIPVIGERYKIDRPIFKAMREAKEC"	/translation="KKAIIPHCERSLRSYVYVHDLVAVYFPLANTYIPLLPAPLAVYAVYVWCCASILGLWVIGHECGHAFSCQWIGDVFILSLPTPYFSWVYSHSHANTSLDNDVYIPKRSKYRANSKIANNPGRFTYVFLTLGFLYLLITVNSKRYERFANHPDWSPIFTEKERIQVAVSDISGLVCAALVLAAKATATWCKYGVAVGVHAFVPLIYVHHTLSLPEVDSWMIKALSTIDRDFGLNRVHDVYVHTVHLHLISYIPHYHAKERADAIIPVIGERYKIDRPIFKAMREAKEC"	/translation="KKAIIPHCERSLRSYVYVHDLVAVYFPLANTYIPLLPAPLAVYAVYVWCCASILGLWVIGHECGHAFSCQWIGDVFILSLPTPYFSWVYSHSHANTSLDNDVYIPKRSKYRANSKIANNPGRFTYVFLTLGFLYLLITVNSKRYERFANHPDWSPIFTEKERIQVAVSDISGLVCAALVLAAKATATWCKYGVAVGVHAFVPLIYVHHTLSLPEVDSWMIKALSTIDRDFGLNRVHDVYVHTVHLHLISYIPHYHAKERADAIIPVIGERYKIDRPIFKAMREAKEC"	/translation="KKAIIPHCERSLRSYVYVHDLVAVYFPLANTYIPLLPAPLAVYAVYVWCCASILGLWVIGHECGHAFSCQWIGDVFILSLPTPYFSWVYSHSHANTSLDNDVYIPKRSKYRANSKIANNPGRFTYVFLTLGFLYLLITVNSKRYERFANHPDWSPIFTEKERIQVAVSDISGLVCAALVLAAKATATWCKYGVAVGVHAFVPLIYVHHTLSLPEVDSWMIKALSTIDRDFGLNRVHDVYVHTVHLHLISYIPHYH				

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
QY	CAV16285	1435 bp mRNA linear	PLN 23-DEC-2000				
Db							
QY	1095	AGAGAGCTAAGGAATGC 1112					
Db	961	AGAGAGCCCAARGARTGC 978					
QY	1035	AAGCCAGTGTGGGCGAGTACTATATAATCGACAGAGCTCCAAATTTTCAAGAATGTAT 10394					
Db	901	ATACCAAGTTTGGTGGAATTTTATTAAGATCGATAGAGCTCCAACTTTAAAGCAATGTGG 960					
QY	975	TTGCATCATTTTGATATCTCATATCCATATATCATATGAAAGGAAGCAAGGATGCAATC 10344					
Db	841	TTGCATCATTTTGATATCTCTTAATTCATCATATATCATATGAAAGGAAGCAAGGATGCAATC 900					
QY	915	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 974					
Db	781	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 840					
QY	721	CTCTGTTGGCTCATTAATGATTCGTCGAAATGGAATCGATCAAAAGAGCTTATTCACA 780					
Db	855	CTCTGACCTCCCTCATTAATGATTCACACGATAGGAATCGATCAAAAGAGCTTATTCACA 914					
QY	661	GTTCCCGATGATAGGCGTACATGCTTTCTTTGTTGATCACTTATTTGACACACACCAT 720					
Db	795	ATTCAGTACTAGTGTAGTGAAGGCTGTTCTCGTTTGTATCACATATTTGCACACACCAT 854					
QY	601	TACGACATCAAAGTCTTGTTGACGCAAAAGAGCCACTTGGGTATGTATGATATGGA 660					
Db	735	TATGCAATCAAGCTTCTTGTTAGACAGCAAAAGGAGGACGCTTGGGTATCAATATGAGCA 794					
QY	675	TTCAACGATCGTGAACGCGTTCAAGTTTGGTATCCGATTTTCGGTCTTCTCGTATATTT 734					
Db	541	TTCAACGAGCGGTGAACGTATCCAAAGTTGTATATCGATCTTGGTATATGCTGTGTGT 600					
QY	1035	AAGCCAGTGTGGGCGAGTACTATATAATCGACAGAGCTCCAAATTTTCAAGAATGTAT 10394					
Db	901	ATACCAAGTTTGGTGGAATTTTATTAAGATCGATAGAGCTCCAACTTTAAAGCAATGTGG 960					
QY	975	TTGCATCATTTTGATATCTCATATCCATATATCATATGAAAGGAAGCAAGGATGCAATC 10344					
Db	841	TTGCATCATTTTGATATCTCTTAATTCATCATATATCATATGAAAGGAAGCAAGGATGCAATC 900					
QY	915	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 974					
Db	781	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 840					
QY	721	CTCTGTTGGCTCATTAATGATTCGTCGAAATGGAATCGATCAAAAGAGCTTATTCACA 780					
Db	855	CTCTGACCTCCCTCATTAATGATTCACACGATAGGAATCGATCAAAAGAGCTTATTCACA 914					
QY	661	GTTCCCGATGATAGGCGTACATGCTTTCTTTGTTGATCACTTATTTGACACACACCAT 720					
Db	795	ATTCAGTACTAGTGTAGTGAAGGCTGTTCTCGTTTGTATCACATATTTGCACACACCAT 854					
QY	601	TACGACATCAAAGTCTTGTTGACGCAAAAGAGCCACTTGGGTATGTATGATATGGA 660					
Db	735	TATGCAATCAAGCTTCTTGTTAGACAGCAAAAGGAGGACGCTTGGGTATCAATATGAGCA 794					
QY	675	TTCAACGATCGTGAACGCGTTCAAGTTTGGTATCCGATTTTCGGTCTTCTCGTATATTT 734					
Db	541	TTCAACGAGCGGTGAACGTATCCAAAGTTGTATATCGATCTTGGTATATGCTGTGTGT 600					
QY	1035	AAGCCAGTGTGGGCGAGTACTATATAATCGACAGAGCTCCAAATTTTCAAGAATGTAT 10394					
Db	901	ATACCAAGTTTGGTGGAATTTTATTAAGATCGATAGAGCTCCAACTTTAAAGCAATGTGG 960					
QY	975	TTGCATCATTTTGATATCTCATATCCATATATCATATGAAAGGAAGCAAGGATGCAATC 10344					
Db	841	TTGCATCATTTTGATATCTCTTAATTCATCATATATCATATGAAAGGAAGCAAGGATGCAATC 900					
QY	915	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 974					
Db	781	ATCGATAGGAGATTTCGGGTTCTCTGATTCGGGTTTCCAGACGTTTACACACATCAGCTC 840					
QY	721	CTCTGTTGGCTCATTAATGATTCGTCGAAATGGAATCGATCAAAAGAGCTTATTCACA 780					
Db	855	CTCTGACCTCCCTCATTAATGATTCACACGATAGGAATCGATCAAAAGAGCTTATTCACA 914					
QY	661	GTTCCCGATGATAGGCGTACATGCTTTCTTTGTTGATCACTTATTTGACACACACCAT 720					
Db	795	ATTCAGTACTAGTGTAGTGAAGGCTGTTCTCGTTTGTATCACATATTTGCACACACCAT 854					
QY	601	TACGACATCAAAGTCTTGTTGACGCAAAAGAGCCACTTGGGTATGTATGATATGGA 660					
Db	735	TATGCAATCAAGCTTCTTGTTAGACAGCAAAAGGAGGACGCTTGGGTATCAATATGAGCA 794					
QY	675	TTCAACGATCGTGAACGCGTTCAAGTTTGGTATCCGATTTTCGGTCTTCTCGTATATTT 734					
Db	541	TTCAACGAGCGGTGAACGTAT					

Query Match 56.7%; Score 728.6; DB 8; Length 1435;  
 Best Local Similarity 77.5%; Pred. No. 1.3e-180;  
 Matches 897; Conservative 0; Mismatches 254; Indels 6; Gaps 1.

ORIGIN

Query 24 TAAATTATATACAAACACATGGGTGCTGTGTGGATGTGGATCCATCTGAGGAAAA 83  
 Db 10 TAAATCATTTATCAACAAAGATGGGTGGCGGTGGCG-----TGGTCGAGCTTCGCCAAAA 63

QY AAACATCCCTTGAACGGTGGCCAGTGGATCCACCGTTACCGTTAAGGATCTGAAGAAAGCG 143  
 Db 64 CCCCTCAGAGAACGGTGTCAAGTGGATCACCCCTTCACCGTAGATCTCAGACAAACA 123

QY 144 ATTCCCTAACCATGGCTTTGAGCGAATCTGTACATCCGGTCATCATATATGTTTCATGAT 203  
 Db 124 ATCCCTCCCATGCTGTTCAAGCAATCTGTATCCGTTCTCTTACTACATATGTCACAGAT 183

QY 204 CTCAATGTGGCTTATGTTCTTACTACTCCCTTGCAAAACAGTATATTCCTTATTTCTACA 263  
 Db 184 GCTATATATGCGCTACATCTTCTACTCTCTTGCCGACAAATACATTTCCGATTTCCCTGCC 243

QY 264 CCTCGGCTTACCTAAGCATGGCCCGCTTTACTGCGTTTGTCAAGCTAAGATCCTACCGGCG 323  
 Db 244 CCTCAGCGCTACCTCGCTTGGCCCTTAACTGCGTTCTGTCAAGCTAAGATCCTACCGGCG 303

QY 324 CTGTGGCTATCGGTCAGCAATGTGGTCAACATGCAATTTAAGCACTACGATTTGAT 383  
 Db 304 TTATGGGTCATCGGTCAAGATGGCGGTCAACATGCTTCAAGCACTACGATGGGTTGAC 363

QY 384 GACATTTGTGATTCGTGCTCCATTCGGGCTCTCCACCCGGTATTTCTTGGAAATAT 443  
 Db 364 GACACTGTGGGCTTCAATCTTCCACCTCGTTTCTCAATGACCCGGTATTTCTCTGGAAATAC 423

QY 444 AGCCACAGGATTCACCAAGCCCAACAAATTCATCTGATTAACGATGAAAGTTTACATTCCT 503  
 Db 424 AGCCACCGGAACACACATGCAACAAATTCGCTTGACCAAGATGAAAGTTTACATTCCTC 483

QY 504 AAACGTATGTGAAGGTCAAGATTTATTCGAAACCTTCTTAACAATTCACCCGGGCGAGTG 563  
 Db 484 AAACGAAAGGCGAAAGTGGCGCTTTACTATTAAGTTCTTCAACACCAACCTGGCGGACTG 543

QY 564 TTCACTTTGTGTTTGGTGTGACTTATTAAGATTTCCGTTATACCTCTTAACATATATCTCG 623  
 Db 544 TTGATTAATGTTCAATCACCCTTCAACCTTGGCTTCCCTGTATACCTTTTACCAATATTTCC 603

QY 624 GGCAGAAATACGGAGGTTTGGCAACACCTTTGATATCCATGAGTCCAAATTTTCAAGAT 683  
 Db 604 GGCAGAAAGTATGAAGGTTTGGCAACCATTTTCAACCCCATGAGTCGATTTTCAAGAG 663

QY 684 CGTGAAGCGCTTCAAGTTTGTCTATTCGATTTGGCTTTCTTCGCTGTATTTTATGCAATC 743  
 Db 664 CGTGAAGCGTTCAAGTTTGTCTATTCGATTTGGCTTTCTTCGCTGTATTTTATGCAAGTT 723

QY 744 AAGCTTCTTAGCAGCAAAAGGGGACCTTGGATATCAATGTACGCAATTCAGTA 803  
 DB 724 AAACCTTGGGTAGCAGCAAAAGGCGCGCTGGGTGAGTGATTTAAGGAATTCAGTT 783  
 QY 804 CTAGGTGTACGCGTCTCTGTTTGTATACATATTTGACACACACCATTCTCACTC 863  
 DB 784 TTAGCGGTGTATCTTTTGTATATCACTCTTGACACACACCATTCTCTGCTG 843  
 QY 864 CCTCATATGATATCAACGGAATGAACTGSAATCAAAAGGCGCTTATCAACATGATAGG 923  
 DB 844 CCTCATATGATATCACTGAAATGAACTGCTCAAGAGGGCTTTGTCAACATTCATAGG 903  
 QY 924 GATTTGGGTTCTGAAATCGGGTTTTCACGACGTTAACAACACTCAAGCTTTGATCAT 983  
 DB 904 GACTTGGGTTCTGAAATGAGTGTCTCCATGATGTATACACACACTCAAGTATGATCAT 963  
 QY 984 TTGATCTATATCTTCCACATTTATATGCAAAAGGAGCAAGGATGCAATCAAGCCAGTG 1043  
 DB 964 CTGTTTTCATATCTTCCACACTATATGCAAGGAGCAAGGATGCAATCAACACATTC 1023  
 QY 1044 TTGGCGAGTACTATTAATGCAAGCACTCCATTTTCAAGCAATGATATGAGAGGCT 1103  
 DB 1024 TTGGCGAGTCTTTATTAAGATGATGAGCTCCATTTCTGAAGCAATGTGAGAGAGGCC 1083  
 QY 1104 AAGGATGCACTATCATCGAGCCCGATGAGATAGCAGCAAAAGTGTCTGTGATAC 1163  
 DB 1084 AAGGATGCACTTCTCATCGAGCTGAAAAAGGTGAGGGGTCCAAAGGTATATTTGTATC 1143  
 QY 1164 CACAAAGATGTAATCAA 1180  
 DB 1144 AATAAATTCATCATTA 1160

RESULT 7  
 AR367437 1358 bp DNA linear PAT 12-SEP-2003  
 LOCUS AR367437  
 DEFINITION Sequence 1 from patent US 6329518.  
 ACCESSION AR367437  
 VERSION AR367437.1 GI:34600636  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1358)  
 AUTHORS Green, A., Singh, S., Lenman, M. and Styenne, S.  
 TITLE Plant fatty acid epoxigenase genes and uses therefor  
 JOURNAL Patent: US 6329518-A 11-DEC-2001;  
 FEATURES  
 source 1..1358  
 /organism="Unknown"  
 /mol\_type="genomic DNA"  
 ORIGIN

Query Match 55.7%; Score 715.8; DB 6; Length 1358;  
 Best Local Similarity 78.2%; Pred. No. 3e-177;  
 Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;  
 QY 29 ATATATCAACAACATGGGTCTGTGTGTCGATGTCGATCGATGAGGAAAAACAT 88  
 DB 17 ATCATTTATCAACATGGGTCTGTGTGTCGATGTCGATCGATGAGGAAAAACATCGGT 70  
 QY 89 CCTGAAGCTGTGCGATGCAATCC--ACGTTACGTTAGCGATCGAAGAAAGCAT 145  
 DB 71 CATGAAAGCTGTGCGATGCAATCC--ACGTTACGTTAGCGATCGAAGAAAGCAT 130  
 QY 146 TCCTAACCATGCTTTAGCGATGTCATCCGATCATCATATGTTGTTCAATGATCT 205  
 DB 131 CCCGCCCATGCTTCCAGAGATGTAATCGGTCATCTTACTATGTTGTTCAAGATCT 190  
 QY 206 CATGTGTGCTTATGTTCTTACTACTGTTGCAACAGGTAATCCCTTTATTTCTACACC 265  
 DB 191 CATTAATGCTTCAATCTTCTACTTCTTGCCAAACATATATCTTACTTCTCTACTAG 250

QY 266 TCTGGCTTACCTAGATGCGCCGTTTACTGGTTTGTCAAGCTAGCATCTCACGGGCT 325  
 DB 251 TCTAGCCTACTTAGGTTGGCCGTTTACTGGTTGTCAAGCTAGCATCTCACGGGCTT 310  
 QY 326 CTGGGTCACTGGGTCAAGATGTGTGTCACATGATCTTATAGGACATTCAGTGTATGATGA 385  
 DB 311 ATGATCTCTCGGCAAGATGTGTGTCACATGATCTTATAGGACATTCAGTGTATGATGA 370  
 QY 386 CATGTGGATTTGCGTCCATTTGGGCTCTCTCAACCCCGATTTCTTGGAAATATAG 445  
 DB 371 CACTGGGCTTCACTCTCACTCAATTTCTCTCAACCCCGATTTCTTGGAAATATAG 430  
 QY 446 CCAGAGATACCAACGCCCAACAATTCATCTGATACAGTAAAGTTTACATCTCTTA 505  
 DB 431 TCACCGGAATACCATTTCCAAACAAGTTGATGATGATGATGATGATGATGATGATGATGATG 490  
 QY 506 ACGTAACTGGAAGTCAAGATTTATTCCAAACCTTTTAAACAATCCACCGGCGAGTGT 565  
 DB 491 AAGCAAGTCCAAACCTCGCGCTATCTATTAACCTTTTAAACAACCACTGGTCCGCTGT 550  
 QY 566 CACTTGGTGTGTGGTTGATTTAGATTTCCGTTATACCTTTAATATATCTCGGG 625  
 DB 551 GGTTTGATTAATCAATGTTCACTTGAATTTCTTTATACCTTTGACAAATATTTCCGG 610  
 QY 626 CAAGAAATACGGAAGGTTTGGCAACACTTGTATCCCATGATGCAATTTTCAACGATCG 685  
 DB 611 CAAGAAATACGAGTTTGGCAACACTTGTATCCCATGATGCAATTTTCAAGAAAGC 670  
 QY 686 TGAACGCGTTCAAGTTTGTCTATTCGATTTGCTGCTCTGTATTTATGCAATCAA 745  
 DB 671 TGACGCGTTTCAAGTCTTCTTGGATCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 730  
 QY 746 GCTTCTTGTACACAAAGGGGCACTTGGGTATCAACATTAACGAATTTCCAGTACT 805  
 DB 731 AGTTGCTGTACAAATGAAGAGCTGTGGTATGCGTGAATGATGATGATGATGATGATGATG 790  
 QY 806 AGGTGTAAAGCGTGTCTTCTGTTTGTATCAATTTTGCACACACACCATCTCACTCCC 865  
 DB 791 AGCGATATTAATCTTTTTCATGATGATCACTTTTGCACACACACCATCTCACTCCC 850  
 QY 866 TCATTAATGATTAACCGAATGAACTGATGAAAGGCGCTTATCAACATGATGATGAA 925  
 DB 851 TCATTAATGATTAACCGAATGAACTGATGAAAGGCGCTTATCAACATGATGATGAA 910  
 QY 926 TTTGGGTTCTGATGAGGTTTTCACAGATTAACACACTCAAGTCTTGCATCATTT 985  
 DB 911 CTTTGAATTCCTGAATGATGTTTTCATGATGATTAACACACTCAAGTCTTGCATCATTT 970  
 QY 986 GATCTCATATCTTCCATTAATCATGCAAGAAAGGAGCAAGGATGCAATCAAGCCAGTGT 1045  
 DB 971 GTTTTCATATCTTCCATTAATCATGCAAGAAAGGAGGATGCAATCAAGCCATTTT 1030  
 QY 1046 GGGCGAGTACTATAAATTCACAGACTCCATTTTCAAGCAATGATATAGAGGCTTA 1105  
 DB 1031 GGGGAGCTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1090  
 QY 1106 GGAATGATCTTACATCGAGCCGATGAGATGAGGACCAAGAGTGTCTTGTGATCA 1165  
 DB 1091 GGAATGATCTTACATCGAGCC--TGATGCAAGCTCAAGAGTGTCTTGTGATCA 1144  
 QY 1166 CAAGATGAATCAA 1180  
 DB 1145 TBAATTTGATCATTA 1159

RESULT 8  
 AX031160 1358 bp DNA linear PAT 20-SEP-2000  
 LOCUS AX031160  
 DEFINITION Sequence 1 from Patent W09846762.  
 ACCESSION AX031160  
 VERSION AX031160.1 GI:10278513  
 KEYWORDS



ORIGIN

/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"

Query Match 55.7%; Score 715.8; DB 6; Length 1358;  
Best Local Similarity 78.2%; Pred. No. 3e-177;  
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;

29 ATATATCAACAACATGGGTGCTGGTGTGCGATGTCGATCCATCTGAGGAAAAAATCAT 88  
Db 17 ATCATTTATCAACATGGGTGCTGGGTGCG-----TGCTGGACATCGGAAAAATCGCT 70  
Qy 89 CCTTGAACGTGTGCGCATGATCC---ACCGTTACGTTAAGCGATCGAAGAAAGCGAT 145  
Db 71 CATGGAAGCTGTCTAGTTGATCCAGTAACTCTTCACTGAGTAATGAAAGCAAGCAAT 130  
Qy 146 TCTTACCATTCCTTTGAGCATCTGTATCCGGTATCATATCATATGTTTCATGATCT 205  
Db 131 CCGTCCCATTCCTTCAGAGATCTGTATCCGGTATCATATGTTTGTCAAGATCT 190  
Qy 206 CATTTGGCCATATGCTTCTACTACCTTGAAACAGATATCCCTTATTCCTAGAC 265  
Db 191 CATTTGGCCATATGCTTCTACTACCTTGAAACAGATATCCCTTATTCCTAGAC 250  
Qy 266 TCTGCTTACCTAGCATGCGCCGTTTACTGTTTGTCAAGCTAGCATCTCACCGGCT 325  
Db 251 TCTAGCCATTAAGCTTGTGCGGTTTACTGTTTGTCAAGCTAGCATCTCACCGGCT 310  
Qy 326 CTGGGTCACTGGTCAACCAATGTGTGTCACATGATTTAGCACTACCATGATTTGATGA 385  
Db 311 ATGGATCTCGGCAACAGATGTGTGTCACATGATTTAGCACTACCATGATTTGATGA 370  
Qy 386 CATTTGGATTCGTTGCTTCATTCGCTCTCTGACCCGATTTCTTGGAAATATAG 445  
Db 371 CACTGTGGCTTCACTCTCCACTCATTTCTCTGACCCCGATTTCTTGGAAATATAG 430  
Qy 446 CCACAGAAATCAACACCGCAACAAATTCATCGATAGATGAAGTTTACATTCCTAA 505  
Db 431 TCACCGGAATACCATTCACACAGATGTGTGTCACATGATTTAGCACTACCATGAT 490  
Qy 506 ACCTAATTCGAAGTCAAGATTTATTCGAATCTTTTACCAATTCACCCGGGCGAGTGT 565  
Db 491 AAGGAATTCGAAGTCAAGTGTGTGTCACATGATTTAGCACTACCATGATTTAGCA 550  
Qy 566 CACTTGTGTTGCTGATGATTTAGATTTCCGTTATTCCTTAACTATATCTGCGG 625  
Db 551 GCTTTGATTTATCATGTTTACCTTAGATTTCTTTATACCTTTCGACAAATATTTCCGG 610  
Qy 626 CAAGAAATACGGAAGTTTGCACACATTTGATCCATGATCCAAATTTTCAAGATCG 685  
Db 611 CAAGAAATACGGAAGTTTGCACACATTTGATCCATGATCCAAATTTTCAAGATCG 670  
Qy 686 TGAACGGGTTCAGTTTGTCTATCCGATTTGCTTCTGCTGTATTTTATGCAATCAA 745  
Db 671 TGAACGGGTTCAGTTTGTCTATCCGATTTGCTTCTGCTGTATTTTATGCAATCAA 730  
Qy 746 GCTTCTTGTAGCAGCAAAAGGGGAGCTTGGGATATCAAGATGATGCAATTCAGTACT 805  
Db 731 AGTTGCTGTAGCAGCAAAAGGGGAGCTTGGGATATCAAGATGATGCAATTCAGTACT 790  
Qy 806 AGGTGAAGCGTGTCTTCTGTTTGTATCAATTTTGCACACACCATCTCTCACTCCC 865  
Db 791 AGGGGTATTTACCTTTTGTATGATCACTTTTGCACACACCATCTCTCACTCCC 850  
Qy 866 TCAATTAATGATTCACCGAATGGAATGATTAAGGCGCTTATTCACATTCATGATGGA 925  
Db 851 TCAATTAATGATTCACCGAATGGAATGATTAAGGCGCTTATTCACATTCATGATGGA 910  
Qy 926 TTTGGGTTCTGATGAGGTTTTCACAGATTCACACACTACGCTGATTCATCTT 985  
Db 911 CTTTGGATTCCTGAATGAGTGTTCATGATTTACACACTCATGATGATCATTT 970  
Qy 986 GATCTCATACATTCACATTAATGCAAGAAAGGATGCAATCAAGCAAGTGT 1045

Db 971 GTTTTCATATCATTCACACTATCATGCAAGGAGCAAGGATCAATCAAGCCAACTTT 1030  
Qy 1046 GGGGAGTACTATAAATTCAGACAGACTCCAAATTTTCAAGCAATGATATAGAGGCTAA 1105  
Db 1031 GGGGAGTACTATAAATTCAGACAGACTCCAAATTTTCAAGCAATGATATAGAGGCTAA 1090  
Qy 1106 GGAATGATCTACATTCAGACCCGATGAGATAGGACACAAAGTGTCTGCTGATCA 1165  
Db 1091 GGAATGATCTACATTCAGACCCGATGAGATAGGACACAAAGTGTCTGCTGATCA 1144  
Qy 1166 CAAGATGATCAAA 1180  
Db 1145 TAAATGATCATTA 1159

## RESULT 10

CPY16283 1358 bp mRNA linear PLN 13-MAY-1998  
LOCUS Crepis palaestina mRNA for delta 12 fatty acid epoxigenase.  
DEFINITION Y16283  
ACCESSION Y16283  
VERSION Y16283.1 GI:3135017  
KEYWORDS delta 12 fatty acid epoxigenase.  
SOURCE Crepis palaestina  
ORGANISM Crepis palaestina  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Crepis.

## REFERENCE

1 Lee, M., Lennan, M., Banas, A., Bafor, M., Singh, S., Schweizer, M.,  
Nilsen, R., Liljeborg, C., Dahlqvist, A., Gummesson, P., Sjoedahl, S.,  
Green, A., and Stymne, S.  
Identification of non-heme diiron proteins that catalyze triple  
bond and epoxy group formation  
Science 280 (5365), 915-918 (1998)  
MEDLINE 98239771  
PUBMED 9572738  
REFERENCE 2 (bases 1 to 1358)

AUTHORS Lennan, M.E.  
TITLE Direct Submission  
SUBMITTED (21-JAN-1998) M.E. Lennan, Dept of Plant Breeding  
Research, SLU, Herman Ehles V 2-4, 26831 Svalov, SWEDEN

## FEATURES

LOCATION/Qualifiers  
1..1358  
/organism="Crepis palaestina"  
/mol\_type="mRNA"  
/db\_xref="taxon:72611"  
/clone="pcp12"  
/clone\_1bp="lambda ZAP"  
/dev\_stage="developing seed"  
30..1154  
/codon\_start=1  
/product="delta 12 fatty acid epoxigenase"  
/protein\_id="CAI76156.1"  
/db\_xref="GI:3135018"  
/db\_xref="GOA:O65771"  
/db\_xref="SPTREMBL:O65771"  
/translation="MGAGGRTSEKSMERVSVDVPTSLSEIKOAIIPPHCFORSVI  
RSSYVVDLILAVIFPLANTYIPLPTSLAVLAWVWFQASVLTGLMIGHECG  
HHAFSYTWEDDVGFILSHFLTPYSWFSRHHNSNTSISIDNDEVIPKSKSLA  
RIYKLNPPRGLVLIIMPTLGPILVILNISGKKDRFANHPDPMSPIFKBEREQ  
VPLSDILAVPGYIVAVANKGAAWACWGVPGVFPFVPTFLHTTHOSSPHY  
DSTBMKIRKALSAIDRDFPLNSVPHDVTHVMMHLPSYIPIHTAKERDAIKPIL  
GDFYMDRITPLKAMWREGRCMYIEPDSKLKQVYVYHKL"

## CDS

## ORIGIN

Query Match 55.7%; Score 715.8; DB 8; Length 1358;  
Best Local Similarity 78.2%; Pred. No. 3e-177;  
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;

29 ATATATCAACAACATGGGTGCTGGTGTGCGATGTCGATCCATCTGAGGAAAAAATCAT 88



Db 17 ATCAATTATCAACATGGGTGCGCGGTG-----TGGTGGACATGGAAAAATCGGT 70  
Qy 89 CCTTGAAGCTGTGCGCATGATCC--ACGGTTCAGTTAAGCATCTGAAGAAAGCAT 145  
Db 71 CATGGAAGGTGTCTGATGATCCAGTACCTTCCATGATGATGATGAAAGCAAGCAT 130  
Qy 146 TCTTACCATGCTTTGAGCGATCTGTCACTCCGATCATATATGTTGTTGATGATCT 205  
Db 131 CCTCCCATGCTTCCAGAGATCTGTATCCGATCATCTTATATGTTGTTCAAGACT 190  
Qy 206 CATTTGTCCTATGCTTCTACTACCTGCAAGAGATATCCCTTATTTCCATGAC 265  
Db 191 CATTTATGCTTACATCTTCTTCTCTTCCCAACATATATCTTCTTCTTCTACTAG 250  
Qy 266 TCTGCTTACCTAGCATGCGCGCTTACTGTGTTTGTCAAGTACATCTTCAAGCGCT 325  
Db 251 TCTAGCTTACTAGTGTGCGCGCTTACTGTGTTTGTCAAGTACATCTTCAAGCGCT 310  
Qy 326 CTGGGTCACTGCGTCAAGATGTGTCACTGATGATGATGATGATGATGATGATGAT 385  
Db 311 ATGATATCTGCGCCCAAGATGTGTCACTGATGATGATGATGATGATGATGATGAT 370  
Qy 386 CATTTGTCCTATGCTTCTACTACCTGCAAGAGATATCCCTTATTTCCATGAC 445  
Db 371 CATTTGTCCTATGCTTCTACTACCTGCAAGAGATATCCCTTATTTCCATGAC 430  
Qy 446 CCACAGATATCAACACGCAACCAAAATTCATCTGATACATGATGATGATGATGAT 505  
Db 431 TCACCGGATATCACTTCAACACAGATGATGATGATGATGATGATGATGATGATGAT 490  
Qy 506 ACCTTATGCTGAAAGTCAAGATTTATCCAACTTTTAAACAATCAACCCGCGCATG 565  
Db 491 AAGCAAGTCAAACTGCGCGATCTATTAACCTTTTAAACAACCACTGCGCATG 550  
Qy 566 CACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625  
Db 551 GCTTTGATTTATCATGTTCACTTCAAGATTTCTTTAATCTTTGCAAAATTTTCCG 610  
Qy 626 CAAGAAATACGGAAGTTCGCAACCACTTGTATCCATGATGATGATGATGATGATG 685  
Db 611 CAAGAAATACGGAAGTTCGCAACCACTTGTATCCATGATGATGATGATGATGATG 670  
Qy 686 TGAAGCGCTCAAGTTTGTCTATCCGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 745  
Db 671 TGAGGCTTCAAGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730  
Qy 746 GCTTCTGATGAGCAAAAGGCGAGCTTGGTATCAACATGATGATGATGATGATGAT 805  
Db 731 AGTTCCTGATGAGCAAAAGGCGAGCTTGGTATCAACATGATGATGATGATGATGAT 790  
Qy 806 AGGTGTAAGCGTGTCTTCTGTTTGTATCATATTTGCAACAACCATCTCTCACTCC 865  
Db 791 AGGTGTAAGCGTGTCTTCTGTTTGTATCATATTTGCAACAACCATCTCTCACTCC 850  
Qy 866 TCAATTTATGATCAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 925  
Db 851 TCAATTTATGATCAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 910  
Qy 926 TTTGGGTTTCTGATGCGGTTTCTCAAGAGTTTCAACAACCTCAAGCTTGTGATCAT 985  
Db 911 CTTTGGATTTCTGATGCGGTTTCTCAAGAGTTTCAACAACCTCAAGCTTGTGATCAT 970  
Qy 986 GATCTCATATCTTCAATTTATCATGATGATGATGATGATGATGATGATGATGATGAT 1045  
Db 971 GTTTTCAATATCTTCAATTTATCATGATGATGATGATGATGATGATGATGATGATGAT 1030  
Qy 1046 GGGGGAAGTATTAATAATGACAGATCTCAATTTTCAAGCAATGATGATGATGATGAT 1105  
Db 1031 GGGGGAAGTATTAATAATGACAGATCTCAATTTTCAAGCAATGATGATGATGATGATGAT 1090  
Qy 1106 GGAATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1165  
Db 1091 GGAATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1144

Qy 1166 CAAGATGATCAAA 1180  
Db 1145 TAAATGTGATCAT 1159  
RESULT 11  
AR367438  
LOCUS AR367438 1312 bp mRNA linear PAT 12-SEP-2003  
DEFINITION Sequence 3 from patent US 6329518.  
ACCESSION AR367438  
VERSION AR367438.1 GI:34600637  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1312)  
AUTHORS Green,A., Singh,S., Ienman,M. and Styhme,S.  
TITLE Plant fatty acid epoxigenase genes and uses therefor  
JOURNAL Patent: US 6329518-A 3 11-DEC-2001;  
FEATURES  
location/Qualifiers  
1..1312  
/organism="unknown"  
/mol\_type="mRNA"  
ORIGIN  
Query Match 54.9%; Score 705.4; DB 6; Length 1312;  
Best Local Similarity 78.6%; Pred.No. 1.6e-174;  
Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;  
Qy 77 GGGAAAAACATCTCTTGAACGTGTGCGATGATCC--ACGGTTCAGTTAAGCATCT 133  
Db 55 GGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 114  
Qy 134 GAAAGAGCGATCTCTTGAACGTGTGCGATGATCCGATCATCATATATG 193  
Db 115 GAAAGAGCGATCTCTTGAACGTGTGCGATGATCCGATCATCATATATG 174  
Qy 194 TGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253  
Db 175 TGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 234  
Qy 254 TATTTCTTACACTGCTGCTTACCTGATGATGATGATGATGATGATGATGATGAT 313  
Db 235 TCTCTCTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 294  
Qy 314 CCTCAGCGCTCTGCGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 373  
Db 295 CTTCACTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 354  
Qy 374 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433  
Db 355 ATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414  
Qy 434 TTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 493  
Db 415 TTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
Qy 494 TTACATTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 553  
Db 475 TTACATTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 534  
Qy 554 CGGGGAGTGTCTTCTGTTTGTGATGATGATGATGATGATGATGATGATGATGAT 613  
Db 535 TGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594  
Qy 614 TAAATCTGCGGCAAGAAATGCGGAGGTTTGGCAACCACTTTGATCCATGATGAT 673  
Db 595 AAATATTTCCGCAAGAAATGCGGAGGTTTGGCAACCACTTTGATCCATGATGAT 654  
Qy 674 TTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733  
Db 655 TTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714



QY 734 TTATGATCAAGCTTCTTGTAGCAGCAAAAGGGGAGCTTGGGTAATCAATGTAAGC 793  
DB 715 TTATGATTAATTAAGTGTGAGCAATAAAGAGAGCTCTGGTGGCGGTGATGTAAG 774  
QY 794 AATTCCAGTACTAGGTGTAAGCGTGTCTCTTTTGTATCATATTTGGACCAACCA 853  
DB 775 AGTTCGGGTGTAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 834  
QY 854 TCTCTCACTCCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 913  
DB 835 TCAAGTCGCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 894  
QY 914 AATGATAGGATTTGGGTTCTGTAATCGGTTTTCACGACGTTTACACACTCAAGT 973  
DB 895 AATGATAGGACCTTTGGGTTCTGTAATGTTTTCATGATGTAACACACTCAAGT 954  
QY 974 CTTCATCATTTGATCTCATACATTTCCACATTTATGCAAAAGAGAGGATGCAAT 1033  
DB 955 CATCATCATTTGTTTTCATCATTTCCACATTTATGCAAAAGAGAGGATGCAAT 1014  
QY 1034 CAAGCCAGTGTGGGCGAGTACTATAAATGACAGCACTCAATTTTCAAGCAATGTA 1093  
DB 1015 CAAGCCAGTGTGGGCGAGTACTATAAATGAGATGAGACTCAATTTAAAGCAATG 1074  
QY 1094 TAGAGAGGCTAAGATGATCATCTATCATGAGCCGATGAGATGAGCAAAAGGATG 1153  
DB 1075 GAGAGAGGCGAGGAGATGATCATGATGAGCC-----TGATGCAAGCTCAAGGATG 1128  
QY 1154 GTTCTGTACCAAGATGTAATCAAA 1180  
DB 1129 TTATGATCATTAATTTGATGATCA 1155

RESULT 12  
AX031162  
LOCUS 1312 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 3 from Patent WO9846762.  
ACCESSION AX031162  
VERSION AX031162.1 GI:10278515  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Green, A., Singh, S., Styenne, S. and Lemman, M.  
TITLE Plant fatty acid epoxidase genes and uses therefor  
JOURNAL Patent: WO 9846762-A 3 22-OCT-1998;  
GREEN ALLAN (AU); SINGH SURINDER (AU); COMM SCIENT IND RES ORG  
(AU); STYENNE STEN (SE); LEMMAN MARIT (SE)  
FEATURES  
SOURCE  
1. 1312  
/organism="Crepis sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:137775"  
26. 1150  
/note="unassigned protein product"  
/codon\_start=1  
/protein\_id="CAC09645.1"  
/db\_xref="GI:10278516"  
/translation="MGAGRGRTSEKSMVESVDYPTPSISLDAKQAIIPHCPRSVI  
RSSYVVDLAIAYFYFLANTYIPNLPHPLAYLWPCQASVLTGLMILHEG  
HHAYSNYWDVDTGFIHSFLTPYPSMKSHRNHSNTSSINDDEVILPKSKK  
RIYLANNPRLVLVIMTIGPPLVLTNI SGKDRANHPDPMSPKXERRO  
VFLSDGLIAVFGIKVAVANKAAMVAAGVPLGVTPEFVITLHHTHOSPHY  
DSTEMNIRGLSAIDKDFGLNSVFDVYTHYMHLSIIPHYHAKRADAIKPLI  
GDFYMDITPLKAMRBRECMTEIPDSKLGKGYWYHKL"

ORIGIN

Query Match 54.9%; Score 705.4; DB 6; Length 1312;  
Best Local Similarity 78.6%; Pred. No. 1.6e-174;  
Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;  
QY 77 GGGAAAAACATCTTGAAGGTGCGAGTCAATCC--ACCGTTCAAGTTAAACGATCT 133  
DB 55 GGAAGAGTGGTCAATGGAAGGTGCTCAAGTGAATCAAGTCACTTCACTCAAGATGATTT 114  
QY 134 GAAGAAAGCATCTTCAACCATTTGCTTGAAGCATCTGTCAATCCGGTCAATCAATATGT 193  
DB 115 GAAGAAAGCATCTTCAACCATTTGCTTGAAGCATCTGTCAATCCGGTCAATCAATATGT 174  
QY 194 TGTTCAATGATCTCAATTTGCTTGAATGCTTCTTCAATCTTGAAGCAAGATATATCTCT 253  
DB 175 TGTTCAAGATCTCAATTTGCTTGAATGCTTCTTCAATCTTGAAGCAAGATATATCTCT 234  
QY 254 TATTCCTACACTTGGCTTACCTAGCATGAGCCGCTTATCGTGTGTTGTCAAGTAGAT 313  
DB 235 TCTCCCTCATCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 294  
QY 314 CCTCAGCGGCTCTGGGTCATCGGTCAAGATGAGTCAACCATGATTTAGCACTACCA 373  
DB 295 CCTCAGCTGGTATGATGATCTCGGCAATGATGATGATGATGATGATGATGATGATGAT 354  
QY 374 GTTGATTTGATGATCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 433  
DB 355 ATGGTTGAGCACTGAGGCTTCAATCATCTTCAATTTCTCTCAACCCGCTATTTCTC 414  
QY 434 TTGAAATATATGCAAGATGATCAACAGCCCAACAAATTTCACTCGATTAAGTGAAGT 493  
DB 415 TTGAAATATGCAAGTCAAGATGATCAACAGCCCAACAAATTTCACTCGATTAAGTGAAGT 474  
QY 494 TTACATTTCTTAAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 553  
DB 475 TTACATTTCTTAAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 534  
QY 554 CGGCGAGTGTCACTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 613  
DB 535 TGCTGACGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 594  
QY 614 TATATCTCGGCGAAGAAATACGAGAGTTTGGCAACCACTTTATGCCATGATCCAAAT 673  
DB 595 AATATTTCCGCGAAGAAATACGAGAGTTTGGCAACCACTTTATGCCATGATCCAAAT 654  
QY 674 TTCAAGATGATGAAGCGGTTTCAAGTTTGTGATTTGATTTGATTTGATTTGATTTGATTT 733  
DB 655 TTCAAGATGATGAAGCGGTTTCAAGTTTGTGATTTGATTTGATTTGATTTGATTTGATTT 714  
QY 734 TTATGATCAAGCTTCTTGTAGCAGCAAAAGGGGAGCTTGGGTAATCAATGTAAGC 793  
DB 715 TTATGATTAATTAAGTGTGAGCAATAAAGAGAGCTCTGGTGGCGGTGATGTAAG 774  
QY 794 AATTCCAGTACTAGGTGTAAGCGTGTCTCTTTTGTATCATATTTGGACCAACCA 853  
DB 775 AGTTCGGGTGTAGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 834  
QY 854 TCTCTCACTCCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 913  
DB 835 TCAAGTCGCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 894  
QY 914 AATGATAGGATTTGGGTTCTGTAATCGGTTTTCACGACGTTTACACACTCAAGT 973  
DB 895 AATGATAGGACCTTTGGGTTCTGTAATGTTTTCATGATGTAACACACTCAAGT 954  
QY 974 CTTCATCATTTGATCTCATACATTTCCACATTTATGCAAAAGAGAGGATGCAAT 1033  
DB 955 CATCATCATTTGTTTTCATCATTTCCACATTTATGCAAAAGAGAGGATGCAAT 1014  
QY 1034 CAAGCCAGTGTGGGCGAGTACTATAAATGACAGCACTCAATTTTCAAGCAATGTA 1093  
DB 1015 CAAGCCAGTGTGGGCGAGTACTATAAATGAGATGAGACTCAATTTAAAGCAATG 1074  
QY 1094 TAGAGAGGCTAAGATGATCATCTATCATGAGCCGATGAGATGAGCAAAAGGATG 1153







GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 12:44:38 ; Search time 2555 Seconds  
(without alignments)  
15018.748 Million cell updates/sec

Title: US-10-069-772-1  
Perfect score: 1285  
Sequence: .1 aaaaagcctctctctcgtcga.....aaaaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hlc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hlc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vtc:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_prc:*
25:	em_gss_rpd:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	505.6	39.3	691 13	BQ994479 OG97F12.Y
2	495.4	38.6	725 13	BQ866257 OG97F15.Y
3	437	34.0	613 14	CF098768 QHN8F08.Y
4	406.4	31.6	624 14	CF096571 QHN23019.

5	358.6	27.9	530 14	CF091557 QHM8J13.Y
6	358.2	27.9	989 14	CK269848 EST715926
7	352	27.4	1856 11	AY104050 Zee maye
8	350.6	27.3	1080 13	BQ238570 D801.13f0
9	349	27.2	973 14	CK262936 EST709014
10	342	26.6	918 14	CK269030 EST715108
11	336.6	26.2	963 14	CK270183 EST716261
12	332.2	25.9	764 10	AM201738 g106f08.Y
13	330.4	25.7	948 14	CK278983 EST725061
14	330	25.7	616 13	BQ973950 QH114314.
15	329.8	25.7	831 14	CF511517 CAPud00002
16	327.6	25.5	756 13	BQ836275 T084F10.P
17	323.4	25.2	911 14	CF215372 CAST0001
18	322.4	25.1	784 12	B1925058 EST544947
19	321.8	25.0	763 13	BQ853589 QCB20018.
20	320.4	24.9	1807 12	B1683572 Rocheferd
21	318.2	24.8	809 10	BE988745 EST430532
22	311.6	24.2	753 13	BQ857435 QGB7104.Y
23	304.6	23.7	891 14	CK250323 EST733960
24	302.6	23.5	714 9	AM100780 sdb1b05.Y
25	302	23.5	870 14	CF212392 QGB9F12.Y
26	300.8	23.4	798 13	BQ858101 QGB9F12.Y
27	300.8	23.4	901 14	CK263172 EST709250
28	300.4	23.4	772 12	B1933814 EST553703
29	294.6	22.9	876 14	CD760583 L1nfAD2.L
30	294	22.9	676 14	CD715491 VVB212E12
31	294	22.9	676 14	CD715677 VVB215F08
32	294	22.8	676 14	CD719893 VVB166C10
33	293.6	22.8	823 14	CF511848 CBud00004
34	293	22.8	676 14	CD717551 VVB140E01
35	292.4	22.8	705 13	BQ939824 QGF5J04.Y
36	291.8	22.7	755 12	BM109924 EST557460
37	291.2	22.7	901 14	CB978093 CAB40005
38	290.2	22.6	905 14	CB349164 CAB2SG000
39	290	22.6	558 13	BQ981901 QCB15A08
40	289.8	22.6	667 14	CD717827 VVB143D12
41	289.8	22.6	757 14	CA801285 sauo3e10.
42	288.2	22.5	696 13	BU010610 QGJ13P22.
43	288.2	22.4	707 14	CA782495 sat29e08.
44	287.8	22.4	704 14	CF809003 pshB041XL
45	286.8	22.3	665 14	CD717639 VVB141D06

## ALIGNMENTS

RESULT 1  
BQ994479  
LOCUS  
DEFINITION  
OG97F12.YG.ab1 OG EFGHU lettuce serricola Lactuca sativa cDNA clone  
ACCESSION  
BQ994479  
VERSION  
BQ994479.1 GI:22414014  
KEYWORDS  
EST.  
SOURCE  
Lactuca sativa  
ORGANISM  
Lactuca sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
1 (bases 1 to 691)  
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
Ellison,P., Kolkmann,J., Stabaugh,M.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compogenomics.ucdavis.edu/  
unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Agriculture Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742

TITLE  
JOURNAL  
COMMENT



Db 102 AGATCTGGAGAGCTGCTCCAGT-GATCCACCGCTTTTCAATTAAGTATTAAGAAAGCGA 160  
 Qy 145 TTCTACCATTCATTCCTTTGAGGATCTGTATCCGGTCACTCATATGATGTTGATGATC 204  
 Db 161 TCCCTGCGCATTCCTTCAAGGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATC 220  
 Qy 205 TCATTTGTTGCTATGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 264  
 Db 221 TGATTTGTTGCTATGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 280  
 Qy 265 CTCTGCTTACCTGATCCAGGCGGCTTCACTGCTTCTTCACTGATGATGATGATGATGATG 324  
 Db 281 CTCTGCTTACCTGATCCAGGCGGCTTCACTGCTTCTTCACTGATGATGATGATGATGATG 340  
 Qy 325 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 384  
 Db 341 TATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400  
 Qy 385 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 444  
 Db 401 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460  
 Qy 445 GCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 504  
 Db 461 GCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 520  
 Qy 505 AACGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 564  
 Db 521 AACGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 580  
 Qy 565 TCATTTGTTGCTATGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 624  
 Db 581 TCATTTGTTGCTATGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 640  
 Qy 625 GCAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 684  
 Db 641 GCAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 700  
 Qy 685 GTGAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 709  
 Db 701 GCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725

RESULT 3  
 CF098768/c 613 bp mRNA linear EST 22-JUL-2003  
 LOCUS QHN8F08.Y9.ab1 QH\_N sunflower H. argophyllus (drought stress)  
 DEFINITION Helianthus argophyllus cDNA clone QHN8F08, mRNA sequence.  
 ACCESSION CF098768  
 VERSION GI:33137835  
 KEYWORDS EST.  
 SOURCE Helianthus argophyllus  
 ORGANISM Helianthus argophyllus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Helianthus.  
 1 (bases 1 to 613)  
 Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,  
 Lan, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
 Ellison, P., Kolman, J., Slabaugh, M. S., Livingston, K., Zhou, Y.,  
 Lai, Z., Church, S., Jackson, L. and Bradford, K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compositae.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Armadillo Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
 belongs to contig QH\_CA\_Contig6400, see http://cgdb.ucdavis.edu/

for details.  
 Plate: QHN8 row: F column: 08.  
 Location/Qualifiers  
 1..613  
 /organism="Helianthus argophyllus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:73275"  
 /clone="QHN8F08"  
 /lab\_host="E. coli"  
 /clone\_lib="QH\_N sunflower H. argophyllus (drought stress)"  
 /note="Vector: pGEM-T. The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and cloned into a high-copy vector pGEM-T. Details of library construction can be obtained at http://cgdb.ucdavis.edu/"

# ORIGIN

Query Match 34.0%; Score 437; DB 14; Length 613;  
 Best local similarity 85.8%; Pred. No. 7.9e-54;  
 Matches 485; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 37 AACATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 96  
 Db 565 AACATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506  
 Qy 97 GTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 156  
 Db 505 GTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446  
 Qy 157 GCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 216  
 Db 445 GCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 386  
 Qy 217 ATGCTTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 276  
 Db 385 ATGCTTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 326  
 Qy 277 TAGATGAGCGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 336  
 Db 325 TAGATGAGCGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 266  
 Qy 337 GTCAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 396  
 Db 265 GTCAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 206  
 Qy 397 TCGTCTTCACTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 456  
 Db 205 TCGTCTTCACTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146  
 Qy 457 ACCAGCGCAACAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 516  
 Db 145 ACCAGCGCAACAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 86  
 Qy 517 AGGTCAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 576  
 Db 85 AAGTTCAGTTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26  
 Qy 577 TTGCTGATCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 601  
 Db 25 TTGCTGATCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1

RESULT 4  
 CF096571 624 bp mRNA linear EST 22-JUL-2003  
 LOCUS QHN23J19.Y9.ab1 QH\_N sunflower H. argophyllus (drought stress)  
 DEFINITION Helianthus argophyllus cDNA clone QHN23J19, mRNA sequence.  
 ACCESSION CF096571  
 VERSION GI:33135638  
 KEYWORDS EST.  
 SOURCE Helianthus argophyllus  
 ORGANISM Helianthus argophyllus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.  
1 (bases 1 to 624)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Assumdeon Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
belong to contig QH\_Ca.Contig3889, see http://cgdb.ucdavis.edu/ for details.  
Plate: QHN23 row: J column: 19.  
Location/Qualifiers  
1..624  
/organism="Helianthus argophyllus"  
/mol\_type="mRNA"  
/db\_xref="taxon:73275"  
/clone="QH23J19"  
/lab\_host="E.coli"  
/note="Vector: pGBM-T. The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and cloned into a high-copy vector pGBM-T. Details of library construction can be obtained at http://cgdb.ucdavis.edu/"

ORIGIN

Query Match 31.6%; Score 406.4; DB 14; Length 624;  
Best Local Similarity 84.2%; Pred. No. 2e-49;  
Matches 458; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

606 CTTTAACTAATATCGGGCAAGAAATACGGAGGTTGCCAACCTGATCCCATG 665  
|||||  
1 CTTGACTAATCTTGGCAAGAAATACGGAGGTTGCCAACCTGATCCCATG 60  
666 AGTCAATTTTCAAGATCGTGAACGCTTCAAGTTTGTATCCGATTCGCTCTC 725  
61 AGTCGATTTTCAAGATCGTGAAGAAATACGTTTATATCGATATGATTTCTT 120  
726 GCTGATTTTATGATCAAGCTTTTGTAGCAAGAAAGGGGCGCTTGGTATCAAC 785  
121 GCGGTTTGTATGCAACTAAGCTTGTAGAAAGGAGGGGTAACTTGGGTGCAAGC 180  
786 ATGTACGAATTCAGTACTAGTGAACGCTTCTCGTTTGTATCAATATTGGAC 845  
181 ATGTATTAATTCGCTGCTAGGTTTCAATGTTTTCGTTTATCATATTTGCAC 240  
846 CACACCATCTCTCACTCCCTCATTAATGATCAACCGATGGAAGTGAAGCGCC 905  
241 CATACCATCTCTCATTAATGATGATTCACCGATGGAAGTGAAGGAGGCA 300  
906 TTATTAACAATGATGAGGATTCGGGTTCCGATCGGGTTTCCAGAGCTTACAC 965  
301 TTATTCGAACAATGATGAGGATTCGGATTCCTAAATAGGGTTTCCAGATGTCAC 360  
966 ACTCAGCTTTCGATCATTTGATCTCATACATTCACATTAATCATGCAAGAGCAAG 1025  
361 ACTCAGCTTTCGATCATTTGATCTCTGATCATTCACATTAATCATGCAAGAGCAAG 420  
1026 GATGCAATCAAGCCAGTGTGGCGAGTACTATAAATGACAGGACTTCATTTTCAA 1085  
421 GACGCGATCAAGCCAGTGTGGCGAGTATTATAAGATGATGAGACCCCATTTTCAAG 480  
1086 GCATGTATAGAGGCTTAAGGATGATCTATCATGACGCCGATGAGGATGCGAGCAC 1145

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.  
1 (bases 1 to 530)  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Assumdeon Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]  
belong to contig QH\_Ca.Contig36400, see http://cgdb.ucdavis.edu/ for details.  
Plate: QHM8 row: J column: 13.  
Location/Qualifiers  
1..530  
/organism="Helianthus argophyllus"  
/mol\_type="mRNA"  
/db\_xref="taxon:73275"  
/clone="QH8J13"  
/lab\_host="E.coli"  
/note="Vector: pBRCNVAS11ab. The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector. Details of library construction can be obtained at http://cgdb.ucdavis.edu/"

ORIGIN

Query Match 27.9%; Score 358.6; DB 14; Length 530;  
Best Local Similarity 84.7%; Pred. No. 1.7e-42;  
Matches 414; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

481 GCAATGTGAGAGGCGCAAGAAATGATCTTACATCGAACCGAGTGAAGATGCGAAGC 540  
1146 AAAG 1149  
541 AAGG 544

CF091557 530 bp mRNA linear EST 22-JUL-2003  
DEFINITION QHM8J13.yg.ab1 QH M sunflower H. argophyllus Helianthus argophyllus  
CDNA clone QHM8J13, mRNA sequence.  
CF091557  
CF091557.1 GI:33130624  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Helianthus argophyllus  
Helianthus argophyllus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

10 CTTCTGTGAGGATTAATTAATATATCAACATGAGGCTGTGTGATGTGATC 69  
42 CTCATCTCTGAGGTTATCAACATCCACCAATGAGGCTGAGTGGCCGATGTGAGC 101  
70 CATCGAGGAGAAAAAACAATCTTGAACGTGTGCCAGTGCATCCAGTTTCAAGTGAAG 129  
102 CATCGAGGAGGAGAAAAACAATCTTGAACGTGTGCCAGTGCATCCAGTTTCAAGTGAAG 161  
130 ATCTGAAGAAAGCGATTCCTACCATTCCTTTGAGCGATCTGTCAATCGGTCATCATCT 189  
162 ATCTGAAGAAAGCGATTCCTACCATTCCTTTGAGCGATCTGTCAATCGGTCATCATCT 221  
190 ATGTGTTCAATGATCTCATTTGTGCTTATGTTCTTACTACTTGCAGAAACAGTATATCC 249



Db 222 ATGTGTTACAGACCTCATTTGTCCTTATGATTTACTTCTTCCCAACATCATCACC 281  
 Oy 250 CTCTTATTCCTTACACCTTGGCTTACCTAGACAGGCGGTTTACGTTTGTCAAGCTA 309  
 Db 282 CTCTTCTTCTTCAACCCCGGCGGTTTACTTACGAGGCGGTTTACTGTTTGTCAAGCTA 341  
 Oy 310 GCATCTTCAACCGGCTTGGTTCATCTGTCACGAAATGTGTCAACCATCATTTAGCAGCT 369  
 Db 342 GCATCTTCAACCGGCTTGGTTCATCTGTCACGAAATGTGTCAACCATCATTTAGTACT 401  
 Oy 370 ACCAGTTGATGATGACATTTGTTGATTTGTTCTTCAATTCGGCTCTC-CTCAACCCGTTAT 428  
 Db 402 ACCAATTTGATGATGACATTTGTTGATTTGTTCTTCAATTCAGCTCTTATACCCCTTAT 461  
 Oy 429 TTCTCTTGAATATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGAT 488  
 Db 462 TTCTCTTGAATATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGATGACGAGAT 521  
 Oy 489 GAGGTTTAC 497  
 Db 522 GAGGTTTAC 530

RESULT 6  
 CK269848 989 bp mRNA linear EST 12-DEC-2003  
 LOCUS CK269848  
 DEFINITION EST15926 potato abiotic stress cDNA library Solanum tuberosum cDNA  
 clone POACP38 5' end, mRNA sequence.

ACCESSION CK269848  
 VERSION CK269848.1 GI:39826826  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum

Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum.  
 Buell, C.R., Hart, A., Ziemann, V., Karameycheva, S.A. and Baker, B.  
 1 (bases 1 to 989)  
 Generation of ESTs from abiotic stressed potato tissue  
 Unpublished (2003)  
 CONTACT: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 Clones can be requested from TIGR via potato@tigr.org  
 Seq primer: ATT TAG GTG ACA CTA TAG.  
 Location/Qualifiers

FEATURES  
 Source

1..989  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="POACP38"  
 /tissue\_type="abiotic stress treated leaf and root tissue"  
 /lab\_host="DH10B-Toni"  
 /clone\_lib="potato abiotic stress cDNA library"  
 /note="vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;  
 supplier: Solanum tuberosum var. Kennebec plants were  
 grown from cuttings on a 16hr light/8 hr dark cycle at 25  
 C for 3-4 weeks. Abiotic stress conditions were applied to  
 four separate sets of plants. Set 1 involved saturation of  
 the soil with 150 mM NaCl and tissues were harvested at  
 following application of the salt stress (leaves: 2hr,  
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
 Set 2 were grown under the standard conditions and then  
 were water stressed by withdrawal of further watering  
 applications. Drought stressed plants were harvested after  
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
 and 5d). Set 3 were grown under the standard conditions  
 and then were cold stressed by placement at 4 C. Cold  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,

2d. Set 4 were grown under the standard conditions and  
 then were heat stressed by placement at 35 C. Heat  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d and 4d and heat-stressed roots were harvested at 6 hr,  
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
 equal RNA from each tissue and stress was pooled to  
 construct the cDNA library. RNA sample."

ORIGIN  
 Query Match 27.9%; Score 358.2; DB 14; Length 989;  
 Best Local Similarity 62.9%; Pred. No. 1.3e-42;  
 Matches 555; Conservative 0; Mismatches 328; Indels 0; Gaps 0;

Oy 109 ATCCACGGTTACCTTAAAGCATCTGAAGAAAGGATCTTACCATTGCTTGGAGCAT 168  
 Db 107 AGCCCCCTTTACAGTTGGTGTATCAAGAAAGGATCTTACCATTGCTTGGAGCAT 166  
 Oy 169 CTGTATCCGGTTCATCTATGTTGTTCAATGATCTTCAATGTTGCTTATGCTTACT 228  
 Db 167 CTGTATCCGGTTCATCTATGTTGTTCAATGATCTTCAATGTTGCTTATGCTTACT 226  
 Oy 229 ACCTTGAAACAGTATATCTCTTATCTTCAACCTTGGCTTACTTACATGCGCCG 288  
 Db 227 ACCTTGAAACAGTATATCTCTTATCTTCAACCTTGGCTTACTTACATGCGCCG 286  
 Oy 289 TTACTGGTTTGTCAAGCTAGCATCTCACCAGGCTCTGGGTCATCGGTCAAGATGTG 348  
 Db 287 TTACTGGTTTGTCAAGGTTGTGTGTGCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 346  
 Oy 349 GTCAACATGATTTAGGACATACCAAGTTGATGATGATGATGATGATGATGATGATGATGAT 408  
 Db 347 GCCATACAGCTTTCAGATATTAACATGAGGTTGATGATGATGATGATGATGATGATGATGAT 406  
 Oy 409 CGGCTTCTTCAACCCGATTTCTTGTGAATATAGCAAGAAATCAAGAAATCAAGCA 468  
 Db 407 CTGTCTGT 466  
 Oy 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528  
 Db 467 CTGTCTGT 526  
 Oy 529 ATTCAAACTTCTTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588  
 Db 527 ATTCAAACTTCTTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586  
 Oy 589 TAGATTTCCGTTTATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 648  
 Db 587 TTGCTGCGCGTTGATCTTGGCTTCAATGTTTCTGCGAGACCATGACGATTTGCTAT 646  
 Oy 649 ACCACTTGTATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
 Db 647 GTCACTATGACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706  
 Oy 709 CCGATTTCCGTTTCTGCTGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 768  
 Db 707 CTGATGCGGAGGTTCTGAGATTTGTTATCTGATACCGGTTGCTTATGATGATGATGATGAT 766  
 Oy 769 CAGCTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
 Db 767 TAGCTTGGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826  
 Oy 829 TGATCAATTTTTCACACACCATGCTCACTCCCTCAATTTATGATTTCAACGATGATGATGAT 888  
 Db 827 TGATCACTTCTTACACACCATGCTCACTCCCTCAATTTATGATTTCAACGATGATGATGAT 886  
 Oy 889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 948  
 Db 887 ATTGCTTAAAGGAGGCTTTGGGACCTGTGACAGAGCTATGAGGCTTTTAAACAGGCT 946  
 Oy 949 TCCACGACGTTTACACATCTCAGCTTTCGATCATTTGATCTC 991  
 Db 947 TCCACACATCAACGACATCTCAGCTTTCGATCATTTGATCTC 989

RESULT 7	AY104050	1856 bp	mRNA	linear	HTC 16-OCT-2002
LOCUS	AY104050				
DEFINITION	Zea mays PC0088038 mRNA sequence.				
ACCESSION	AY104050				
VERSION	AY104050.1	GI:21207128			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 1856) Hainey,C.E., Dolan,M., Miao,G.H., Vogel,J.M., Whitesett,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 1856)				
AUTHORS	Coe,E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maize map.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.				
FEATURES	location/Qualifiers				
source	1..1856				
	/organism="Zea mays"				
	/mol_type="mRNA"				
	/db_xref="MaizeDB:634972"				
	/db_xref="taxon:4577"				
	/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"				
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"				
ORIGIN					
Query Match	27.4%;	Score 352;	DB 11;	Length 1856;	
Best Local Similarity	59.6%;	Pred.No. 7,1e-42;			
Matches	636;	Conservative	0;	Mismatches 420;	Indels 12; Gaps 2;
QY	109 ATCCACCGTTCACGTTAAGCATCTGAAGAAAGCATTCATCCATTGCTTTGAGCAT	168			
DB	265 AGCCTCCGTTCACTCTGGGTGAGATCAGAAAGGCATCCCGCAGACACTGCTTCAGGCCT	324			
QY	169 CTGTCAATCCGGTATCATACTATGTTGTCATGATCTCATGTTGCTCATGCTTCTACT	228			
DB	325 CGGTCTCAAGCTCTTCTGTACAGGTGTCACGACCTGGTGAATCCCGCGGCTCTCT	384			
QY	229 ACCTTGCAACACGATATTCCTCTTATTTCCACACCTGTGGCTTACCTAGAGAGCCCG	288			
DB	385 ACTTGCGCGTGGCATCAATACCGGGGCTCCCAAGCCGCTCCGCTAAGCCCGCTGGCCGC	444			
QY	289 TTATCTGTTTTGTACAGTACATCTCAACCGGCTCTGGGTCAATCGGTACAGATGTG	348			
DB	445 TGTATGTGATCGCGAGGGGTGCGTGTGACCGGCGGTGTGATCTCCGACAGATGCG	504			
QY	349 GTACCATGATTTAGCGACTACCAAGTTGATGATGAATGTTGGATTCGTGCTCAAT	408			
DB	505 GCCACCAAGCTTCTTCGGACTACTGCTCTTCGAGAGAGATGGTCCGGCTGGGTGCTACT	564			
QY	409 CGGCTCTCTACCCCGATTTCTTGTGAATATAGCCAGGAATACCAACGCGCAACA	468			

Db	565	CGTGGCTCATGATGAGCCCTCACTTCTCGTGGAAAGTACAGCACCGGGCGCACACCACTCCACA	624
Qy	469	CAAAATCACTCGATTAAGATGAAGTTTACATCTCTAAACGTAAGTCGAAGTCAAGATT	528
Db	625	CGGGGTCCCTGGACCGGACGAGGTGTTCGGCCCAAGAAAGAGAGCGCTGCCGTGGT	684
Qy	529	ATTGCG---AAACTCTTAAACAATCACCGGGGCGAGTGTTCATTGGTGTTCGGTTGA	585
Db	685	ACACCCCGTACGTGTACACAAACCCGGTGGCGGGGTGGTGCACATGTGTGTGACGTCA	744
Qy	586	CTTTAGATTTCCGTTATACCTCTTAACTATATCTCGGGCAGAAATTAACGAGGTTTG	645
Db	745	CCCTCGGGTGGCGCTGTACTGTGGCGACAAACGGTGGGGCGGCGGTACCCGCGTTCG	804
Qy	646	CCAAACCACTTTGATGCCATGATGTCATTTTTCACACGATCGTGAAACGGGTTCAGTTTGC	705
Db	805	CCTCCCACTTCGACCCCTTACCGGCCCATCTTACACGACCGGAGCGGCCCAAGTCTTCG	864
Qy	706	TATCCGATTTGCGTCTCTGCTGTATTTTATGCAATCAAGCTTCTTGAGCAGCAAAAG	765
Db	865	TCTGGACGCGCGGCGTGTGGCCGTGGCGTTCGGGCTGTACAGCTGGCGGCGTTCG	924
Qy	766	GGGACGCTTGGGTATCAACAATGACCAATTCAGTACTAGTGAACGCTGTTCCTTCG	825
Db	925	GGGTCTGGTGGTGTGTGGCGGTACGCGTACGCGGTGCTGTATGTGAAGCGGTGGCTGG	984
Qy	826	TTTGTATCAATATTGTGACCAACCCACTCTCTCACTCCCTCATTTAGATTCAACCGAAT	885
Db	985	TGCTCATCACTTACCTGTGACGACACCCACCGTGTCTCCCACTTACGACTCGACGAT	1044
Qy	886	GGAACTGGATCAAAAGGGGCGCTTATCAACATGCAATAGGAATTTGGGGTCTCGAATCGGG	945
Db	1045	GGGACTGGCTGCGGGCGCGCTGGCGACCAATGAGACCGGACTACGGCATCTTCAACCGCG	1104
Qy	946	TTTTTCCAGAGTTTACACACTGACGTCTTGTGACTATTTGATCTCATATTCATTCACATT	1005
Db	1105	TGTTTCACAAATCATACGGACACGACGTCGGGACACACCTCTTCCACATGCGGACT	1164
Qy	1006	ATCATGCAAGAGACCAAGGAGTGCATCAAGCCAGTGTGGCGAGTACTATATAATCG	1065
Db	1165	ACCAAGCCATGAGAGGCCACCAAGGCGATCAAGGCCCATCTCGGGGACTACTACCACTTCG	1224
Qy	1066	ACAGAGCTCCCAATTTTCAAGCAATGATATGAGAGGCTAAGAGATGCATCATCTGAGC	1125
Db	1225	ACCGACCCCTGTTGCCAGGCGACCTGGCGCGAGGCCAGGAGTGCATCTACCTCGAGC	1284
Qy	1126	CCGATGAGATAGCGACCAAAAGTGTGTCTGTGTACCAACAAGATTG	1173
Db	1285	CCGA-----GGACCGCAAGGGCGTCTTCTGTGTACACAAGAAGT	1323
RESULT 8			
LOCUS	BU238570		
DEFINITION	Ds01_13f05_A Ds01_AAPC_ECORC_cold stressed Fltxweed seedlings	1080 bp	linear mRNA EST 06-SEP-2002
ACCESSION	BU238570		
VERSION	BU238570.1	GI:22750395	
KEYWORDS	EST.		
SOURCE	Descurainia sophia		
ORGANISM	Descurainia sophia		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.		
AUTHORS	Singh,J.A., Piche,C., Couroux,P., De Moor,A., Harris,L.J., Hattori,I.I., Ouellet,T., Robert,L.S., Sprout,D. and Tinker,N.A.		
TITLE	Expressed Sequence Tags From Cold-Stressed Descurainia sophia Seedlings		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Singh,J.A.		
	Eastern Cereal and Oilseed Research Centre		
	Agriculture and Agri-food Canada		





Db 321 GCCATCAGCTTTCAGTATTAACCAATGGGTGATGACACCTTGACCTTATCTTCACT 380  
Oy 409 CGGCTTCCTCAACCCCGTATTTCTTGGAATATAGCAAGAAATCAACCGCAACA 468  
Db 381 CTGCTCTTGTGGCCGACTCTTCTTGGAATATAGTATGTGCGCACACTCCACA 440  
Oy 469 CAATTCAGTACGATGAGTGAAGTTTACCTTCAACGTAAGTGAAGTCAAGATT 528  
Db 441 CTGGCTCCCTCGAGGGTATGAGTCTTGTGCGCAAGCAAAATCTCAGCTCGATGAT 500  
Oy 529 ATTCAAACTTCTTAACATTCACCCGCGAGTGTCACTTTGGTGTGCTGACTT 588  
Db 501 ATTCAGATCTGTAACATTCACGAGCGAGGCTCTCTCACTTCAATCACTCCACATC 560  
Oy 589 TAGATTTCCGTTATACCTTAACTAATATCTCGGGCAAGAAATACGAGGTTGCA 648  
Db 561 TTGGCTGGCCGTTGACTTGGCTTCAATGATCTGGGACACATACGACGATTTGAT 620  
Oy 649 ACCACTTGTATCCCATGAGTCCCAATTTTCAACGATCGTGAACGCGTCAAGTTTGTAT 708  
Db 621 GTCACTATAGCCCTTACGAGCCCAATCAACACGATGAGGCTACAGATCTTCTT 680  
Oy 709 CCGATTTGGTCTTCTGCTGTATTTATGCAATCAAGCTTCTTGAAGCAAGAGG 768  
Db 681 CTGATGCTGAGATCTCGAGATTTGTATCTGCTATACCGTATCTTGAAGAGGTC 740  
Oy 769 CAGCTGGGATATCAACATGTAACGAAATTCAGTACTAGTGTAGCGTGTCTTCTT 828  
Db 741 TAGCTGGCTAGTGTGATCACTACGATGTAACCGCTCTGCTGTAACGCGTCTTCTT 800  
Oy 829 TGATCAATATTTGGACCAACCCATCTCTCACTCCCTCATATGATTTCAACGATGGA 888  
Db 801 TGATCACTACTTGAAGCACTCACTCCATCTATTCACATCTACGATTTCAACGAGG 860  
Oy 889 ACTGATCAAAAGCGCTTATCAACATGATGAGGATTTGGGTTCTGAAATCGGAT 946  
Db 861 ATGGCTTGAAGGAGCTTGGCACTGTGACAGAGATGAGGAGGTTCTAAACAAGAT 918

RESULT 11  
CK270183 963 bp mRNA linear EST 12-DEC-2003  
LOCUS EST716261 potato abiotic stress cDNA library Solanum tuberosum cDNA  
DEFINITION CK270183  
ACCESSION CK270183.1 GI:39827161  
VERSION EST  
KEYWORDS Solanum tuberosum (potato)  
SOURCE Solanum tuberosum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.  
REFERENCE Buell, C.R., Hart, A., Ziemann, V., Kazmychewa, S.A. and Baker, B.  
TITLE Generation of ESTs from abiotic stressed potato tissue  
JOURNAL Unpublished (2003)  
COMMENT Other ESTs: EST716262  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potatocenter@tigr.org  
Clones can be requested from TIGR via potatocenter@tigr.org  
Seq primer: ATT TAG GTG ACA CTA TAG.  
Location/Qualifiers  
1..963  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="POACR59"  
/tissue\_type="abiotic stress treated leaf and root tissue"  
/lab\_host="DH10B-Tona"

/clone\_lib="potato abiotic stress cDNA library"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d. Set 4 were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cDNA library. RNA sample."

## ORIGIN

Query Match 26.2%; Score 336.6; DB 14; Length 963;  
Best Local Similarity 61.4%; Pred. No. 1.7e-39;  
Matches 540; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

Oy 375 TTGATGATGACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 434  
Db 3 TGGGTGATGACACCGTTGACCTATCTTCACTGCTGCTGTTGGTCCGACTTCTCT 62  
Oy 435 TGAATATGACACAGAAATCAACGCAACAAATTAATCTGATGATGATGATGATGAT 494  
Db 63 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 122  
Oy 495 TACATTCCTTAACGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 554  
Db 123 TTGTGCGCAAGCCAAATCTCAGCTCGAGTATGATGATGATGATGATGATGATGATGAT 182  
Oy 555 GGGGAGTGTCTACCTTGTGTTGCTGTTGATGATGATGATGATGATGATGATGATGAT 614  
Db 183 GGGAGGTCCTCTCACTTCAACATCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242  
Oy 615 AATATCTGGGCAAGAAATACGAGGATTTGCCAACACTTGTATGCCATGATGATGAT 674  
Db 243 AATGATCTGGCAGACCATACGACCGATTTGATGATGATGATGATGATGATGATGATGAT 302  
Oy 675 TTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 734  
Db 303 TACAACAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362  
Oy 735 TATGCAATCAAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 794  
Db 363 TATCTGATATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422  
Oy 795 ATTCAGTACTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854  
Db 423 GTACCCCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482  
Oy 855 CTTCACCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 914  
Db 483 CCATCATTTGCACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542  
Oy 915 ATTCAGTACTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 974  
Db 543 TGTGACAGAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602  
Oy 975 TTGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034  
Db 603 GTGACCATCTGTTCTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1035	AAGCAGGTTGGGGAGATACCTATTAATAATCGACAGAGACTCCAAATTTTCAAGCAATGTAT	1094	1035	AAGCAGGTTGGGGAGATACCTATTAATAATCGACAGAGACTCCAAATTTTCAAGCAATGTAT
663	AAGCCACTACTCGAGACTACTACCAATTCATGGAACCCGATTTTCAGGCAATGTGG	722	663	AAGCCACTACTCGAGACTACTACCAATTCATGGAACCCGATTTTCAGGCAATGTGG
1095	AGAGAGCTAAGAAATGCATTCATCATCGAGCCCGAATGAGATAGCAAGCAAAAGTGTG	1154	1095	AGAGAGCTAAGAAATGCATTCATCATCGAGCCCGAATGAGATAGCAAGCAAAAGTGTG
723	AGGAGAGCTAAGAGTGTCTCTAGCTCGAAGAAACGATATCATCTCAAGCAAGAAAGTGTG	782	723	AGGAGAGCTAAGAGTGTCTCTAGCTCGAAGAAACGATATCATCTCAAGCAAGAAAGTGTG
1155	TTCTGTATCCACAGAGATATATCAAAAAGTATATGATATCAATGATATATGCTTAATTA	1214	1155	TTCTGTATCCACAGAGATATATCAAAAAGTATATGATATCAATGATATATGCTTAATTA
783	TTCTGTATCAAAAAACAAGCTCTGAAATATCTAGAACAGAACTCAGCTTGTGAATTTGG	842	783	TTCTGTATCAAAAAACAAGCTCTGAAATATCTAGAACAGAACTCAGCTTGTGAATTTGG
1215	AGTTGTAACTTCTATTCCTCGGTGAATTAATTAATTCATT	1253	1215	AGTTGTAACTTCTATTCCTCGGTGAATTAATTAATTCATT
843	TCCTTTGGTATATGTTTGTCTCAGTGTCTTGAATTAATTCATT	881	843	TCCTTTGGTATATGTTTGTCTCAGTGTCTTGAATTAATTCATT
RESULT 12				
LOCUS	AM201738	764 bp	mrna	linear
DEFINITION	AM201738	764 bp	mrna	linear
VERSION	AM201738	764 bp	mrna	linear
KEYWORDS	AM201738	764 bp	mrna	linear
SOURCE	AM201738	764 bp	mrna	linear
ORGANISM	AM201738	764 bp	mrna	linear
REFERENCE	AM201738	764 bp	mrna	linear
AUTHORS	AM201738	764 bp	mrna	linear
TITLE	AM201738	764 bp	mrna	linear
JOURNAL	AM201738	764 bp	mrna	linear
COMMENT	AM201738	764 bp	mrna	linear

Query Match	Best Local Similarity	25.9%	Score 332.2	DB 10	Length 764
Matches 484	Conservative	0	Mismatches 262	Indels 0	Gaps 0
294	TGGTTTGTCAAGCTAGACATCTCCACCGGCTCTGGGTCAATCGGTCAAGATGTGTAC	353			
18	TGGGCTGTCCAAAGGTGCATCTTACTGAGATTGGGTCAATGGCCATGATGTGGCCAC	77			
354	CATGCAATTTAGCACTACCAAGTTGATTTGATGACATTGTGGATTCTGCTCCATTCGGCT	413			
78	CATGCAATTCAGTGCCTACCAAGTTCGATGATATTTGTGGCTGTCTCCACTTCGGCT	137			
414	CTCCTCAACCCGGTATTTCTCTTGGAAATATATGACAGCAAGATTCACACGCAACAAT	473			
138	CTCTAGTCCCATTCCTTTTCAATGAAATACAGCCATGCGGTACACCTCCACACTGGT	197			
474	TCACCTGCATACGATGAAATTTTCAATCTTAAAGTAAGTGAAGTCAAGATTATTC	533			
198	TCTCTTAGAGGGGATGAAAGTATTTGTGCCAAAGCAAGATCTGTATCAAGTGTACTCT	257			
534	AAACTTTTAAACAATCCACCGGGCGAGTGTTCACITTTGTTGGTTCGTTGACTTATGA	593			
258	AAATACCTTAAACATCTCCAGGCGAGAGTCTCACTCTTGTGTGCACCCCTCACACTGGT	317			
594	TTTCCGTTATACCTTAACTAATATCTCGGGCAAGAAATACGGGAGGTTTGCACACAC	653			
318	TGGCCCTTGATCTGGCTTAAAGTTTCTGGAAGGCTTATGATATTTGCTTGCAC	377			
654	TTTGTATCCCATGATGATCCAAATTTTCAAGATCGTAAAGCGCTTCAAGTTTGTATCCGAT	713			
378	TATGATCCCATATGTTCCCATTTTACTCGATTCGTGAAAGCACTTCAAAATATATATCATGAT	437			
714	TTGCGTCTTCTCGGTATTTTATGCAATCAAGCTTTTGTAGACGAAAGGGGACGT	773			
438	GCAGAGATACCTTGACAGATGTATGAGGCTTTTCCGTTCCGATGCGCAAAAGGACTTGGC	497			
774	TGGGTATTCACAGATGATGCAATTCACAGTACTGAGGTATGAGCGGTCTTTCGTTTATGC	833			
498	TGNTGTGTGTGTATATGAGATTCATGTGTATGTGTCAATGATATTTTGTGTATGAT	557			
834	ACATATTTGACACACCACTCTCACTCCCTCATATGATTTTCAACCGATGAGACTGG	893			
558	ACATTTCTTGACGACTACTCACTCCGATGATGACATTTACACTTCTCTGATGGGACTGG	617			
894	ATCAAAGGCGCTTATCAACATGATAGGAGTTTGGGTTCTGAAATCGGTTTTCAC	953			
618	TTGAGAGAGATCTTAGCAACAGTGGATATGAGATTATGAGGATATTCGAAACAGGTCTTNNCA	677			
954	GAGCTTACACACTCACTGCTTCGATCATTTTATCTCATATCATTTCCACATTTATCATGCA	1013			





REFERENCE		1 (bases 1 to 616)
AUTHORS		Kozik A., Michelmore R.W., Knapp S., Matvienko M., Riesberg J., Lin H., van Damme M., Lavelle D., Chevalier P., Ziegler J., Ellison P., Kolman J., Slabaugh M.S., Livingston K., Zhou Y., Lai Z., Church S., Jackson L. and Bredford K.
TITLE		Lectuce and Sunflower ESTs from the Compositeae Genome Project <a href="http://compgenomics.ucdavis.edu/">http://compgenomics.ucdavis.edu/</a>
JOURNAL		Unpublished (2002)
COMMENT		Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmunden Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.org [michelmore@vegmall.ucdavis.edu] belongs to contig OH_CA_Contig3889, see <a href="http://cgpdb.ucdavis.edu/">http://cgpdb.ucdavis.edu/</a> for details. Plate: QH14 row: E column: 14.
FEATURES		Location/Qualifiers
source		1..616
		/organism="Helianthus annuus"
		/mol_type="RNA"
		/cultivar="RHAB01"
		/db_xref="taxon:4232"
		/clone="QH14B14"
		/lab_host="E.coli"
		/clone_lib="OH_ABRCDI sunflower RHAB01"
		/note="Vector: pBRCDN5f1AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <a href="http://cgpdb.ucdavis.edu/tag_SEQ=Not found">http://cgpdb.ucdavis.edu/tag_SEQ=Not found</a> "
ORIGIN		
Query Match	25.7%; Score 330; DB 13; Length 616;	
Best Local Similarity	83.5%; Pred. No. 2e-38;	
Matches 386; Conservative	0; Mismatches 75; Indels 1; Gaps 1	
Dy	718 GTCCTCGCAGTATTTATGACCAAGCTCTTGAGACCAAAGGGGAGACTGGG	777
Db	616 GTTCTCGGTAGTAGTGAAGCACTCAAGCTCTTGAGACCAAAGGGGTTGCTGGG	557
Dy	778 TAATCAAGATGACGCAATTCCAGACTAGTAGTAAGCGTGTCTCGTTTGATCATAT	837
Db	556 TAACTGATGATGATGAGAGTCCCGGTAGGGTAAAGTGTCTTGTGTTGATCACAT	497
Dy	838 ATTGCACCAACCACCATCTCTACTCCCTCATTAATGATTCAACCGAATGGAAC-TGATC	896
Db	496 ATTTGACACCCCCCATCTCTCTGTACCTTATGATTCACAACGATGGAATCTGGATC	437
Dy	897 AAAGCGCGCTTATCAACAATCGATGAGGGATTCGGGTTCTGTAATCGGGTTTTCCAGAC	956
Db	436 AAAAGGGGCTTATTGACATTCATAGAGACTTCGGGTTCTTAAACAGGGTTTTACATGAC	377
Dy	957 GTTACACACTCACGCTCTTGATCATATTTGATCTATACTTCCACATTTATCATGCAAG	1014
Db	376 GTTACACATACGCAAGCTTGATCATATTTGATTTGATTCATTCACATTTATCATGCAAG	317
Dy	1017 GAAGCAAGGATGCAATCAAGCAATGTTGGGCGAGTACTATAAATTCAGACAGACTCCA	1074
Db	316 GAGGCAAGAAGAGCAATCAAGCCAGTGTGGGTGAGATTAATTAAGATTCATGAGACCCCG	257
Dy	1077 ATTTTCAAGCATATATATAGAGGCTAAGAGATCATCTTATCATCGAGCCCATGAGAT	1133
Db	256 ATTTTCAAGGCGATGTGAGAGAGAGGCAAGAGATGATTTTCAATTTGAGCCGATGAGAT	197
Dy	1137 AGCGACACAAAAGTGTGTCTTGATGCCAACAAATGATATCA	1178

DB	196	AGTGAACCCAAAGGTATATTGGTTCATTAACCTTAATCA	155
RESULT 15			
CF511517			
LOCUS	CF511517	831 bp	mRNA linear EST 09-SEP-2003
DEFINITION	Cabud0002 IIIR_E01 Vitis vinifera cv. cabernet sauvignon (Clone 8)		
	Bud - CABUD Vitis vinifera cDNA clone Cabud0002_IIIR_E01 3', mRNA sequence.		
ACCESSION	CF511517		
VERSION	CF511517.1	GI:34543285	
KEYWORDS	EST.		
SOURCE	Vitis vinifera		
ORGANISM	Vitis vinifera		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.		
AUTHORS	1 (bases 1 to 831) Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and Cook, D.		
TITLE	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drcocok@ucdavis.edu Seq primer: GCCAAGCAAGTCTTAG. Location/Qualifiers 1..831 /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon (Clone 8)" /db_xref="taxon:29760" /clone="Cabud0002_IIIR_E01" /sex="hermaphrodite" /dev_stage="Pre-bloom (10-11 days before bloom)" /lab_host="ID5Alpha" /clone_id="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD" /note="Organ: Bud; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CABUD is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-ATTGAGTGTGATCGACGAGATGGCCATTACGGCCGGG-3' and 5'-ATTGAGTGTGATCGACGAGCGCCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."		
FEATURES	Source		
Query Match	25.7%;	Score 329.8;	DB 14; Length 831;
Best Local Similarity	64.5%;	Pid. No. 1.8e-38;	
Matches 509;	Conservative 0;	Mismatch 277;	Indels 3; Gaps 1
DB	1	GTGGATTCGAGTCATTTGGCTCTCTCTACCCCGTATTTCTCTGTGAATATATAGCAC	449
GY	390		
DB	61	CGCGGCATCATTTCTTAATACCGGTTTCCCTCAGAAAGATGAAGTCTTTGTCCCCAAAC	120
GY	450	AGGATCCACCAAGCCACACAAATTCATCTGATACGATGAAGTTTACATTTCTTAACGT	509
DB	61	CGCGGCATCATTTCTTAATACCGGTTTCCCTCAGAAAGATGAAGTCTTTGTCCCCAAAC	120
GY	510	AAATTCGAAAGTCAGATTTATTTCCAACTTTTAACATTCACCGGCGGAGTCTTACT	569
DB	121	AAATTCGAAAGTCAGATTTATTTCCAACTTTTAACATTCACCGGCGGAGTCTTACT	180



QY 570 TTGGTGTTCGGTTGACTTTAGATTTCGGTATACCTTTAATAATATCTCGGCAAG 629  
 Db 181 CTCACCAATTCAACACACTCTAGGCTGGCTTTGTATCTAATGTTCACAGTTTCAAGCAGG 240  
 QY 630 AAATACGGGAGGTTTGCCACCACTTTGATCCCATGAGTCCAAATTTTCAACAGATGTGAA 689  
 Db 241 CGTACAGTAGATTGTGCGCACTTTGATCCACATGAGTCCAAATTTTCAAGATGTGAG 300  
 QY 690 CGCGTTCAAGTTTGTCTATCCGATTTGGTCTTCGCTGATTTTATGCAATCAAGCTT 749  
 Db 301 CGACTGCAGATATACATTTACAGATGCTGTGTTCTTGCAATCACTATGACTTTACCT 360  
 QY 750 CTTGTAGACGCAAAAGGGCAGCTTGGTAAATCAACATGTACGCAATTCAGTACTAGGT 809  
 Db 361 CTTGCAAGTATCAAAAGGCTCAGATGGTTTTGTGTGTTATGATGTCCCTGTGTGATT 420  
 QY 810 GTAAAGCGTGTCTTGTTTATCATATATTTGACACACACCATCTCTCACTCCCTCAT 869  
 Db 421 GTGATGATTTCTGTGCTGATTAAGTATTTGACAGATACCAACCGCTCTGTGCAAC 480  
 QY 870 TATGATTCACCGAATGGAATGATCAAGGCGCTTATCAACAATGATAGGATTTT 929  
 Db 481 TATGATTCCTGTGATGGAGCTGTGAGAGAGCTTTGGCCACCATGATAGAGACTAT 540  
 QY 930 GGGTTCCTGAATCGGGTTTTCACGACGTTACACACTCAAGTCTTGATCATTTGATC 989  
 Db 541 GGAATTCCTTAAGGTTTTCATATATACGATATCTCATGTGGCACACCATTTGTTT 600  
 QY 990 TCATACATTCACATTTATCATGCAAAAGGACAAAGGATGCAATCAAGCCAGTGTGGGC 1049  
 Db 601 TCAACATTCGCGCATTTATCATGCAATGAGGCTACAAAGGCCATTAAGCCAGTATTAGA 660  
 QY 1050 GAGTACTATAAATCGACAGACTCCCAATTTTCAAGCAATGTATAGAGGCTTAAGAA 1109  
 Db 661 GATTATTAATCAAGTTTATGAGGACTTCATTTTACAAAGGCAATGTGAAAGAGGCAAGAG 720  
 QY 1110 TGCATCTACATCGAGCCGATGAGATAGCAGACAAAGGTGTGTTCTGTATCCACAAG 1169  
 Db 721 TGTGTCTATGTCCAGTGGATGTGA---CAAGGCAAGAGTGTCTGTGTACCAAGAT 777  
 QY 1170 ATGTAAATCA 1178  
 Db 778 AAGTTTGA 786

Search completed: June 23, 2004, 14:43:21  
 Job time : 2561 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using bw model

Run on: June 18, 2004, 17:35:18 ; Search time 23 Seconds  
(without alignments)  
846.217 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGRMSDSEGNILERV.....IYIEPDESEHKGVFWYHKM 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUTS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/bacflilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	79.9	375	4	US-09-161-994A-2 Sequence 2, Appli
2	1598.5	78.1	374	4	US-09-059-769-4 Sequence 4, Appli
3	1589.5	77.7	374	4	US-09-059-769-2 Sequence 2, Appli
4	1578.5	77.1	384	2	US-08-872-302-4 Sequence 4, Appli
5	1396.5	68.2	383	4	US-09-638-937-15 Sequence 15, Appli
6	1348.5	65.9	383	4	US-09-059-769-12 Sequence 12, Appli
7	1348.5	65.9	383	4	US-09-161-994A-16 Sequence 16, Appli
8	1325.5	64.8	383	4	US-09-059-769-11 Sequence 11, Appli
9	1325.5	64.8	383	4	US-09-161-994A-15 Sequence 15, Appli
10	1318	64.4	384	2	US-08-675-650B-2 Sequence 2, Appli
11	1318	64.4	384	4	US-09-354-231B-14 Sequence 14, Appli
12	1318	64.4	384	4	US-09-128-602B-14 Sequence 14, Appli
13	1318	64.4	384	4	US-09-995-297-14 Sequence 14, Appli
14	1317	64.3	384	4	US-09-354-231B-10 Sequence 10, Appli
15	1317	64.3	384	4	US-09-133-962A-4 Sequence 4, Appli
16	1317	64.3	384	4	US-09-128-602B-10 Sequence 10, Appli
17	1317	64.3	384	4	US-09-995-297-10 Sequence 10, Appli
18	1313	64.1	384	4	US-09-354-231B-12 Sequence 12, Appli
19	1313	64.1	384	4	US-09-128-602B-12 Sequence 12, Appli
20	1313	64.1	384	4	US-09-995-297-12 Sequence 12, Appli
21	1312	64.1	384	3	US-08-907-608-6 Sequence 6, Appli
22	1312	64.1	384	4	US-09-354-231B-6 Sequence 6, Appli
23	1312	64.1	384	4	US-09-128-602B-6 Sequence 6, Appli
24	1312	64.1	384	4	US-09-482-287-6 Sequence 6, Appli
25	1312	64.1	384	4	US-09-966-888-6 Sequence 6, Appli
26	1312	64.1	384	4	US-09-995-297-6 Sequence 6, Appli
27	1311	64.0	384	2	US-08-675-650B-6 Sequence 6, Appli

28	1311	64.0	384	4	US-09-354-231B-16 Sequence 16, Appli
29	1311	64.0	384	4	US-09-128-602B-16 Sequence 16, Appli
30	1311	64.0	384	4	US-09-995-297-16 Sequence 16, Appli
31	1310	64.0	384	4	US-09-354-231B-18 Sequence 18, Appli
32	1310	64.0	384	4	US-09-128-602B-18 Sequence 18, Appli
33	1310	64.0	384	4	US-09-995-297-18 Sequence 18, Appli
34	1307	63.8	384	2	US-08-675-650B-4 Sequence 4, Appli
35	1305	63.8	384	4	US-09-354-231B-8 Sequence 8, Appli
36	1305	63.8	384	4	US-09-128-602B-8 Sequence 8, Appli
37	1305	63.8	384	4	US-09-995-297-8 Sequence 8, Appli
38	1301	63.6	384	4	US-09-059-769-10 Sequence 10, Appli
39	1300.5	63.5	383	1	US-08-314-596-41 Sequence 41, Appli
40	1300.5	63.5	383	1	US-08-320-982-41 Sequence 41, Appli
41	1300.5	63.5	383	3	US-08-819-037-41 Sequence 41, Appli
42	1300.5	63.5	383	3	US-08-530-862B-6 Sequence 6, Appli
43	1300.5	63.5	383	4	US-08-597-313D-6 Sequence 6, Appli
44	1300.5	63.5	383	4	US-09-059-769-9 Sequence 9, Appli
45	1300.5	63.5	383	4	US-09-161-994A-14 Sequence 14, Appli

ALIGNMENTS

```
RESULT 1
US-09-161-994A-2      Application US/09161994A
; Sequence 2, Appli
; Patent No. 6333448
; GENERAL INFORMATION:
; APPLICANT: BAFOR, Maureen
; APPLICANT: BANAS, Antoni
; APPLICANT: DAHLOVIST, Anders
; APPLICANT: GUMMELSON, Per-Olov
; APPLICANT: LEE, Michael
; APPLICANT: SJODAL, Staffan
; APPLICANT: STYRNE, Sten
; APPLICANT: LENNAN, Marit
; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: BAFOR-1
; CURRENT APPLICATION NUMBER: US/09/161,994A
; CURRENT FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 9601236.4
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Crepis alpina
US-09-161-994A-2
Query Match      79.9%; Score 1636; DB 4; Length 375;
Best local Similarity 76.9%; Pred. No. 1.1e+164;
Matches 289; Conservative 40; Mismatches 45; Indels 2; Gaps 1;
QY      1 MGAGRMSDSEGNILERVVDPPTLSDDKKAIPTHCFERSYIRSSYYVHDLIVAYV 60
      1 MGGGGR--GRSQRPMEWERSVDPPTVSDKQAIIPHCFRASVIRSSYIVHDAIIYVI 58
DB      1 LHSALTPYFSGKSHRNHNNTSLNDEYIIRKSKYKIVYKRLNNPGRVPTLVFR 180
QY      119 LHSALTPYFSGKSHRNHNNTSLNDEYIIRKSKYKIVYKRLNNPGRVPTLVFR 178
DB      61 FYTLANTYIPIPPPLAYLAMPVYVPCOASITLTGLWVIGHEGCHAFSDYLLIDIVGFV 120
QY      59 FYPLADKIIPIPLAPLAYLAMPVYVPCOASITLTGLWVIGHEGCHAFSDYVMDVDFGI 118
DB      121 LHSALTPYFSGKSHRNHNNTSLNDEYIIRKSKYKIVYKRLNNPGRVPTLVFR 180
QY      119 LHSALTPYFSGKSHRNHNNTSLNDEYIIRKSKYKIVYKRLNNPGRVPTLVFR 178
DB      181 LTLGFPYLITNIGSKYGRFANHFDPMSPIFNDRERVOVLISDFGLAVFYAIKLVAA 240
QY      179 FTLGFPLTLFNLGSKYGRFANHFDPMSPIFKRERFQVLISDFGLAVFYVYKLVAA 238
DB      241 KGAAVIMVYAIPLYGVSVFVLLITTYLHHTLSLPHYDSTEMWNIKGALSTIDRDFGLN 300
QY      239 KGAAVIMVYAIPLYGVSVFVLLITTYLHHTLSLPHYDSEWNIKGALSTIDRDFGLN 298
```

Qy 301 RVFHDVTHVHLHLISYIPHYHAKARDAIKPVIGYKIDRPIPFKAMTREAKECIYI 360  
Db 299 SVLHDVTHVHMLHLSYIPHYHAKARDAINVLDGPKIDRPIFKAMTREAKECIPI 358  
Qy 361 EPDESEHKGVFWYHKM 376  
Db 359 EPEKGRSKGVWYHKM 374

## RESULT 2

US-09-059-769-4  
; Sequence 4, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Stymer, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feider, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-059-769-4

Query Match 78.1%; Score 1598.5; DB 4; Length 374;

Best Local Similarity 75.7%; Pred. No. 1e-160; Matches 286; Conservative 41; Mismatches 46; Indels 5; Gaps 3;

Qy 1 MGAGRMSDPSEGNILKRVDP-PFTLSDLKKAIPHCERSYIRSSYYVVDLIVAY 59  
Db 1 MGAGR--GRTSKSVMERVSVDPTFSLDLKKAIPHCGRSVIRSSYYVVDLIVAY 58  
Qy 60 VFYLIANTYIPLIPPLAYLAMPVYVFCOASITLGLMWIGHCGHHAESYQDLIDIVGF 119

Db 59 IFYFLANTYIPLNPLPLAYLAMPVYVFCOASVLTGLMWIGHCGHHAESNTWDDIVGF 118  
Qy 120 VHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKLNNDPGVFTLVF 179  
Db 119 IHSFLITPYFSWKYSHRNHNSNTSIDNDEVYIPKRSKYKRYKLNNDPGSLVLVI 178  
Qy 180 RLITGFPYLYLTNLSGKKYGFANHPDMSTIFNDRERVOYLSDFGLAVFYAIKLVA 239  
Db 179 MFTLGFPLLYLTNLSGKKYGRFANHPDMSPIFKRRERFQVLSDLGLAVFYAIKVA 238  
Qy 240 AKGAWVYNVAIVLGVSVFVLTLYLHHTLSLPHYDSTKMWIKGALSTIDRDFGL 299  
Db 239 NKGAWVACMGVVLGVFTTFDYITFLHHTQSSPHYDSTKMWIKGALSIDRDFGL 298  
Qy 300 NRVDVTHVTHVHLHLISYIPHYHAKARDAIKPVIGYKIDRPIPFKAMTREAKECIY 359  
Db 299 NSVFDVTHVHMLHLSYIPHYHAKARDAIKPIGLGFYVIDRPIFKAMWREGRECMY 358  
Qy 360 IEPDESEHKGVFWYHKM 377  
Db 359 IEP--DSKLGKVWYHKM 374

## RESULT 3

US-09-059-769-2  
; Sequence 2, Application US/09059769  
; Patent No. 6329518  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Marit  
; APPLICANT: Stymer, Sten  
; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,769  
; FILING DATE: April 14, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06223  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU P06226  
; FILING DATE: 15-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043706  
; FILING DATE: 16-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/050403  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feider, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-059-769-2

Query Match 77.7%; Score 1589.5; DB 4; Length 374;  
Best Local Similarity 75.4%; Pred. No. 9e-160;  
Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGGRMSDPEGKRLERVPVD-PPTLSDLKKAIPHCERSVIRSSYVVDLIVAY 59  
DB 1 MGAGGR--GRTSKSVKERSVSDPTFSLSEKQAIIPHCFORSVIRSSYVVDLIVAY 58  
QY 60 VFYLLANTYIPLIPTPLAYLAMPVYVFCQASILTLGAWIGHCGHNAFSDYQOLIDIYGF 119  
DB 59 IFYLLANTYIPLIPTPLAYLAMPVYVFCQASVLTGLMVLGHCGHNAFNTWPDITGCF 118  
QY 120 VLHSAFLTPTYSWKYSHRNHANTNSLNDDEVYIPKRSKVYIS-KLANNPGRVFTLVF 179  
DB 119 ILHSAFLTPTYSWKYSHRNHANTNSLNDDEVYIPKRSKVYIS-KLANNPGRVFTLVF 178  
QY 180 RLITGFPLYLTLNTSGKKYGRFANHPDMSPIFNDREVOVLSDGLAVFAIKLVA 239  
DB 179 MPTLGFPLYLTLNTSGKKYGRFANHPDMSPIFKERERQVFLSDGLAVFYIKLVA 238  
QY 240 AKGAAMVIMYAIPLYGVSEFVLITLHHTLSLPHYDSTEMWIKGALSTIDRDFGL 299  
DB 239 NKGAAVAMCVGVPLGVFTFVDVITPLHHTHOSPHDSTEMWIRGALSAIDRDFGL 298  
QY 300 NRVDVHTHTVHLHLISYIPHYNAKEARDAIKPVLSGYIKIDRTPIKAMYREKECIY 359  
DB 299 NSVDVHTHTVHMLHLSYIPHYNAKEARDAIKPILGDFYIMIDRTPIKAMREKECIY 358  
QY 360 IEPDSEHKGVMYHKM 377  
DB 359 IEP--DSKLGVMYHKM 374

RESULT 4

US-08-872-302-4  
Sequence 4, Application US/08872302  
Patent No. 5846784  
GENERAL INFORMATION:  
APPLICANT: Hitz, William D  
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From  
TITLE OF INVENTION: Developing Seeds of Vernonia galamensis  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. duPont de Nemours and Co.  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/872.302  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R  
REGISTRATION NUMBER: P-41,173  
REFERENCE/DOCKET NUMBER: BB-1084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-872-302-4

Query Match 77.1%; Score 1578.5; DB 2; Length 384;  
Best Local Similarity 76.5%; Pred. No. 1.4e-158;  
Matches 280; Conservative 39; Mismatches 44; Indels 3; Gaps 2;

QY 15 NILSRVPVD-PPTLSDLKKAIPHCERSVIRSSYVVDLIVAYVYLLANTYIPLIP 73  
DB 19 NINERAPVDAAPFSLSDLKKAIPHCERSVIRSSYVVDLITPLLYTLANTSTIPLP 78  
QY 74 TPLAYLAMPVYVFCQASILTLGAWIGHCGHNAFSDYQOLIDIYGVFLHSAFLTPTYSWK 133  
DB 79 PPLYLAMPVYVFCQASILTLGAWIGHCGHNAFSEYQVMDNTGFIHSAFLTPTYSWK 138  
QY 134 YSHRNHANTNSLNDDEVYIPKRSKVYIS--KLANNPGRVFTLVRLITGFPYLLT 191  
DB 139 YSHRNHANTNSLNDDEVYIPKRSKVYIS--KLANNPGRVFTLVRLITGFPYLLT 198  
QY 192 NISGKKYGRFANHPDMSPIFNDREVOVLSDGLAVFAIKLVAKGAAMVIMY 251  
DB 199 NISGKKYGRFANHPDMSPIFSEERERQVFLSDGLAVFYIKLVAKGAAMVIMY 258  
QY 252 IPLYGVSEFVLITLHHTLSLPHYDSTEMWIKGALSTIDRDFGLANRVFHDVHTHV 311  
DB 259 APVGLANFIMITLHHTLSLPHYDSTEMWIKGALSTIDRDFGLANRVFHDVHTHV 318  
QY 312 LHLISYIPHYNAKEARDAIKPVLSGYIKIDRTPIKAMYREKECIYIEPDESEHKGV 371  
DB 319 LHLHFPYIPHYNAKEASDAIKPVLSGYIMIDRTPIKAMYREKECIYIEPDESEHKGV 378  
QY 372 FMYHKM 377  
DB 379 YMYHKM 384

RESULT 5

US-09-638-937-15  
Sequence 15, Application US/09638937  
Patent No. 6593514  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Edgar B  
APPLICANT: Hitz, William D  
APPLICANT: Ripp, Kevin G  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNUSUAL  
TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/638,937  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: BB-1371-P1  
PRIOR FILING DATE: 1999-08-16  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 15  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Borago officinalis  
US-09-638-937-15

Query Match 68.2%; Score 1396.5; DB 4; Length 383;  
Best Local Similarity 63.9%; Pred. No. 2.6e-139;  
Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPEGK---NILSRVPVD-PPTLSDLKKAIPHCERSVIRSSYVVDL 55  
DB 1 MGAGGRMPVPTKKSSSDVQVRVSEKPPPTVDDKVIIPHCFCQSVLHSPYVVDL 60  
QY 56 IVAYVFTYLLANTYIPLIPTPLAYLAMPVYVFCQASILTLGAWIGHCGHNAFSDYQOLID 115  
DB 61 VIALFFYTSRYIHLPHPLSVVAMPVYVFCQASVLTGLVWVIAHCGHNAFSDYQWLDD 120



QY 56 IVAVFYLLANTYIPLIPTPLAYLAMPYVWFCQASILTLGLWVIGHECGHAFSDYQIJD 115  
 Db 61 ILVSIIMYVANTYFHLPSFCYIAMPYIWIQCGCVCTGIWNAHECGHAFSDYQIWD 120  
 QY 116 IVGVLHSAITLTPYKSKYSHRNHANTNSLDNDENVYIPKRSKYKITSKILNPPGVF 175  
 Db 121 TVGLILSHALLVPFWSKYSHRRHSNTGSLERDEVFPVKPKSOLGWSKYLNNPPGKVL 180  
 QY 176 TLVRLTLGFPPLYLTLNLSGKKYGRFANHPDMSPIFNDREVOVLSDPGLAVFYAIK 235  
 Db 181 SLITLTLGFWPLYLALFVNSGRPIYDFACHIDYPIYNNRRLQIFISDAGVLGYCYLD 240  
 QY 236 LVAAGKAWYINWYALFVLGVSVFVLITYLHHTHLSLPHYDSTENWIKALSTIDRD 295  
 Db 241 RIALVKGALAVCYGVPLVNGFLVLTLYLQHTHPLPHYDSTENWIKALATCDRD 300  
 QY 296 FGLNRPVHDVTHRVHLISYIPHYAKARDAIKFVLGEYIKIDTPIFKAMYRAK 355  
 Db 301 YGILNKVFHNITDTHVHHLFSTMPHYAMETAKVXKPLDYYQFDGTPIYKEMWREAK 360  
 QY 356 ECIYEPDESEHKGVFWY 374  
 Db 361 ECIYEPDESEHKGVFWY 379

RESULT 8  
 US-09-059-769-11  
 Sequence 11, Application US/09059769  
 Patent No. 6329518  
 GENERAL INFORMATION:  
 APPLICANT: Green, Allan  
 APPLICANT: Singh, Surinder  
 APPLICANT: Lemnan, Maric  
 APPLICANT: Stymne, Sten  
 TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses  
 TITLE OF INVENTION: Therefor  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 STREET: 5370 Manhattan Circle, Suite 201  
 CITY: Boulder  
 STATE: Colorado  
 COUNTRY: US  
 ZIP: 80303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/059,769  
 FILING DATE: April 14, 1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU P06223  
 FILING DATE: 15-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU P06226  
 FILING DATE: 15-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/043706  
 FILING DATE: 16-APR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/050403  
 FILING DATE: 20-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Feider, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089  
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 383 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Glycine max  
 US-09-059-769-11

Query Match 64.8%; Score 1325.5; DB 4; Length 383;  
 Best Local Similarity 61.3%; Pred. No. 8.4e-132;  
 Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPEEGK---NILERVVD-PPTSLDLKKAIPTHCPERSVIRSSYVVDL 55  
 Db 1 MGAGGRDVPANRANKSEVDPLKRVFEPQSLQIKALIPHCFOKSVLASFVYVDL 60  
 QY 56 IVAVFYLLANTYIPLIPTPLAYLAMPYVWFCQASILTLGLWVIGHECGHAFSDYQIJD 115  
 Db 61 TLAFCLYVAATHVPHLPGPLSFRGMATYMAVQCCILTGWVIAHECGHAFSDYQIJD 120  
 QY 116 IVGVLHSAITLTPYKSKYSHRNHANTNSLDNDENVYIPKRSKYKITSKILNPPGVF 175  
 Db 121 TVGLILSHALLVPFWSKYSHRRHSNTGSLERDEVFPVKPKSOLGWSKYLNNPPGKVL 180  
 QY 176 TLVRLTLGFPPLYLTLNLSGKKYGRFANHPDMSPIFNDREVOVLSDPGLAVFYAIK 235  
 Db 181 SLITLTLGFWPLYLALFVNSGRPIYDFACHIDYPIYNNRRLQIFISDAGVLGYCYLD 240  
 QY 236 LVAAGKAWYINWYALFVLGVSVFVLITYLHHTHLSLPHYDSTENWIKALSTIDRD 295  
 Db 241 RIAAKGALAVCYGVPLVNGFLVLTLYLQHTHPLPHYDSTENWIKALATVDRD 300  
 QY 296 FGLNRPVHDVTHRVHLISYIPHYAKARDAIKFVLGEYIKIDTPIFKAMYRAK 355  
 Db 301 YGILNKVFHNITDTHVHHLFSTMPHYAMETAKVXKPLDYYQFDGTPIYKEMWREAK 360  
 QY 356 ECIYEPDESEHKGVFWY 375  
 Db 361 ECIYEPDESEHKGVFWY 380

RESULT 9  
 US-09-161-994A-15  
 Sequence 15, Application US/09161994A  
 Patent No. 6333448  
 GENERAL INFORMATION:  
 APPLICANT: BAFOR, Maureen  
 APPLICANT: BANAS, Antoni  
 APPLICANT: DAHLOVIST, Anders  
 APPLICANT: GIMMESON, Per-Olov  
 APPLICANT: LEE, Michael  
 APPLICANT: SUDAL, Scaflan  
 APPLICANT: STYME, Sten  
 APPLICANT: LENMAN, Maric  
 TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF  
 FILE REFERENCE: BAFOR-1  
 CURRENT APPLICATION NUMBER: US/09/161,994A  
 PRIOR FILING DATE: 1998-09-29  
 PRIOR APPLICATION NUMBER: 9601236.4  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 15  
 LENGTH: 383  
 TYPE: PRT  
 ORGANISM: Glycine max  
 US-09-161-994A-15

Query Match 64.8%; Score 1325.5; DB 4; Length 383;  
 Best Local Similarity 61.3%; Pred. No. 8.4e-132;  
 Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;





Db 241 FRVAAQGVASMCFCYVPLIYNGFLVLTLYLQHTHPSLPHYDSSEMDWIRGALATVDR 300  
 Qy 295 DFGFLNVPFDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354  
 Db 301 DYGILNVPFNHITDTHVAHHLFSTMPHYHAEATKAIKPIIGEYQPGDTVVAKMREA 360  
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375  
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 12

US-09-128-602B-14  
 ; Sequence 14, Application US/09128602B  
 ; Patent No. 6414223  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kodali, Dharma  
 ; APPLICANT: Fan, Zhongong  
 ; APPLICANT: Debonite, Lorin R.  
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
 ; FILE REFERENCE: 07148-072001  
 ; CURRENT APPLICATION NUMBER: US/09/128,602B  
 ; CURRENT FILING DATE: 1998-08-03  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 384  
 ; TYPE: PRT  
 ; ORGANISM: Braessica napus  
 US-09-128-602B-14

Query Match 64.4%; Score 1318; DB 4; Length 384;  
 Best Local Similarity 61.2%; Pred. No. 5.2e-131;  
 Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

Qy 1 MGAGGRM--SDPSECK--NILERVPVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHDL 55  
 Db 1 MGAGGRM-QVSPSPSKSETDRIKRVCEPTPTVGLKKAIPPHCFKSIIPRSFYLWMDI 60  
 Qy 56 IVAVFPYLLANTYPIPIPTPLAYLAMPVYVFCQASILTGMLVIGHECGHAFSDYQIIDD 115  
 Db 61 IIAACFYVATVTPPLPHPLSYFAMPLVWACQCGVLGVVIAHECGHAFSDYQIWLDD 120  
 Qy 116 IGVFVLSALITPFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKILNPPGVVF 175  
 Db 121 TVGLIFHSFLVFPFSKYSIRRHNSNTGSLERDEVFPKKSIDIKWYGTILNPLGRTV 180  
 Qy 176 TLVRLTLGFPYLTLNIGSKY--GRFANHPDPMSPFNDREYQVLLSDPGLAVFYAI 234  
 Db 181 MLTVQFTLGMPLYLAFVNSGRPYDGGFACHFHPAPAYNDRERLQIYISDGLAVCYGL 240  
 Qy 235 KLVAAAGAAVIMYAIPIVLGVSVFVLITYLHHTLSLPHYSTENWIKALSTIDR 294  
 Db 241 FRVAAQGVASMCFCYVPLIYNGFLVLTLYLQHTHPSLPHYDSSEMDWIRGALATVDR 300  
 Qy 295 DFGFLNVPFDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354  
 Db 301 DYGILNVPFNHITDTHVAHHLFSTMPHYHAEATKAIKPIIGEYQPGDTVVAKMREA 360  
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375  
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 13

US-09-995-297-14  
 ; Sequence 14, Application US/0995297  
 ; Patent No. 6649782  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kodali, Dharma  
 ; APPLICANT: Fan, Zhongong  
 ; APPLICANT: Debonite, Lorin R.

; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
 ; FILE REFERENCE: 07148-072002  
 ; CURRENT APPLICATION NUMBER: US/09/995,297  
 ; CURRENT FILING DATE: 2001-11-27  
 ; PRIOR APPLICATION NUMBER: US 09/128,602  
 ; PRIOR FILING DATE: 1998-08-03  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 384  
 ; TYPE: PRT  
 ; ORGANISM: Braessica napus  
 US-09-995-297-14

Query Match 64.4%; Score 1318; DB 4; Length 384;  
 Best Local Similarity 61.2%; Pred. No. 5.2e-131;  
 Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

Qy 1 MGAGGRM--SDPSECK--NILERVPVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHDL 55  
 Db 1 MGAGGRM-QVSPSPSKSETDRIKRVCEPTPTVGLKKAIPPHCFKSIIPRSFYLWMDI 60  
 Qy 56 IVAVFPYLLANTYPIPIPTPLAYLAMPVYVFCQASILTGMLVIGHECGHAFSDYQIIDD 115  
 Db 61 IIAACFYVATVTPPLPHPLSYFAMPLVWACQCGVLGVVIAHECGHAFSDYQIWLDD 120  
 Qy 116 IGVFVLSALITPFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKILNPPGVVF 175  
 Db 121 TVGLIFHSFLVFPFSKYSIRRHNSNTGSLERDEVFPKKSIDIKWYGTILNPLGRTV 180  
 Qy 176 TLVRLTLGFPYLTLNIGSKY--GRFANHPDPMSPFNDREYQVLLSDPGLAVFYAI 234  
 Db 181 MLTVQFTLGMPLYLAFVNSGRPYDGGFACHFHPAPAYNDRERLQIYISDGLAVCYGL 240  
 Qy 235 KLVAAAGAAVIMYAIPIVLGVSVFVLITYLHHTLSLPHYSTENWIKALSTIDR 294  
 Db 241 FRVAAQGVASMCFCYVPLIYNGFLVLTLYLQHTHPSLPHYDSSEMDWIRGALATVDR 300  
 Qy 295 DFGFLNVPFDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354  
 Db 301 DYGILNVPFNHITDTHVAHHLFSTMPHYHAEATKAIKPIIGEYQPGDTVVAKMREA 360  
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375  
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 14

US-09-354-231B-10  
 ; Sequence 10, Application US/09354231B  
 ; Patent No. 6342658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Debonite, Lorin R.  
 ; APPLICANT: Shorlosh, Basil S.  
 ; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
 ; FILE REFERENCE: 07148-063002  
 ; CURRENT APPLICATION NUMBER: US/09/354,231B  
 ; CURRENT FILING DATE: 1999-07-16  
 ; PRIOR APPLICATION NUMBER: US 08/874,109  
 ; PRIOR FILING DATE: 1997-06-12  
 ; NUMBER OF SEQ ID NOS: 69  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 384  
 ; TYPE: PRT  
 ; ORGANISM: Braessica napus  
 US-09-354-231B-10

Query Match 64.3%; Score 1317; DB 4; Length 384;  
 Best Local Similarity 61.3%; Pred. No. 6.7e-131;  
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

QY 1 MGAGRM-----SDPSGKNTLERYVD-PPFTSLDKKALPTCFERSVTRSSYYVHD 54  
 DB 1 MGAGRMQVSPSPSKSETDNI-KRVPCEPPTVGEELKALPPHCFKRSIPRSPSYLIMD 59  
 QY 55 LIVAVFVYLYANTYIPLIPPLAYLAMPVWFCCASILTGLMVGHECGHAFSDYOLID 114  
 DB 60 IILASCFYVATYTPLLPPLPLSTFAMPLWACQCVLTGWVLAHECGHAFSDYOLID 119  
 QY 115 DIVGFVLSALLTPYFSWKYSHRHHNANTNSLDNDVYIPRKSQVLYSLNNPGRV 174  
 DB 120 DTGILFHSFLVYFWSKYSRRHNSNTGSLEREDEVFVPPKKSQDIKMYGKYLNNPLGRT 179  
 QY 175 FTLYVRLTLGFPYLYLTNLSGKTY-GRFANFDPMSPIFNDRERQVLLSPGLLAVFYA 233  
 DB 180 VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFNAPAYNDRERLQIYISDAGILAVCYG 239  
 QY 234 IKLLVAAKGAAMVINMTALPVLAGSVFVPLITLYLHHTLSLPHYDSTEMNIIKGLSTID 293  
 DB 240 LYRYAAVGVASWVCFYGVPLIYNGFLVLTLYLQHTPSLPHYDSSMDWLRGLATVD 299  
 QY 294 RDPFGLNRVFDVTHVLAHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 353  
 DB 300 RDYGLLNKVFNNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEEYQDGPVYKAMWRE 359  
 QY 354 AKECIYIEPDESDSHKGVFWYH 375  
 DB 360 AKECIYVEPDRQGEKKGIVFWYN 381

RESULT 15

US-09-133-962A-4  
 Sequence 4, Application US/09133962A  
 Patent No. 6372965  
 GENERAL INFORMATION:

APPLICANT: JOHN JOSEPH OXLEY  
 TITLE OF INVENTION: GENES FOR MICROSOMAL FATY ACID  
 DELTA-12 DESATURASES AND RELATED  
 ENZYMES FROM PLANTS

NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
 STREET: 1007 MARKET STREET  
 CITY: WILMINGTON  
 STATE: DELAWARE  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 19898

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
 SOFTWARE: MICROSOFT WORD VERSION 7.0A  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/133,962A  
 FILING DATE: 14-Aug-1998  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 07/977,339  
 FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: CHRISTENBURY, LYNN M.  
 REGISTRATION NUMBER: 30,971  
 REFERENCE/DOCKET NUMBER: BB-1043-D  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)992-5481  
 TELEFAX: (302)773-0164  
 TELEK: 835420

INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 384 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-133-962A-4  
 Query Match 64.3%; Score 1317; DB 4; Length 384;  
 Best Local Similarity 61.3%; Pred. No. 6.7e-131;  
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

QY 1 MGAGRM-----SDPSGKNTLERYVD-PPFTSLDKKALPTCFERSVTRSSYYVHD 54  
 DB 1 MGAGRMQVSPSPSKSETDNI-KRVPCEPPTVGEELKALPPHCFKRSIPRSPSYLIMD 59  
 QY 55 LIVAVFVYLYANTYIPLIPPLAYLAMPVWFCCASILTGLMVGHECGHAFSDYOLID 114  
 DB 60 IILASCFYVATYTPLLPPLPLSTFAMPLWACQCVLTGWVLAHECGHAFSDYOLID 119  
 QY 115 DIVGFVLSALLTPYFSWKYSHRHHNANTNSLDNDVYIPRKSQVLYSLNNPGRV 174  
 DB 120 DTGILFHSFLVYFWSKYSRRHNSNTGSLEREDEVFVPPKKSQDIKMYGKYLNNPLGRT 179  
 QY 175 FTLYVRLTLGFPYLYLTNLSGKTY-GRFANFDPMSPIFNDRERQVLLSPGLLAVFYA 233  
 DB 180 VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFNAPAYNDRERLQIYISDAGILAVCYG 239  
 QY 234 IKLLVAAKGAAMVINMTALPVLAGSVFVPLITLYLHHTLSLPHYDSTEMNIIKGLSTID 293  
 DB 240 LYRYAAVGVASWVCFYGVPLIYNGFLVLTLYLQHTPSLPHYDSSMDWLRGLATVD 299  
 QY 294 RDPFGLNRVFDVTHVLAHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 353  
 DB 300 RDYGLLNKVFNNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEEYQDGPVYKAMWRE 359  
 QY 354 AKECIYIEPDESDSHKGVFWYH 375  
 DB 360 AKECIYVEPDRQGEKKGIVFWYN 381

Search completed: June 18, 2004, 17:39:02  
 Job time : 24 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1633.5	79.8	384	9	US-09-981-124-20	Sequence 20, Appl
2	1592	77.8	373	9	US-09-981-124-4	Sequence 4, Appl
3	1599.2	77.7	374	9	US-09-981-124-2	Sequence 2, Appl
4	1386.5	68.12	383	12	US-10-464-631-15	Sequence 15, Appl
5	1356.5	66.3	383	12	US-10-424-559-266787	Sequence 266787, Appl
6	1356.5	66.3	335	12	US-10-425-114-40643	Sequence 40643, Appl
7	1348.5	65.9	333	9	US-09-981-124-12	Sequence 12, Appl
8	1346.5	65.8	332	12	US-10-425-114-56017	Sequence 56017, Appl
9	1332.5	65.1	383	9	US-09-937-751-6	Sequence 6, Appl
10	1335.5	64.8	383	9	US-09-937-751-31	Sequence 31, Appl
11	1333.5	64.7	383	9	US-09-952-399-4	Sequence 4, Appl
12	1318	64.4	384	9	US-09-995-297-14	Sequence 14, Appl
13	1318	64.4	384	10	US-09-771-994-14	Sequence 14, Appl
14	1318	64.4	384	16	US-10-715-100-14	Sequence 10, Appl
15	1317	64.3	384	9	US-09-995-297-10	Sequence 10, Appl

QY 1 MGAGGRSDPSEG-KNLLRVPVD-PPEPLSLDKKAIPTTHCFERSVIRSSYYVVDLIVA 58  
 ||||| : ||: ||| |||:||||| |||:|:|||||:|:|

Db 1 MGAGRMNTTDDQKNLFRQVPAKPFPSLADLKKAIPHCFOBSLSSYYVVDLVVA 60  
 QY 59 VFFYLLANTYIPLIPTPLAY-LAMPVYFCQASILTGLMTVIGHECGHHAFFSDYQIDDIY 117  
 Db 61 VFFYLLANTYIPLIPSLAYLAMPVYFCQASILTGLMTVIGHECGHHAFFSDYQIDDIY 120  
 QY 118 GFVLSALLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 177  
 Db 121 GFVLSALLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 180  
 QY 178 VFFLLGPRVLLTNISGKKYGRFANHPDMSPIFNDREVOYLLSDGGLAVFAIKLL 237  
 Db 181 AFRLIVGPFLLFTNVSGKKYGRFANHPDMSPIFNDREVOYLLSDGGLAVFAIKLL 240  
 QY 238 VAKGAAMVIMVYAIPLVGVSVFVLLITLHTHLSLPHYDSTEMWIKALSTIDRDFG 297  
 Db 241 VLAAGAMVIMVYAIPLVGVSVFVLLITLHTHLSLPHYDSTEMWIKALSTIDRDFG 300  
 QY 298 FLNRFVHDVTHVHLHLISYIPHYHAKARDAIKPVLGSEYKIDRPIFKAMVREAK 355  
 Db 301 FLNRFVHDVTHVHLHLISYIPHYHAKARDAIKPVLGSEYKIDRPIFKAMVREAK 358

RESULT 2  
 US-09-981-124-4  
 ; Sequence 4, Application US/09981124  
 ; Patent No. US2002016144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green, Allan  
 ; APPLICANT: Singh, Surinder  
 ; APPLICANT: Lemman, Marit  
 ; APPLICANT: Styume, Sten  
 ; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
 ; FILE REFERENCE: 26-98A  
 ; CURRENT FILING DATE: 2001-10-17  
 ; PRIOR APPLICATION NUMBER: US 09/059769  
 ; PRIOR FILING DATE: 1998-04-14  
 ; PRIOR APPLICATION NUMBER: US 60/043706  
 ; PRIOR FILING DATE: 1997-04-16  
 ; PRIOR APPLICATION NUMBER: AU P06223  
 ; PRIOR FILING DATE: 1997-04-15  
 ; PRIOR APPLICATION NUMBER: AU P06226  
 ; PRIOR FILING DATE: 1997-04-15  
 ; PRIOR APPLICATION NUMBER: US 60/050403  
 ; PRIOR FILING DATE: 1997-06-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 373  
 ; TYPE: PRT  
 ; ORGANISM: Crepis sp.  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (292)..(292)  
 ; OTHER INFORMATION: The 'Xaa' at location 292 stands for Arg, or Ser.  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (937)..(937)  
 ; OTHER INFORMATION: N is any nucleotide residue  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (901)..(901)  
 ; OTHER INFORMATION: N is any nucleotide residue  
 US-09-981-124-4

Query Match 77.8%; Score 1592; DB 9; Length 373;  
 Best Local Similarity 75.9%; Pred. No. 4e-154;  
 Matches 287; Conservative 40; Mismatches 45; Indels 6; Gaps 4;

QY 1 MGAGRMDSPEGKNILERVVDP-PFTLSDLKKAIPHCERSVIRSSYYVVDLIYAY 59  
 Db 1 MGAGGR--GRSE-KSVMERVSVDVPTLSLKLKAIIPHCFORSVIRSSYYVVDLIYAY 57

QY 60 VFFYLLANTYIPLIPTPLAYLAMPVYFCQASILTGLMTVIGHECGHHAFFSDYQIDDIY 119  
 Db 58 IFVFLANTYIPLIPSLAYLAMPVYFCQASVLTGLMTVIGHECGHHAFFSDYQIDDIY 117  
 QY 120 VLSGALLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 179  
 Db 118 IHSFLLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 177  
 QY 180 RLTLGPFLLYLLTNISGKKYGRFANHPDMSPIFNDREVOYLLSDGGLAVFAIKLL 239  
 Db 178 MFTLGFPLVLLTNISGKKYGRFANHPDMSPIFNDREVOYLLSDGGLAVFAIKLL 237  
 QY 240 AKGAAMVIMVYAIPLVGVSVFVLLITLHTHLSLPHYDSTEMWIKALSTIDRDFG 299  
 Db 238 NKGAMVIMVYAIPLVGVSVFVLLITLHTHLSLPHYDSTEMWIKALSTIDRDFG 297  
 QY 300 NRVFHDVTHVHLHLISYIPHYHAKARDAIKPVLGSEYKIDRPIFKAMVREAK 359  
 Db 298 NSVFHDVTHVHLHLISYIPHYHAKARDAIKPVLGSEYKIDRPIFKAMVREAK 357  
 QY 360 IEPDESEHKGVFWYHKM 377  
 Db 358 IEP--DSKLGKVWYHKL 373

RESULT 3  
 US-09-981-124-2  
 ; Sequence 2, Application US/09981124  
 ; Patent No. US2002016144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green, Allan  
 ; APPLICANT: Singh, Surinder  
 ; APPLICANT: Lemman, Marit  
 ; APPLICANT: Styume, Sten  
 ; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
 ; FILE REFERENCE: 26-98A  
 ; CURRENT FILING DATE: 2001-10-17  
 ; PRIOR APPLICATION NUMBER: US 09/059769  
 ; PRIOR FILING DATE: 1998-04-14  
 ; PRIOR APPLICATION NUMBER: US 60/043706  
 ; PRIOR FILING DATE: 1997-04-16  
 ; PRIOR APPLICATION NUMBER: AU P06223  
 ; PRIOR FILING DATE: 1997-04-15  
 ; PRIOR APPLICATION NUMBER: AU P06226  
 ; PRIOR FILING DATE: 1997-04-15  
 ; PRIOR APPLICATION NUMBER: US 60/050403  
 ; PRIOR FILING DATE: 1997-06-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 374  
 ; TYPE: PRT  
 ; ORGANISM: Crepis palaestina  
 US-09-981-124-2

Query Match 77.7%; Score 1589.5; DB 9; Length 374;  
 Best Local Similarity 75.4%; Pred. No. 7.3e-154;  
 Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGRMDSPEGKNILERVVDP-PFTLSDLKKAIPHCERSVIRSSYYVVDLIYAY 59  
 Db 1 MGAGGR--GRSEKSVMERVSVDVPTLSLKLKAIIPHCFORSVIRSSYYVVDLIYAY 58  
 QY 60 VFFYLLANTYIPLIPTPLAYLAMPVYFCQASILTGLMTVIGHECGHHAFFSDYQIDDIY 119  
 Db 59 IFVFLANTYIPLIPSLAYLAMPVYFCQASVLTGLMTVIGHECGHHAFFSDYQIDDIY 118  
 QY 120 VLSGALLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 179  
 Db 119 IHSFLLTPYFSWKYSRHHNANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTL 178

QY 180 RLTLGFPYLLTNIISGKKYGRFANHPDMSPIFNDRERVOVLLSDPGLLAFAVYAIKLLVA 239  
 DB 179 MFTLGFPYLLTNIISGKKYGRFANHPDMSPIFNDRERVOVLLSDPGLLAFAVYAIKLLVA 238  
 QY 240 AKGAAYINMYAIYVGVSVFVLITTYLHHTHLSLPHYDSTENWIKALSTIDRDFGL 299  
 DB 239 NKGAAWACWGVSVFVLITTYLHHTHLSLPHYDSTENWIKALSTIDRDFGL 298  
 QY 300 NRVPDVTHTVHLHLSIYIPHYAKARDAIKPVLAGERYIDRPTIFKAMYREAKECIY 359  
 DB 299 NSVHDVTHVHMLHSYIPIHYAKARDAIKPVLAGERYIDRPTIFKAMYREAKECIY 358  
 QY 360 IEPDESEHKGVPWYHQM 377  
 DB 359 IEP--DSKLGKGVYWHKL 374

RESULT 4  
 US-10-464-631-15  
 ; Sequence 15, Application US/10464631  
 ; Publication No. US2003020487A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cahoon, Edgar B  
 ; APPLICANT: Hicz, William G  
 ; APPLICANT: Rapp, Kevin G  
 ; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNSUOL  
 ; TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE  
 ; TITLE OF INVENTION: BONDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/464,631  
 ; CURRENT FILING DATE: 2003-06-18  
 ; PRIOR APPLICATION NUMBER: US/09/638,937  
 ; PRIOR FILING DATE: 2000-08-15  
 ; PRIOR APPLICATION NUMBER: BR-1371-P1  
 ; PRIOR FILING DATE: 1999-08-16  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 15  
 ; LENGTH: 383  
 ; TYPE: PRT  
 ; ORGANISM: Boreago officinalis  
 ; US-10-464-631-15

Query Match 68.2%; Score 1396.5; DB 12; Length 383;  
 Best Local Similarity 63.9%; Pred. No. 4.3e-134; Indels 5; Gaps 2;  
 Matches 24; Conservative 62; Mismatches 70;

QY 1 MGAGRMSDSEBGR---NILERVPVD-PPPTLSDLKKAIPTHCFERSVIRSSYYVVDL 55  
 DB 1 MGAGGRMPVPTFKGKKSVDVQFVPSKRPPTVGLDKKVIDPHCFORSVLSFSYVVDL 60  
 QY 56 IVAVFPYLLANTYIPLIPTPLAYLAMPVYWCQSILTLGLVIGHEGCHNAFSYQYLLDD 115  
 DB 61 VIAALFFYTSRYTHLQPHPLSYVAMPVWCQSIVTLGVVVAIHEGCHNAFSYQYLLDD 120  
 QY 116 IVGFVLSALTLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGRVF 175  
 DB 121 TVGLLSALLVFPFSWKYSIRRHNSNTGSLERDEVFPKRSKVSISMSSEVLNPPGRVL 180  
 QY 176 TLVFRLLTGFPLYLITNIGSKKYGRFANHPDMSPIFNDRERVOVLLSDPGLLAFAVYAIK 235  
 DB 181 VLVVQLTLGMPVLYMFPVNSGRPRDPAFCHDPKSPYVDRRLQIYISDAIVAMVGLY 240  
 QY 236 LIVAAGAAYINMYAIYVGVSVFVLITTYLHHTHLSLPHYDSTENWIKALSTIDRD 295  
 DB 241 RLVAAGAAYINMYAIYVGVSVFVLITTYLHHTHLSLPHYDSEMDWMLGALATVDRD 300  
 QY 296 FGFNRPVHDVTHVHLHLSIYIPHYAKARDAIKPVLAGERYIDRPTIFKAMYREAK 355  
 DB 301 YGFLNKVLAHNTTTHVHMLHLSYIPHYAKARDAIKPVLAGERYIDRPTIFKAMYREAK 360  
 QY 356 ECIYIEPDESEHKGVPWY 374  
 DB 359 IEP--DSKLGKGVYWHKL 374

DB 361 ECIYIEADBDGNKKGVFWY 379

RESULT 5  
 US-10-424-599-266787  
 ; Sequence 266787, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovacic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 266787  
 ; LENGTH: 383  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_8292C.1.Dep  
 ; US-10-424-599-266787

Query Match 66.3%; Score 1356.5; DB 12; Length 383;  
 Best Local Similarity 62.4%; Pred. No. 5.4e-130; Indels 5; Gaps 2;  
 Matches 23; Conservative 61; Mismatches 77;

QY 1 MGAGRMSDSEBGR---NILERVPVD-PPPTLSDLKKAIPTHCFERSVIRSSYYVVDL 55  
 DB 1 MGAGRTDVPANRKSSEVDPLKRPFEKPPFSLSQIKVIVPHCFORSVLSFSYVVDL 60  
 QY 56 IVAVFPYLLANTYIPLIPTPLAYLAMPVYWCQSILTLGLVIGHEGCHNAFSYQYLLDD 115  
 DB 61 TIAPCLYVAVTHYHPLPSLPSFLAMPYIYVAVOGCIITLGVVVAIHEGCHNAFSYQYLLDD 120  
 QY 116 IVGFVLSALTLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGRVF 175  
 DB 121 IVGLVLSGLVFPFSWKYSIRRHNSNTGSLERDEVFPKRSKVSISMSSEVLNPPGRVL 180  
 QY 176 TLVFRLLTGFPLYLITNIGSKKYGRFANHPDMSPIFNDRERVOVLLSDPGLLAFAVYAIK 235  
 DB 181 TLATVTLGMPVLYALAVNSGRPRDPAFCHDPYCPISDNERLQIYISDAIVAMVGLY 240  
 QY 236 LIVAAGAAYINMYAIYVGVSVFVLITTYLHHTHLSLPHYDSTENWIKALSTIDRD 295  
 DB 241 RLMAAGLAWVWCYGVPLLVNGFVLITLQHTHPALPHYTSSEMDWMLGALATVDRD 300  
 QY 296 FGFNRPVHDVTHVHLHLSIYIPHYAKARDAIKPVLAGERYIDRPTIFKAMYREAK 355  
 DB 301 YGILNKVFNHNTTTHVHMLHLSYIPHYAKARDAIKPVLAGERYIDRPTIFKAMYREAK 360  
 QY 356 ECIYIEPDESEHKGVPWY 375  
 DB 361 ECIYIEPDQSTESKGVFWY 380

RESULT 6  
 US-10-425-114-40643  
 ; Sequence 40643, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53113)B

```

1 CURRENT APPLICATION NUMBER: US10/425,114
2 CURRENT FILING DATE: 2003-04-28
3 NUMBER OF SEQ. ID NOS: 73128
4 SEQ. ID NO. 40643
5 LENGTH: 395
6 TYPE: PRT
7 ORGANISM: Glycine max
8 FEATURE:
9 OTHER INFORMATION: Clone ID: LIB3028-001-B9_PL1.pepf
10 US-10-425-114-40643

```

Query Match	66.3%	Score 1356.5	DB 12	Length 395
Best Local Similarity	62.4%	Pred. NO. 5.6e-130		
Matches 237, Conservative	61	Mismatches 77	Indels 5	Gaps 2

Qy	1	MAGGMSDSEBCK-----NIBRRVPD--PPLTSDLKKALPTHCERSVIRSSYYVHDL	55
Db	13	MGGGKRDVPPANKKEVDPLKKRPEKPEPFSLSQIKVPIPHCHORQKRVFSSVYDYL	72
Qy	56	IVAIVVFYYLANTYIPLIPTPLAVLAMPVYVFCQASILTLGWLTGHCCHNAFSDYQDLD	115
Db	73	TIATFCLYYAATHFHLLPSPPLSLAMPIMYAAQSGCLTLGWVIAHECHNAFSDYQDLD	122
Qy	116	IVGVFVLSALLTFYFSWKYSHRNHANTNSLDNDEVYIPKRKSKYKYSKLANNPGRVY	175
Db	133	IVGVVHLSGLLVYFPMKYSHRRHSNTSLERDEVFVPOKSCIKWYSKYLANNPGRVY	192
Qy	176	TIIVPRLTIGPLVLLNLSGKKYGRPAHHFDMGSIENDRRVOYQLSDPCLLAVFAIAIK	235
Db	193	TLVAVTLTGMPILYLTALNVSGRPDRPACHYDYGPIYSDRERLQYISDAVGLVTCGLF	252
Qy	236	LIVAAKGAADVIMMYAIPVLGSVVFPEVLITTYLHHTHLSLPHYDSTENWMIKALSTYDRD	295
Db	253	RLMAMGALNAVVCVGPPLLVNNGFVLITFLQHHPRLPHYTSEWMLRGALATYDRD	312
Qy	296	FGLINRVFHDVHTTHVLHLISYIPHYAKKARDAIKVLGEBYYKIDRTPIFKAMYEAKE	355
Db	313	YGLINKVFNHNIPTDTHVAHHLFSTMPHYAMEATKAIKILGSEYRVFDETPFVKAMMBEAR	372
Qy	356	ECTIYIBDEDESKGVFWYTH	375
Db	373	ECTIYVEPDOSTESKGVFWYTH	392

```

RESULT 7
US-09-981-124-12
Sequence 12, Application US/09981124
Patent No. US2002016144A1
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lemman, Marc
APPLICANT: Styrene, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MO
FILE OF INVENTION: 26-98A
FILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU P06223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU P06226
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 383
TYPE: PRT

```

ORGANISM: Solanum commersonii  
US-09-981-124-12

Query Match	65.9%	Score 1348.5;	DB 9;	Length 383;
Best Local Similarity	61.2%;	Pred. No. 3.6e-129;		
Matches 232;	Conservative 65;	Mismatches 77;	Indels 5;	Gaps 2

```

OY 1 GGAGGMRMDPS-----EGKNILIERVVD--PPFLTSLDKKAIPIHCFERSASVRSQVYVHVD 55
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MGAGGRMAEPENGETVKNPDLQKVTSPKDFPVTGDIKKAI PPHCFORSLSRSFYVYIDL 60
OY 56 IVAVVPYLTANTYIPLIPTPLAYLTAMPVYVFCOASLTGLMWYIGHCGHHAESDYOLDID 115
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 61 ILVSLMTYVANTYIFHLPLSPICYIAMPITWIOGCYCGIWNNAHCGHHAESDYQWVVD 120
OY 116 IVGFVLHSALLTPYRSWKYSHRHHNHAANTNSLNDENVYIPKRSKYKVIYSKLLANPPGRVY 175
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 121 TVGLILHSALLVPYRSWKYSHRHHNHSNTGSLERDEVFVFKPSQSLGMYEKYLLANPPGRVYL 180
OY 176 TLVPLFLTLGFLPYLLTNI SGKKYGRFANHDEMSPLFENDREKVOYLLSPGGLAAVYAIK 235
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 SLTITLLTGLWPYLYLAFNVSGRPYDPBACHYDDYGPYNNRERLQITISDAGVLGVCTLYL 240
OY 236 LLVAAGAAWYVNNMAIPVLGVSVFVLTITTYLHTHTLSLPHYDSTEMNNIKGALSTIDRD 255
    | : | : | : | : | : | : | | | | | | | | | | | | | | | | | | | | | | |
Db 241 RIALVKGGLAMVLCYGVPLLVNGLVLTITTYQHHTPRLPHYDSTEMDWLLRGALATCDRD 300
OY 296 FGLNRFVHDVTHVTHVHLISYIDHYHAKEARDAIKPVLGEYKIKDRTPIFKAMTREAK 355
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 301 YGVLNKVFHNITDTHVHHLFSTMPHYNMAEATKAVKPLGDYQYQDGPITYKEMWREAK 360
OY 356 ECIYIEPDEDSHKGVFWY 374
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 361 ECLYVEKDESSQSGKGVFWY 379
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

```

RESULT 8
US-10-425-114-56017
/ Sequence 56017, Application US/10425114
/ Publication No. US2004003488A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 56017
/ LENGTH: 392
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 701211444_FLI.pep
US-10-425-114-56017

```

Query Match	65.8%;	Score 1346.5;	DB 12;	Length 392;
Best Local Similarity	62.1%;	Pred. No. 5.9e-129;		
Matches 236;	Conservative 61;	Mismatches 78;	Indels 5;	Gaps 2

```

QY      1  GAGGGRMDPSGCK---NII,LRVVD--PEPLTSLKKRIAPHCEPRSVIRSSYYVHDL  55
        :      :      :      :      :      :      :      :      :
Db      10  GAGGRTVPPEANRSEVDPKRGVPEKPEPESLSQIKVI PRCHCFORSVFRSSYYVLD  69
        :      :      :      :      :      :      :      :      :
QY      56  IVAYVYYLIANTYIPLIPTPLAYLAMPVYVFCQASITLGLMWIIGHECGHAFSDYOLIDD  115
        :      :      :      :      :      :      :      :      :
Db      70  TIAFLCYVATYIFILPSPSPSLFAMPIYVAOGLITGVWYIAHCGGHAFSDYOLIDD  129
        :      :      :      :      :      :      :      :      :

```



SEQ ID NO 4  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Calendula officinalis  
US-09-852-399-4

Query Match 64.7%; Score 1323.5; DB 9; Length 383;  
Best Local Similarity 61.3%; Pred. No. 1.3e-126;  
Matches 233; Conservative 57; Mismatches 83; Indels 7; Gaps 2;

QY 1 MGAGGRMDPSEKGIILERVVD-----PPETLSDLKKAIPTHCFERSVIRSSYYVHD 54  
DB 1 MGAGGRMODPTNGKKTPEPPIQVRHKEPPTVVDIKAIIPHCFTNSVIRSESYVYD 60  
QY 55 LIVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASITLGLWVIGHECGHAFSDYQI 114  
DB 61 LTIASILYIANNTYISTPLSPYLAAYVAPVMAQCVCVLTVGVVLAHECGHAFSDHQI 120  
QY 115 DIVGFVLSALLTPFSKWKYSHRNHNANTNSLNDDEVYIPKRSKVKIYSKLANNPGRV 174  
DB 121 DTGVIVLHSPFLVPFSWKYSHRRHSNTGSIHDEVEVPKLKSGVRSSTARLANNPGR 180  
QY 175 FTLVERLTGLFPLVLTNLSGKKYGRFANHPDPMSPFNDEBERVOVLSDGILAVFYAI 234  
DB 181 LTLVLTGLMPLVLTFRVSGRYRFRACHDPNSPISKEKRAQIFISDAGILAVFVL 240  
QY 235 KLVAAKGAAMVIMMYAIPVLGVSVFVLTLYLHHTLSLPHYDSTEMNMIKALSTIDR 294  
DB 241 FRLANRKFHDVYTHVLAHLISYIPHYHAKAADAIPVIGEYKIDRTPIFKAMREA 300  
QY 295 DFGFLANRVFDVYTHVLAHLISYIPHYHAKAADAIPVIGEYKIDRTPIFKAMREA 354  
DB 301 DYGLINKVFHNIITDTHVAHLFTSTMPHYHAMEATKAIKPIIGDYQFDGTSIFKAMYRET 360  
QY 355 KECIYIPEDESEHKGVFWY 374  
DB 361 KECIYVDEDEBK-DGVYVY 379

## RESULT 12

US-09-995-297-14  
Sequence 14, Application US/09995297  
Patent No. US20020092038A1

GENERAL INFORMATION:  
APPLICANT: Kodali, Dharma  
APPLICANT: Fan, Zhegong  
APPLICANT: Debonte, Lorin R.  
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
FILE OF INVENTION: PATTY ACID CONTENT  
FILE REFERENCE: 07148-072002  
CURRENT APPLICATION NUMBER: US/09/995,297  
CURRENT FILING DATE: 2001-11-27  
PRIOR APPLICATION NUMBER: US 09/128,602  
PRIOR FILING DATE: 1998-08-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Brassica napus  
US-09-995-297-14

Query Match 64.4%; Score 1318; DB 9; Length 384;  
Best Local Similarity 61.2%; Pred. No. 4.7e-126;  
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

QY 1 MGAGGRM--SDPSSEK--NILERVVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHD 55  
DB 1 MGAGGRMOVSPSKSESTDTIKRVPCETPPPTVGLKKAIPHCFTNSVIRSESYLWDI 60  
QY 56 IVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASITLGLWVIGHECGHAFSDYQI 115  
DB 61 IIASCFYVATTYIFPLRPLRPLSTYFAMPVYMACQCVLTVGVVLAHECGHAFSDYQI 120

QY 116 IVGFVLSALLTPFSKWKYSHRNHNANTNSLNDDEVYIPKRSKVKIYSKLANNPGRV 175  
DB 121 TVGLIFHSFLLVPFSWKYSHRRHSNTGSIHDEVEVPKKKSDIKWYGLANNPLGRTV 180  
QY 176 TFLVRLTGLFPLVLTNLSGKKY--GRFANHPDPMSPFNDEBERVOVLSDGILAVFYAI 234  
DB 181 MLTVQFTLGMPLVLAFAVNSGRFPYDGFACHHAPNAPINDREKQIYISDAGILAVCYGL 240  
QY 235 KLVAAKGAAMVIMMYAIPVLGVSVFVLTLYLHHTLSLPHYDSTEMNMIKALSTIDR 294  
DB 241 FRVAAQGVASMGCFGVPLIIVNGFLVLTLYLQHTHPSLPHYDSEMDWLRGALATVDR 300  
QY 295 DFGFLANRVFDVYTHVLAHLISYIPHYHAKAADAIPVIGEYKIDRTPIFKAMREA 354  
DB 301 DYGLINKVFHNIITDTHVAHLFTSTMPHYHAMEATKAIKPIIGDYQFDGTVVAKAMREA 360  
QY 355 KECIYIPEDESEHKGVFWY 375  
DB 361 KECIYVDEDEBKGVFWY 381

## RESULT 13

US-09-771-904-14  
Sequence 14, Application US/09771904  
Publication No. US20030131379A1

GENERAL INFORMATION:  
APPLICANT: Debonte, Lorin R.  
APPLICANT: Fan, Zhegong  
APPLICANT: Miao, Guo-Hua  
TITLE OF INVENTION: PATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
FILE REFERENCE: 07148-063003  
CURRENT APPLICATION NUMBER: US/09/771,904  
CURRENT FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 08/874,109  
PRIOR FILING DATE: 1997-06-12  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Brassica napus  
US-09-771-904-14

Query Match 64.4%; Score 1318; DB 10; Length 384;  
Best Local Similarity 61.2%; Pred. No. 4.7e-126;  
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

QY 1 MGAGGRM--SDPSSEK--NILERVVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHD 55  
DB 1 MGAGGRMOVSPSKSESTDTIKRVPCETPPPTVGLKKAIPHCFTNSVIRSESYLWDI 60  
QY 56 IVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASITLGLWVIGHECGHAFSDYQI 115  
DB 61 IIASCFYVATTYIFPLRPLRPLSTYFAMPVYMACQCVLTVGVVLAHECGHAFSDYQI 120  
QY 116 IVGFVLSALLTPFSKWKYSHRNHNANTNSLNDDEVYIPKRSKVKIYSKLANNPGRV 175  
DB 121 TVGLIFHSFLLVPFSWKYSHRRHSNTGSIHDEVEVPKKKSDIKWYGLANNPLGRTV 180  
QY 176 TFLVRLTGLFPLVLTNLSGKKY--GRFANHPDPMSPFNDEBERVOVLSDGILAVFYAI 234  
DB 181 MLTVQFTLGMPLVLAFAVNSGRFPYDGFACHHAPNAPINDREKQIYISDAGILAVCYGL 240  
QY 235 KLVAAKGAAMVIMMYAIPVLGVSVFVLTLYLHHTLSLPHYDSTEMNMIKALSTIDR 294  
DB 241 FRVAAQGVASMGCFGVPLIIVNGFLVLTLYLQHTHPSLPHYDSEMDWLRGALATVDR 300  
QY 295 DFGFLANRVFDVYTHVLAHLISYIPHYHAKAADAIPVIGEYKIDRTPIFKAMREA 354  
DB 301 DYGLINKVFHNIITDTHVAHLFTSTMPHYHAMEATKAIKPIIGDYQFDGTVVAKAMREA 360  
QY 355 KECIYIPEDESEHKGVFWY 375



Db 361 KECIYEPDROGKKGWFWYN 381

## RESULT 14

US-10-715-100-14  
; Sequence 14, Application US/10715100  
; Publication No. US20040083503A1  
; GENERAL INFORMATION:  
; APPLICANT: Kodali, Dharm  
; APPLICANT: Pan, Zhegong  
; APPLICANT: Debonite, Lorin R.  
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
; FILE OF INVENTION: FATTY ACID CONTENT  
; FILE REFERENCE: 07148-072002  
; CURRENT APPLICATION NUMBER: US/10/715,100  
; PRIOR FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: US/09/995,297  
; PRIOR FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: US 09/128,602  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Brassica napus  
US-10-715-100-14

Query Match 64.4%; Score 1318; DB 16; Length 384;  
Best Local Similarity 61.2%; Pred. No. 4.7e-126;  
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

Qy 1 MGAGRM--SDPSEK--NILERVVD--PPTLSLKKALPTCHERSVIRSSYYVVDL 55  
Db 1 MGAGRMQVSPSPSKSSTDTIKVPCETPPTVGEKKAIPHCCKRSIPRSFSTYLWDI 60  
Qy 56 IVAVVFYLLANTYIPIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQILD 115  
Db 61 IIAACFYVATTTFFPLPHPLSTFAMPLIYACQCVLTGVWVAHECGHAFSDYQWLD 120  
Qy 116 IVGFVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKVKYISKLNPPGRV 175  
Db 121 TVGILFHSPFLVYFWSKYSRHRHNSNTGSLERDEVFPKCKSDIKWYGKYLNNPLGRTV 180  
Qy 176 TLVFRLLTGFPPLVLTNLSGKCY--GRFANHPDPMSPFINDERVOVLSDGLAVFAI 234  
Db 181 MLTVQFTLGWPLVLAFFVNSGRPYDGGFACHFNAPAIYNDRERLQIYISDAGILAVCYL 240  
Qy 235 KILVAAKGAAMVIMYAIPIVAGSVFFVLTITLHHTLSLPHYDSTEMNMIKALSTIDR 294  
Db 241 FRYAAAGVAVSMVCFCYGVPLIYNGFLVLTITLQHTHPSLPHYDSEMDLKGALATYDR 300  
Qy 295 DFGFLNRVFDVTHVTHVHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 354  
Db 301 DYGLINKVFENITDTHVAHHLFSTMPHYHAMEATKAIKPIIGEYQFDGTPVVKAMWRE 360  
Qy 355 KECIYEPDDESEHKGVFWYH 375  
Db 361 KECIYEPDROGKKGWFWYN 381

## RESULT 15

US-09-995-297-10  
; Sequence 10, Application US/09995297  
; Patent No. US20020092038A1  
; GENERAL INFORMATION:  
; APPLICANT: Kodali, Dharm  
; APPLICANT: Pan, Zhegong  
; APPLICANT: Debonite, Lorin R.  
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
; FILE REFERENCE: 07148-072002

; CURRENT APPLICATION NUMBER: US/09/995,297  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: US 09/128,602  
; PRIOR FILING DATE: 1998-08-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Brassica napus  
US-09-995-297-10

Query Match 64.3%; Score 1317; DB 9; Length 384;  
Best Local Similarity 61.3%; Pred. No. 6e-126;  
Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

Qy 1 MGAGRM-----SDPSEKNILERVVD--PPTLSLKKALPTCHERSVIRSSYYVVD 54  
Db 1 MGAGRMQVSPSPSKSSTDTIKVPCETPPTVGEKKAIPHCCKRSIPRSFSTYLWDI 59  
Qy 55 LIVAVVFYLLANTYIPIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQILD 114  
Db 60 IIAACFYVATTTFFPLPHPLSTFAMPLIYACQCVLTGVWVAHECGHAFSDYQWLD 119  
Qy 115 DIVGFVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKVKYISKLNPPGRV 174  
Db 120 DTGILFHSPFLVYFWSKYSRHRHNSNTGSLERDEVFPKCKSDIKWYGKYLNNPLGRT 179  
Qy 175 FTVFRLLTGFPPLVLTNLSGKCY--GRFANHPDPMSPFINDERVOVLSDGLAVFAI 233  
Db 180 VMLTVQFTLGWPLVLAFFVNSGRPYDGGFACHFNAPAIYNDRERLQIYISDAGILAVCYG 239  
Qy 234 IKLVAAKGAAMVIMYAIPIVAGSVFFVLTITLHHTLSLPHYDSTEMNMIKALSTID 293  
Db 240 LYRYAAAGVAVSMVCFCYGVPLIYNGFLVLTITLQHTHPSLPHYDSEMDLKGALATVD 299  
Qy 294 RDFGFLNRVFDVTHVTHVHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 353  
Db 300 RDYGLINKVFENITDTHVAHHLFSTMPHYHAMEATKAIKPIIGEYQFDGTPVVKAMWRE 359  
Qy 354 KECIYEPDDESEHKGVFWYH 375  
Db 360 KECIYEPDROGKKGWFWYN 381

Search completed: June 18, 2004, 17:43:53  
Job time : 49 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 17:34:22 ; Search time 20 Seconds  
(without alignments)  
1813.210 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEKGVFWYHKM 377

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1348.5	65.9	383	2 T10480	Delta12 fatty acid
2	1336	65.3	382	2 T15042	omega-6 fatty acid
3	1332.5	65.1	383	2 T10789	omega-6 desaturase
4	1325.5	64.8	383	2 T07688	omega-6 desaturase
5	1296.5	63.3	385	2 T09880	omega-6 desaturase
6	1273.5	62.2	387	2 T09839	oleate 12-hydroxyl
7	1241.5	60.6	383	2 T15043	funeral elicitor-in
8	1237.5	60.5	387	2 T07687	omega-6 desaturase
9	1220	59.6	378	2 T14269	Delta12 fatty acid
10	1160.5	56.7	333	2 T07009	omega-6 fatty acid
11	926.5	45.3	359	2 JC7871	stearyl-CoA 9-des
12	658.5	32.2	356	2 AG2005	omega-3 fatty acid
13	653	31.9	359	2 SS2650	omega-3 fatty acid
14	645	31.5	441	2 T03029	omega-3 fatty acid
15	639.5	31.2	460	2 T10063	omega-3 fatty acid
16	632.5	30.9	381	2 T03923	probable omega-3 f
17	627	30.6	431	2 T07685	omega-3 fatty acid
18	620.5	30.3	386	1 J02335	omega-3 fatty acid
19	612	29.9	379	2 J02555	omega-3 fatty acid
20	607	29.7	398	2 T01686	omega-3 fatty acid
21	607	29.7	404	2 PQ0812	omega-3 fatty acid
22	606	29.6	418	2 JC7872	stearyl-CoA 9-des
23	606	29.6	446	1 J02336	omega-3 fatty acid
24	604.5	29.5	443	1 T01697	omega-3 fatty acid
25	602.5	29.4	453	1 J02339	omega-3 fatty acid
26	593.5	29.0	380	2 T10898	probable omega-3 f
27	593	29.0	438	2 T15039	omega-3 fatty acid
28	590.5	28.8	377	1 J02337	omega-3 fatty acid
29	590.5	28.8	383	2 T06238	omega-3 fatty acid

30	588.5	28.7	383	1 A44227	omega-3 fatty acid
31	585	28.6	380	2 T06235	omega-3 fatty acid
32	574	28.0	380	2 J02338	omega-3 fatty acid
33	428.5	20.9	376	2 T26075	hypothetical prote
34	339	16.6	350	2 A43772	phosphatidylcholin
35	339	16.6	350	2 A42005	phosphatidylcholin
36	330	16.1	424	2 JC5891	omega 6 desaturase
37	319	15.6	347	2 S43771	phosphatidylcholin
38	316.5	15.5	447	2 S53309	n-6 fatty acid des
39	309.5	15.1	351	2 S11519	phosphatidylcholin
40	306	14.9	349	2 S43770	phosphatidylcholin
41	306	14.9	424	2 T07742	omega-6 desaturase
42	301	14.7	448	2 D85362	hypothetical prote
43	293.5	14.3	443	2 T08136	probable omega-6 d
44	292	14.3	351	2 S54259	Delta12 fatty acid
45	214	10.5	352	2 B69901	fatty-acid desatur

## ALIGNMENTS

RESULT 1	T10480	Delta12 fatty acid desaturase (EC 1.14.99.-) [imported] - Commerson's wild potato
C:Species:	Solanum commersonii (Commerson's wild potato)	
C:Date:	16-Jul-1999	#sequence_revision 16-Jul-1999 #text_change 09-Jun-2000
C:Accession:	T10480	
R:Consiglio, F.; Amatruda, M.R.; Leone, A.; Costa, A.; Grillo, S.		
Submitted to the EMBL Data Library, November 1995		
A:Reference number: 217044		
A:Accession: T10480		
A:Status: preliminary; translated from GB/EMBL/DBJ		
A:Molecule type: mRNA		
A:Residues: 1-383 <CON>		
A:Cross-references: EMBL:X92847; NID:G1054842; PID:G1054843		
A:Experimental source: Clone SCDS D11		
C:Superfamily: omega-3 fatty acid desaturase		
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis		
Query Match	65.9%	Score 1348.5; DB 2; Length 383;
Best Local Similarity	61.2%	Pred. No. 1.6e-105;
Matches 232; Conservative 65; Mismatches 77; Indels 5; Gaps 2;		
QY	1 MGAGGRMSDPS-----EGNIIERVPVD-PPTLSDLKKAIPTHGFERSVIRSYVVDL	55
DB	1 MGAGGRMSAPNGERBYKRNPLQKVPSTKPEPTVGDIKAIIPKCFQRLISFSVYVDL	60
QY	56 IVAVVFYLLANTYIPLIPTPLAYLAMPYWFQASILTLGWLVIHGCCHNAFSDYQLDD	115
DB	61 ILVSIWYVANTYVPHLLPSFYCYIAMPYIWCQCVCCTGIVWNAHCGHNAFSDYQVDD	120
QY	116 IVGVVLSALITPPFSWKYSRRNHNTNSLDNDEVYIPKSKKVKYISKILNPPRGVVF	175
DB	121 TVGILHSALLVPPFSWKYSRRHNSNGSLERBEVFPKPKSQLGWWSKYLNNPPGVL	180
QY	176 TLVRLTGFPLLYLLTNSGKCYGRPANHPDPMSPIFDRBRVOVLLSDFGLAVFYAIK	235
DB	181 SLTTLTGMPLYLAFNVSGRPRDFACHYDPYGRYINRRRLQIFISDAVLYGVLYLY	240
QY	236 LILVAKGAWINNYAIPVLGVSVFVLLITVLAHTHSLSPHYDSTENWIMKALSTTD	295
DB	241 RIALVKGIAWVCYGVPLAVVNGFVLITLQHTHSLPHYDSTENWIMKALATCORD	300
QY	296 FGLNRYPHVDYTHVHLHLISYIPHYAKARDAIKPVLCGYIKIDTPIPKMYRPAK	355
DB	301 YGVINKYFHNITDTHVHHLFSTPHYNAEMATRAVPLDYYQFDGTPIYKEMWRAK	360
QY	356 ECIYIPDESEKGVFWY 374	
DB	361 ECLYVEKDESQKGVFWY 379	
RESULT 2		



Qy 236 LVAAGAAVYNNATVGVSVFVLTITLHTLSTLPHYSTERNWIKALSTIORD 295  
 Db 241 RLAAAGLAWVVCYGVPLVNGFLVLTPLQHTHPLPHTYSSSEWMLGALATVORD 300  
 Qy 296 FGLNRFVHDVTHVTHLHLSYIPHYAKKARDAIKVLSYXKIDRTPIFKAMVREAK 355  
 Db 301 YGLINKVFHNTIDTHVAHLSSTMPHYAMERATKAIKILGSIYKFDTPVYKAMWREAK 360  
 Qy 356 ECIYIEPDEDESHKGVFWYH 375  
 Db 361 ECIYIEPDESHKGVFWYH 380

## RESULT 5

T09880  
 omega-6 desaturase - upland cotton  
 C:Species: Gossypium hirsutum (upland cotton)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 20-Jun-2000  
 C:Accession: T09880  
 R:Lit, Q.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z16895  
 A:Accession: T09880  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-385 <Lit>  
 A:Cross-references: EMBL:X97016  
 A:Experimental source: cultivar Deltapine-16  
 A:Function:  
 A:Description: introduces a cis double bond at omega-6 position of oleic acids  
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 63.3%; Score 1296.5; DB 2; Length 385;  
 Best Local Similarity 59.6%; Pred. No. 3.6e-101;  
 Matches 227; Conservative 61; Mismatches 66; Indels 7; Gaps 3;

Qy 1 MGAGGRM---SDPSBGNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYYVHDI 56  
 Db 1 MGAGGRMPIDGIIKENRGSVNRVPEKPPFTLGQIKQAI PPHCFRSLRSFSYVHDL 60  
 Qy 57 VAVYFYLLANTYIPLIPTPLAYLAMPVYVPCQASITLGLMTLGHGCGHNASDYQLIDI 116  
 Db 61 LASFFYIATSYFHFLLPQFSYIAMPVYVVLQGLTGVWVIAHEGHAERDYQWVD 120  
 Qy 117 VGFILSHALTPYRSWKYSHRNHANTSLDNDEYVIRPKRSKYIKSLANNPGRFT 176  
 Db 121 VGLILSHALTPYRSWKYSHRNHANTSLDNDEYVIRPKRSKYIKSLANNPGRFT 180  
 Qy 177 LVFRLTGLFPLYLTLNISGKRYGRFANFDPMSPIFNDRERVOVLLSDPGLAVFYAKL 236  
 Db 181 LVVTLTGMPVYLAFAVNSGRYDRLASHYNYGPIYSRERLQVYISDTGIFAVIYVLYK 240  
 Qy 237 LVAAGAAVYNNATVGVSVFVLTITLHTLSTLPHYSTERNWIKALSTIORD 296  
 Db 241 IAAKGLAMLCCTGVPLIYNAFVLTLYLQHTHSAIPHYDSSSEWMLRQALSTMDDF 300  
 Qy 297 GFLNRFVHDVTHVTHLHLSYIPHYAKKARDAIKVLSYXKIDRTPIFKAMVREAK 356  
 Db 301 GVLNKFVHNTIDTHVAHLSSTMPHYAMERATKAIKILGSIYKFDTPVYKAMWREAK 360  
 Qy 357 CIIYIEPD---EDSEHKGFWYH 374  
 Db 361 CIIYIEPDVGGGGGSGKGVFWYH 381

## RESULT 6

T09839  
 oleate 12-hydroxylase - castor bean  
 C:Species: Ricinus communis (castor bean)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
 C:Accession: T09839  
 R:van de Loo, F.J.; Brown, P.; Turner, S.; Somerville, C.R.  
 Proc. Natl. Acad. Sci. U.S.A. 92, 6743-6747, 1995

A>Title: An oleate 12-hydroxylase from Ricinus communis L. is a fatty acyl desaturase ho.  
 A:Reference number: Z16877; MUID:95350145; PMID:7624314  
 A:Accession: T09839  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <Del>  
 A:Cross-references: EMBL:U22378; NID:9722350; PIDN:AAC49010.1; PID:9722351  
 A:Experimental source: strain Baker 296; tissue-type developing endosperm  
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 62.2%; Score 1273.5; DB 2; Length 387;  
 Best Local Similarity 56.9%; Pred. No. 3.1e-99;  
 Matches 218; Conservative 68; Mismatches 88; Indels 9; Gaps 2;

Qy 1 MGAGGRM-----SDPSBGNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYYV 51  
 Db 1 MGAGGRMSTVITSNNSKGGSSHLKAPRHPFTLGLDLRAIPPHCFERSVIRSSYYV 60  
 Qy 52 VHDIVAVFYLLANTYIPLIPTPLAYLAMPVYVPCQASITLGLMTLGHGCGHNASDYQ 111  
 Db 61 AYDVCLSFYSIATNFPPYISPLSYAVMLVYVLFQGLITGLMTLGHGCGHNASDYQ 120  
 Qy 112 LIDIVGVVLSALTPYRSWKYSHRNHANTSLDNDEYVIRPKRSKYIKSLANNP 171  
 Db 121 IADIVGLVLSALTPYRSWKYSHRNHANTSLDNDEYVIRPKRSKYIKSLANNP 180  
 Qy 172 GRVFTLVRLTGLFPLYLTLNISGKRYGRFANFDPMSPIFNDRERVOVLLSDPGLAVF 231  
 Db 181 GRVITLAATLGLMPVYLAFAVNSGRYDRLASHYNYGPIYSRERLQVYISDTGIFAVIYVLYK 240  
 Qy 232 YAIKLVAAGAAVYNNATVGVSVFVLTITLHTLSTLPHYSTERNWIKALST 291  
 Db 241 FVLQATMAKGLAWVNRVYGVPLILVNCFLVMTLYLQHTHSAIPHYDSSSEWMLRQALST 300  
 Qy 292 IDRPGLNRFVHDVTHVTHLHLSYIPHYAKKARDAIKVLSYXKIDRTPIFKAMV 351  
 Db 301 VDRYGVLANVFHNTIDTHVAHLSSTMPHYAMERATKAIKILGSIYKFDTPVYKAMW 360  
 Qy 352 REAKCIYIEPDEDESHKGVFWYH 374  
 Db 361 REAKCIYIEPDEDESHKGVFWYH 383

## RESULT 7

T15043  
 fungal elicitor-induced protein - parsley  
 C:Species: Petroselinum crispum (parsley)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: T15043  
 R:Kirsch, C.; Hahlbrock, K.; Somssich, I.E.  
 Plant Physiol. 115, 283-289, 1997  
 A>Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desat.  
 A:Reference number: Z18274; MUID:97451781; PMID:9306702  
 A:Accession: T15043  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-383 <KIR>  
 A:Cross-references: EMBL:U86374; NID:92501791; PIDN:AA80697.1; PID:92501792  
 C:Genetics:  
 A:Gene: EL112  
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 60.6%; Score 1241.5; DB 2; Length 383;  
 Best Local Similarity 58.2%; Pred. No. 1.5e-96;  
 Matches 221; Conservative 64; Mismatches 88; Indels 7; Gaps 4;

Qy 1 MGAGGRMSDPSBGNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYYVHDI 55  
 Db 1 MGAGGRMSDPSBGNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYYVHDI 60  
 Qy 56 IVAVFYLLANTYIPLIPTPLAYLAMPVYVPCQASITLGLMTLGHGCGHNASDYQLIDI 114  
 Db 61 FMAAYLVAVTNYIDQYLTPTPFNFVMAAAYAVAGCVLTGAMVVGHCCHDAFNTYWIN 120

[illegible]

## RESULT 8

omega-6 desaturase FAD2-1, microsomal - soybean  
 C:Species: Glycine max (soybean)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-May-2000  
 C:Accession: T07687  
 R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.  
 plant Physiol. 110, 311-319, 1996  
 A:Title: Developmental and growth temperature regulation of two different microsomal  
 A:Reference number: Z16095, MUID:96151506, PMID:8587990  
 A:Accession: T07687  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <HEP>  
 A:Cross-references: EMBL:U43920, NID:g904151, PIDD:AA00859.1, PIR:g904152  
 A:Experimental source: seed  
 C:Genetics:  
 A:Gene: FAD2-1  
 C:Function:  
 A:Description: involved in production of polyunsaturated lipids; plays a major role in c  
 A>Note: strongly expressed in developing seeds  
 C:Superfamily: omega-3 fatty acid desaturase

Query Match	60.5%	Score 1237.5;	DB 2;	Length 387;
Best Local Similarity	56.6%	Pred. No. 3.3e-96;		
Matches 213; Conservative	70;	Mismatches 90;	Indels 3;	Gaps 3

Qy	1	GGAGGRMSDPS-EGKNILIERVP-VDRPPTLSDLKAIPTTHCEESVIRSSVYVVDLIVA	58
Db	9	MGRGRVAKVEQGGKPSLRVPNTKPPPTVQQLKALIPHCFSRSLTFSFYVYDLSFA	68
Qy	59	YVYFYANTYTPILPTPLAYLAMPYWFECQASILGLVWIGHECHHAFSPYOLIDDIVG	118
Db	69	FIF-YIATTFPHLEQPSLSIAMPYWLQGLLGWAVIAHBCGHAFSXTQWVDVWG	127
Qy	119	FVLHSALLTPYFSWKYSHRNHHANTNSLNDNEVYIPKRSKYKITYSKLNNPGSRFVLY	178
Db	128	LTHSHTLVVPFSWKISHRRHSHNSGSLDRBEVFPKRSKSYAMPSTKLNNPLGRASLL	187
Qy	179	FRLLGFLPYLLTINSKKYGRFANHPDPMSPFIENDRERVOLLSDGFLLAIFYAIKLLV	238
Db	188	VLTIQWPMYLAFNVSGRPYDSFASHYHPAYPIYENRERLLIYVSVALFVYISLYRVA	247
Qy	239	AAKGAAMVIMTAIVLGVSVFFVLLITYLHHTHLSLPHYDSTENWIMGALSTIDRQGF	298
Db	248	TLKGWMLLCVYGVPLLLVNGFLVITIYLOHTHFALPHYDSEMDWMLKGALATMDRDYGI	307
Qy	299	LNRVHDVTHTHVHLHLSYIPHYNAKKAARDAIKRVAGEYVKIDRTPIFKMYEAAKXCI	358
Db	308	LNRVHATHTDTHVAHLSFPMFYHAMEATYNAIKRILDEYQOFDTPKXKMLMRARCCJ	367

QY	359	YIEPDESEHKGVFWY	374
		:     :	:
Db	368	YIEPDEGTSEKGVWY	383

## RESULT 9

Delta12 fatty acid desaturase (EC 1.4.99.-) [imported] - common sunflower  
C|Species: Helianthus annuus (common sunflower)  
C|Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C|Accession: T14269  
R|Hongtrakul, V.; Slabaugh, W.B.; Knapp, S.J.  
submitted to the EMBL Data Library, February 1997  
A|Description: Sunflower delta-12 olate desaturase.  
A|Reference number: Z17949  
A|Accession: T14269  
A|Status: preliminary; translated from GB/EMBL/DBJ  
A|Molecule type: mRNA  
A|Residues: 1-378 <HON>  
A|Cross-references: EMBL:U91341; NID:g22290403; P1D:g22290404  
A|Experimental source: Strain Mammoth  
C|Function:  
A|Description: desaturates oleic acid to linoleic acid  
C|Superfamily: omega-3 fatty acid desaturase  
C|Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match	59.6%	Score 1220;	DB 2;	Length 378;
Best Local Similarity	56.7%	Pred. No. 9.4e-95;		
Matches 215; Conservative	69;	Mismatches 91;	Indels 4;	Gaps 4;

```

QY 1 MGAGGRMBDPSHGKQIILERV- VDPFPFLSLDKAKIPTHCFERSVYRSZYVVDHILVAV 59
QY 1 MGAGEYTSVWNE- NNPDLBRVPAKPPFTIGDIKKAI PRHCFORSILTRSTSYYSLDITITA 59
QY 60 VFYUANTANYIPLIPPLAVIAMPVYVWFCOASILITGLMTVGHCEGCHNAFSDYOLDIDIVGF 119
QY 60 VLYHATITTYHHILPRPLSSIMASTVYVQCVLTIGWVIYAHGCHHAFEDYQVMDYTVGF 119
QY 120 VJHSAALLTPYFSWKYSHRNHNANTNSLNDDEVYIIPKRSKVKYIYSKLLNPPGRVFTLVF 179
QY 120 VJHSSLVLPYFSWKYSHRHHSNTQSLERDEYFVPRSKSVPMWSKYFNNTVGRIVSMFV 179
QY 180 RUTLGFPLYLNTNIGSKKYGFRANFPDMSPIFNDREKQVULSDPGLLAVFYAICLYA 239
QY 180 TLLTGMPPLYLAFNVSGRPYDRFACHYVPTSPPMYNEKRQIVMSDGIYITSFILRVAM 239
QY 240 AKGAMVNVNMAIPIVIGSVFVLITLYLHHTHLSLPHYVSTENMWIKALSTIDRDFGL 299
QY 240 AKGLVWVICVGVPLWVNAFVLVLTLYLOHTHPGLPHYDSSENEWKALATYDRYGVU 299
QY 300 NKVFHDVTHVTHVHLISYIPHYAHKEARDAIKPVLGEYXKIDRPIFKAMVREACEYI 359
QY 300 NKVFHIHIDTHVHHLFSFMPIYNNMBAQKALRPVLGEYRRDKTFPVYAMWREMECEJF 359
QY 360 IEPDEDSHKGVFWY-HKM 377
QY 360 VEODDEGK-GGVFWYXNMK 377

```

## RESULT 10

omega-6 fatty acid desaturase (EC 1.14.99.-) defense-related - tomato  
C.Species: Lycopersicon esculentum (tomato)  
C.Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 21-Jul-2000  
C.Accession: T07009  
R.Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.  
Mol. Plant Microbe Interact. 9, 409-415, 1996  
A.Title: Characterization of defense-related genes ectopically expressed in virid-infected  
A.Reference number: Z15859; PMID:96252900; PMID:8672818  
A.Accession: T07009  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-333 <GAD>

A:Cross-references: EMBL:X94944, NID:g1161567, PIDN:CAA64414.1, PID:g1161568  
A:Experimental source: cultivar Rutgers; leaf  
C:Genetics:  
A:Gene: cev119  
C:Superfamily: omega-3 fatty acid desaturase  
C:Keywords: oxidoreductase

Query Match 56.7%; Score 1160.5; DB 2; Length 333;

Best Local Similarity 55.1%; Pred. No. 8e-90; Matches 209; Conservative 54; Mismatches 61; Indels 55; Gaps 5;

QY 1 MGAGRM-----SDSEGNILIERVVD--PPTLSLKKALPFCFERSVIRSSYVVDL 55  
DB 1 MGGGNNAMTSKOEQKNPLERVPSSKRPPTLGVKKALIPPCFERSLVKVSFSLIDL 60  
QY 56 IVAVFYIANTYIPLIPPLAYLAMPYVFCQASILGLMWIGHCNHAFSDYQDL 115  
DB 61 ILVYIFYYIANTYIHLITPFRYVAMTYWIAQGCVCIGVIGHCNHAFSDYQVDD 120  
QY 116 IVGFVLSALLTPYFWMKYSRHHNANTNSLDNDEVYIPKRSKVYKSLNPPGRVF 175  
DB 121 IVGLHSALLTPYFAMGSHRRHANTGSLNDEIYIPRLKSKLR----- 166  
QY 176 TLVRLITGLFPLYLITNSGKKYGFANHPFMSPIFNDREVOYLLSDFLAVFAIK 235  
DB 167 -----GKKYDFACHYDPSPISYNSRRLQIYIDVAVIATVILLY 207  
QY 236 LIVAAGAAWVINYAIPLVGSVFVLTLYLHHTLSLPHYDSEMMWIKALSTDRD 295  
DB 208 RVTITQGLAG-----FVITLHHTHSLPHYDSEMDHLGALATVDRD 253  
QY 296 FGLNRFVHDVTHVHLHLSYIPHYAKARDAIKFVLGEYKIDRTPIFKMYREAK 355  
DB 254 YGLNKFVHNTDTHVHLHFSYISHYAMEAKAIKFLDEYKYDDTPIKMMWRDTK 313  
QY 356 ECIYIEPDESEHKGVPYH 374  
DB 314 ECIYIEPDESEHKGVPYH 329

## RESULT 11

JC7871  
stearyl-CoA 9-desaturase (EC 1.14.19.1), FAD2 - *Chlorella vulgaris*  
N:Alternate names: acyl-CoA desaturase; delta12 stearyl-CoA desaturase; delta9-desatura  
C:Species: *Chlorella vulgaris*  
C>Date: 09-Dec-2002 #sequence\_revision 09-Dec-2002 #text\_change 31-Mar-2003  
A:Accession: JC7871  
R:Stuga, K.; Honjo, K.; Furuya, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.;  
BioSci. Biotechnol. Biochem. 66, 1314-1327, 2002  
A:Title: Two low-temperature-inducible *Chlorella* genes for delta12 and omega-3 fatty ac  
s cerevisiae, and expression of omega-3 fad in *Nicotiana tabacum*.  
A:Reference number: JC7871, MUID:22152188, PMID:12162554  
A:Accession: JC7871  
A:Molecule type: mRNA  
A:Residues: 1-376 <SUG>  
A:Cross-references: DDBJ:AB075526  
C:Comment: This enzyme is involved in low temperature adaptation, and is also involved i  
C:Genetics:  
A:Gene: fad2  
C:Keywords: oxidoreductase

Query Match 45.3%; Score 926.5; DB 2; Length 376;  
Best Local Similarity 45.9%; Pred. No. 4.1e-70;  
Matches 175; Conservative 76; Mismatches 117; Indels 13; Gaps 8;

QY 3 AGGMSDPSSEGNILIERVVD--PPTLSLKKALPFCFERSVIRSSYVVDL 60  
DB 2 AATRRASABG---WTRQPVVTKPAFSYSTLRKAIIPACWQSLPRSCAYLAADLALAA 58  
QY 61 FYIYANTYIPLIPPLA--YLA-WPVYVFCQASILGLMWIGHCNHAFSDYQDL 117  
DB 59 LVW-ASTFIDAPFVPAVRLWALMPAYWILAGAVATGIVIAHCGHAFSDYQVNDGV 117

QY 118 GFVLSALLTPYFWMKYSRHHNANTNSLDNDEVYIPKRSKVYKSLNPPGRVFTL 177  
DB 118 GLVLSLLVYFWMKYSRHHNANTGAVVDEVFVPTREVEDKMWLEQAWPRLVKL 177  
QY 178 VFRITGLFPLYLITNSGKKYGFANHPFMSPIFNDREVOYLLSDFLAVFAIKL 236  
DB 178 FITLGLPFLYLAENVASRPFEKSVWNHFDWSPISFGRLEVEVAASDAALVAVICGRQ 237  
QY 237 LVAAGAAWVINYAIPLVGSVFVLTLYLHHTLSLPHYDSEMMWIKALSTDRD 296  
DB 238 LAASFQAMLVKTMVLVPLVNVFVLVITLMLQSHPELPHIGEDMDLRLGALLTVDDY 297  
QY 297 GF-LNRFVHDVTHVHLHLSYIPHYAKARDAIKFVLGEYKIDRTPIFKMYREAK 355  
DB 298 GMLNLSLHHTIADTHVAHLFSQMPHYAQAETALKVLDYRSDSRPILQAIWQDFG 357  
QY 356 ECIYIEPDESEHKGVPYH 376  
DB 358 SCRVAADPTGD--GVLMFRK 376

## RESULT 12

AG2005  
omega-3 fatty acid desaturase [imported] - *Nostoc* sp. (strain PCC 7120)  
C:Species: *Nostoc* sp. PCC 7120  
A:Notes: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
A:Accession: AG2005  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaoto, S.; Watanabe, A.; Iriuguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A:Reference number: AB1807, MUID:21595285, PMID:11759840  
A:Accession: AG2005  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-359 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA87963.1; PID:g17135417; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1597  
C:Superfamily: omega-3 fatty acid desaturase

Query Match 32.2%; Score 658.5; DB 2; Length 359;  
Best Local Similarity 35.7%; Pred. No. 1.2e-47;  
Matches 121; Conservative 76; Mismatches 123; Indels 19; Gaps 6;

QY 25 PFTLSLKKALPFCFERSVIRSSYVVDLIVAVFYIANTYIPLIPPLAYLAMPVY 84  
DB 24 PFTLQDLKALIPACFPQPNVSKSLFYFPRDVLVGLLYAVAH-YLD-----SWYFWDIF 76  
QY 85 WFCQASILGLMWIGHCNHAFSDYQDLIDIVFVLSALLTPYFWMKYSRHHNANTN 144  
DB 77 WLIQGTWFMALFVVGHDGCHQSFQKXKMLNDLIGLHTFTFLVYHQMRSIRHTRHNTGT 136  
QY 145 SLNDEVYIPKRSKVYKSLNPPGRVFTLVRITLGLPFLYLITNSGKKYGRFANH 204  
DB 137 NIDNDESWYPTQGYK-----EMPLGQKIGRYVVLAVPVILFKRSPKE-----GSH 186  
QY 205 FDPMSPIFNDREVOYLLSDFLAVFAIKLIVAAGAAWVINYAIPLVGSVFVFLI 264  
DB 187 FLPESSLPFKSEKMDVITSTVLMSCWGLGFLVYQGMWMLKXYAARYIVFVITWDLV 246  
QY 265 TYLHHTLSLPHYDSEMMWIKALSTDRDGLNRFVHDVTHVHLHLSYIPHYA 324  
DB 247 TFLHHTRADLPWRGSEWTFPLKGAISSIDRYGLVNHIIHDI-GTHVAHHIPLNIPIHYNL 305  
QY 325 KEARDAIKPVLGEYKIDRTPIFKMYREAKECYIYEPD 363  
DB 306 LKATRAIKPVWGEYIRKSEBPIKSLMRSCVSCHFV-PD 343

## RESULT 13

```

A/Status: preliminary; translated from GB/EMBL/DDBU
A/Molecule type: mRNA
A/Residues: 1-441 <HAM>
A/Cross-references: EMBL:D79979; NID:G1694624; PID:BAA11475.1; PID:G1694625
A/Experimental source: cultivar SRI
C/Genetics:
A/Gene: FAD7
C/Superfamily: omega-3 fatty acid desaturase
C/Keywords: oxidoreductase

Query Match      31.5%; Score 645; DB 2; Length 441;
Best Local Similarity 39.6%; Pred. No. 2,Je-46;
Matches 137; Conservative 56; Mismatches 113; Indels 40; Gaps 9;

Qy 3 AGGMRSPSGKNILERVDPPTTSDLKAIPTCFERSVIRSSYYVVHDLIVAYF- 61
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 SGGEFFPDG-----APPKSLDIAIKAIPIKCOWNPKMSMSYVRD--VALVFG 129

Qy 62 -----YYLANTYIPLIPTPLAYITAMPYWCQSILGLWVTIGEGCHNAFSYQILDID 116
Db  LAAAAAFENN-----WWVWELPYWFQSTMFNALFVLGHDCGGSPNNHKINSV 178

Qy 117 VGFVLSALITPEYPSWKYSRHNHNANTNSLDNDENVYIPKRKSXYKIISKLIANDPGRVET 176
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 VGHIIHSIIIVPGYHGWHISRTHQNHQNGHVENBESMHPDEP--KIYNSIDLATKULFT 235

Qy 177 LVPLTLGFPRLYLITNISGKKYGFAHFNPMPSPIFNDRREVOYLLDSDFGLAVFYAKL 236
Db  LPPFL-LAPPEYILMSRSPGKK---GSHFPNSDLFEPSEKDDWTSLCTANPAALLVG 290

Qy 237 LVAKGAAMVINMWAIPEVLGVSVFPEVLTLYLHH--THLSLPHYDSTEMNMKGALSTIDR 294
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
291 LSPFMGPQYLAKIXGIYWGCVMLDLVTYLHHGHODKLFMYRGEMSYLEGGTLTLDR 350

Qy 295 DPFGLNFVFHDVTHTVHLHLISYIPHYHAKENDAIKEPVIGEYRK 340
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
351 DYGINNIITHDI-GTHVIHLFPQIPHYHLVEATEAKPAVLGYKYX 395

RESULT 15
T110063
omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - castor bean
N/Alternate names: linoleoyl desaturase
C/Species: Ricinus communis (castor bean)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T110063
R/de Ioo, F.J.; Somerville, C.
Plant Physiol. 105, 443-444, 1994
A>Title: Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.
A/Reference number: Z16930; MUID:94302177; PMID:8029360
A/Accession: T110063
A/Status: preliminary; translated from GB/EMBL/DDBU
A/Molecule type: mRNA
A/Residues: 1-460 <DBL>
A/Cross-references: EMBL:L25897; NID:G414731; PID:NAAA73511.1; PID:G414732
A/Experimental source: cultivar Baker 296; tissue-type seed
C/Genetics:
A/Gene: FAD7
C/Function:
A/Pathway: fatty acid biosynthesis
C/Superfamily: omega-3 fatty acid desaturase
C/Keywords: oxidoreductase

Query Match      31.2%; Score 639.5; DB 2; Length 460;
Best Local Similarity 35.5%; Pred. No. 6,Se-46;
Matches 134; Conservative 72; Mismatches 134; Indels 37; Gaps 9;

Qy 12 EGKNILERVDPPTTSDLKAIPTCFERSVIRSSYYVVHDLIVAY----VFYYLANT 67
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
96 EGKEFEFDAGAPRPFTIADIIPAIPKICOWNPKMSYLVIRDVVVVGGLAAVAAYENN- 154

Qy 68 YIPIPIPIALAPVPVWFCASILTGLMVIGHGCHNAFSDYQLIDIIVGFVLSALT 127
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



[illegible]

Search completed: June 18, 2004, 17:38:26  
Job time : 21 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 17:30:33 ; Search time 18 seconds  
(without alignments)  
1090.580 Million cell updates/sec

Title: US-10-069-772-2

Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEGRNLEERV.....IYIEPDESEHKGVFWYHKM 377

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	79.6	375	D12_CREAL	O81931 crepis alpi
2	1325.5	64.8	383	PD62_SOYBN	P48631 glycine max
3	1301	63.6	384	PD6E_BRARU	Q32877 brassica ju
4	1300.5	63.5	383	PD6E_BRARU	P46313 arabidopsi
5	1237.5	60.5	387	PD61_SOYBN	P48630 glycine max
6	782	38.2	400	PD12_MORIS	P55668 mortierella
7	781	38.2	400	PD12_MORAP	Q97855 mortierella
8	642	31.4	447	PD3C_SESIN	P48620 sesamum ind
9	639.5	31.2	460	PD3C_RICCO	P48619 ricinus com
10	620.5	30.3	386	PD3E_ARATH	P48623 arabidopsi
11	612	29.9	379	PD3E_TOBAC	P48626 nicotiana t
12	607	29.7	404	PD3C_BRANA	P48618 brassica na
13	606	29.6	446	PD3C_ARATH	P46310 arabidopsi
14	602.5	29.4	453	PD3C_SOYBN	P48621 glycine max
15	598.5	29.2	435	PD3D_ARATH	P48622 arabidopsi
16	593.5	29.0	380	PD3E_PHARU	P33291 phaseolus a
17	588.5	28.7	383	PD3E_BRANA	P48624 brassica na
18	574	28.0	380	PD3E_SOYBN	P48625 glycine max
19	316.5	15.5	447	PD3C_SPIOL	P48629 spinacia ol
20	309.5	15.1	351	PD3A_SYNY3	P20388 synchocyst
21	306	14.9	424	PD6C_SOYBN	P48628 glycine max
22	301	14.7	448	PD6C_ARATH	P46312 arabidopsi
23	293.5	14.3	443	PD6C_BRANA	P48627 brassica na
24	292	14.3	351	PD3A_SYNY3	Q54794 spirulina p
25	169.5	8.3	359	PD6C_SYNY3	Q08871 synchocyst
26	110	5.4	1191	S122_SQUAC	P55013 squaalus aca
27	101	4.9	1212	S122_HUMAN	P55011 homo sapien
28	97	4.7	320	CRTW_HARPL	Q39982 haemacococc
29	96.5	4.7	390	ARP2_SCHPO	Q9uu11 sciliosacch
30	95.5	4.7	711	FRE3_YEAST	Q09857 saccharomyc
31	95.5	4.7	1044	YAF3_SCHPO	Q09857 sciliosacch
32	94	4.6	313	CCSA_TOBAC	P12216 nicotiana t
33	94	4.6	794	POT2_ARATH	O22881 arabidopsi

34	94	4.6	973	1	HYPA_CLOPE	Q46205 clostridium
35	93	4.5	888	1	POL_SMRVA	P03364 squitrel mo
36	93	4.5	1205	1	S122_MOUSE	P55012 mus musculu
37	92.5	4.5	514	1	MYIN_BUCAP	Q8K913 buchnera ap
38	92	4.5	1353	1	CYAG_MOUSE	P51830 mus musculu
39	91.5	4.5	359	1	ACOD_BOVIN	Q9rt94 bos taurus
40	91	4.4	444	1	FADS_BRARE	Q9dex7 brachydanto
41	91	4.4	1353	1	CYAG_HUMAN	O60503 homo sapien
42	90.5	4.4	346	1	FMLR_MACMU	P79189 macaca mula
43	89.5	4.4	1026	1	EXSB_CHLMU	Q9P1t8 chlamydia m
44	89	4.3	870	1	POL_TSRV	P31623 sheep pulmo
45	88	4.3	499	1	PTRA_ECOLI	P37308 escherichia

## ALIGNMENTS

RESULT 1	ID	D12_CREAL	STANDARD;	PRT;	375 AA.
AC	O81931;				
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepennate synthase) (Delta-12 fatty acid acetylase).				
OS	Crepis alpina.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.				
OX	NCBI_TaxID=72610;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96239771; PubMed=9572738;				
RA	Lee M., Leeman M., Banas A., Bator M., Singh S., Schweizer M., Nilsson R., Liljenberg C., Dahlqvist A., Gummesson P.O., Sjodahl S., Green A., Stymer S.;				
RT	"Identification of non-heme diiron proteins that catalyze triple bond and epoxy group formation.";				
RL	Science 280:915-918(1998).				
CC	-1- FUNCTION: Changes the delta-12 double bond of linoleic acid into a triple bond in the biosynthesis of crepennic acid.				
CC	-1- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepennate + A + H(2)O.				
CC	-1- COFACTOR: Iron.				
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC	-1- TISSUE SPECIFICITY: Seed.				
CC	-1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.				
CC	-1- SIMILARITY: Belongs to the fatty acid desaturase family.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL, Y16285; CAAT6158.2; -				
DR	InterPro, IPR005804; FA_desat_fam.				
DR	Pfam, PF00487; FA_desaturase_1.				
DR	ProDom, PD001081; FA_desat_fam; 2.				
KW	Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Iron.				
FT	TRANSMEM	54	74	POTENTIAL.	
FT	TRANSMEM	77	97	POTENTIAL.	
FT	TRANSMEM	110	130	POTENTIAL.	
FT	TRANSMEM	172	192	POTENTIAL.	
FT	TRANSMEM	218	238	POTENTIAL.	
FT	TRANSMEM	242	262	POTENTIAL.	
FT	DOMAIN	98	102	HISTIDINE BOX-1.	

FT DOMAIN 134 138 HISTIDINE BOX-2.  
 FT DOMAIN 308 312 HISTIDINE BOX-3.  
 SQ SEQUENCE 375 AA; 43362 MW; B31F5A64DD0C2926 CRC64;  
 Query Match 79.6%; Score 1629; DB 1; Length 375;  
 Best Local Similarity 76.6%; Pred. No. 7, 8e-124;  
 Matches 288; Conservative 40; Mismatches 46; Indels 2; Gaps 1;

QY 1 MGAGRMSDPSEBGRKILERVDPDPTLSDLKKAIPTHCFERSVIRSSYYVHDLIVAV 60  
 1 MGGGR--GRISQKPLMERVSVDPPFTVSDLKQALPHCFKRSVIRSSYYIVHDAIAYI 58  
 DB 61 FYIYANTYIPLIPLATAYLAWPVWPCQASITGLMVGHEGCHHAFSDYQILDYGV 120  
 59 FYFLADKRIPIIPALAYLAWPLWPCQASITGLMVGHEGCHHAFSDYQVWDVTVGI 118  
 QY 121 LHSALLTPFWSKYSRHRNHANTNSLDNDEVYIPKRSKVKIYSLKLNPPGRVFTLVER 180  
 119 LHSPLMTYFWSKYSRHRNHANTNSLDNDEVYIPKRSKAKVLYVNLNHPGRLLIMPT 178  
 QY 181 LTLGFPVLLTINISGKTYGRFANHPDPMSPFNDREVOVLLSDFGLLAVFYAIIKLVAA 240  
 179 FTLGFPVLLTINISGKTYGRFANHPDPMSPFNDREVOVLLSDFGLLAVFYAIIKLVAA 238  
 DB 241 KGAANVIMMYAIPVGVSVFVLLTYLHTHTLSLPHYSTENNVIKALSTIDRPFGLN 300  
 239 KGAANVTCIYGVIPVGVPIFDIILYHHTHTLSLPHYSSSENMWRGALSTIDRPFGLN 298  
 QY 301 RVFHVHTHVLHHLISYIPHYAKARDAIKPVIGEVYKIDRTPIFKAMYREAKCIYI 360  
 299 SVLHVHTHVLHHLISYIPHYAKARDAIKPVIGEVYKIDRTPIFKAMYREAKCIYI 358  
 DB 361 EPEDESEHKGVFWYK 376  
 359 EPEKGRSGKVYWNK 374

QY 361 EPEDESEHKGVFWYK 376  
 359 EPEKGRSGKVYWNK 374

RESULT 2  
 F62\_SOYBN STANDARD; PRT; 383 AA.  
 AC P48631;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2  
 (EC 1.14.19.-).  
 GN FAD2-2.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 NX NCBI\_TaxID=3847;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Epicotyl;  
 RX MEDLINE=96151506; PubMed=8587990;  
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;  
 RT "Developmental and growth temperature regulation of two different  
 RT microsomal omega-6 desaturase genes in soybeans.";  
 RL Plant Physiol. 110:311-319(1996).  
 CC -1- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces  
 CC the second double bond in the biosynthesis of 18:3 fatty acids,  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>  
 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL, L43921; AA00860.1; -.  
 DR PIR; T07688; T07688.  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.  
 DR Prodom; PD001081; FA\_desat\_fam; 2.  
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
 KW Transmembrane.  
 FT TRANSMEM 61  
 FT TRANSMEM 81  
 FT TRANSMEM 85  
 FT TRANSMEM 105  
 FT TRANSMEM 117  
 FT TRANSMEM 137  
 FT TRANSMEM 179  
 FT TRANSMEM 199  
 FT TRANSMEM 225  
 FT TRANSMEM 245  
 FT TRANSMEM 249  
 FT TRANSMEM 269  
 FT TRANSMEM 299  
 FT TRANSMEM 315  
 FT TRANSMEM 319  
 FT TRANSMEM 339  
 FT TRANSMEM 359  
 FT TRANSMEM 375  
 FT TRANSMEM 383  
 FT TRANSMEM 395  
 FT TRANSMEM 405  
 FT TRANSMEM 415  
 FT TRANSMEM 425  
 FT TRANSMEM 435  
 FT TRANSMEM 445  
 FT TRANSMEM 455  
 FT TRANSMEM 465  
 FT TRANSMEM 475  
 FT TRANSMEM 485  
 FT TRANSMEM 495  
 FT TRANSMEM 505  
 FT TRANSMEM 515  
 FT TRANSMEM 525  
 FT TRANSMEM 535  
 FT TRANSMEM 545  
 FT TRANSMEM 555  
 FT TRANSMEM 565  
 FT TRANSMEM 575  
 FT TRANSMEM 585  
 FT TRANSMEM 595  
 FT TRANSMEM 605  
 FT TRANSMEM 615  
 FT TRANSMEM 625  
 FT TRANSMEM 635  
 FT TRANSMEM 645  
 FT TRANSMEM 655  
 FT TRANSMEM 665  
 FT TRANSMEM 675  
 FT TRANSMEM 685  
 FT TRANSMEM 695  
 FT TRANSMEM 705  
 FT TRANSMEM 715  
 FT TRANSMEM 725  
 FT TRANSMEM 735  
 FT TRANSMEM 745  
 FT TRANSMEM 755  
 FT TRANSMEM 765  
 FT TRANSMEM 775  
 FT TRANSMEM 785  
 FT TRANSMEM 795  
 FT TRANSMEM 805  
 FT TRANSMEM 815  
 FT TRANSMEM 825  
 FT TRANSMEM 835  
 FT TRANSMEM 845  
 FT TRANSMEM 855  
 FT TRANSMEM 865  
 FT TRANSMEM 875  
 FT TRANSMEM 885  
 FT TRANSMEM 895  
 FT TRANSMEM 905  
 FT TRANSMEM 915  
 FT TRANSMEM 925  
 FT TRANSMEM 935  
 FT TRANSMEM 945  
 FT TRANSMEM 955  
 FT TRANSMEM 965  
 FT TRANSMEM 975  
 FT TRANSMEM 985  
 FT TRANSMEM 995  
 FT TRANSMEM 1005  
 FT TRANSMEM 1015  
 FT TRANSMEM 1025  
 FT TRANSMEM 1035  
 FT TRANSMEM 1045  
 FT TRANSMEM 1055  
 FT TRANSMEM 1065  
 FT TRANSMEM 1075  
 FT TRANSMEM 1085  
 FT TRANSMEM 1095  
 FT TRANSMEM 1105  
 FT TRANSMEM 1115  
 FT TRANSMEM 1125  
 FT TRANSMEM 1135  
 FT TRANSMEM 1145  
 FT TRANSMEM 1155  
 FT TRANSMEM 1165  
 FT TRANSMEM 1175  
 FT TRANSMEM 1185  
 FT TRANSMEM 1195  
 FT TRANSMEM 1205  
 FT TRANSMEM 1215  
 FT TRANSMEM 1225  
 FT TRANSMEM 1235  
 FT TRANSMEM 1245  
 FT TRANSMEM 1255  
 FT TRANSMEM 1265  
 FT TRANSMEM 1275  
 FT TRANSMEM 1285  
 FT TRANSMEM 1295  
 FT TRANSMEM 1305  
 FT TRANSMEM 1315  
 FT TRANSMEM 1325  
 FT TRANSMEM 1335  
 FT TRANSMEM 1345  
 FT TRANSMEM 1355  
 FT TRANSMEM 1365  
 FT TRANSMEM 1375  
 FT TRANSMEM 1385  
 FT TRANSMEM 1395  
 FT TRANSMEM 1405  
 FT TRANSMEM 1415  
 FT TRANSMEM 1425  
 FT TRANSMEM 1435  
 FT TRANSMEM 1445  
 FT TRANSMEM 1455  
 FT TRANSMEM 1465  
 FT TRANSMEM 1475  
 FT TRANSMEM 1485  
 FT TRANSMEM 1495  
 FT TRANSMEM 1505  
 FT TRANSMEM 1515  
 FT TRANSMEM 1525  
 FT TRANSMEM 1535  
 FT TRANSMEM 1545  
 FT TRANSMEM 1555  
 FT TRANSMEM 1565  
 FT TRANSMEM 1575  
 FT TRANSMEM 1585  
 FT TRANSMEM 1595  
 FT TRANSMEM 1605  
 FT TRANSMEM 1615  
 FT TRANSMEM 1625  
 FT TRANSMEM 1635  
 FT TRANSMEM 1645  
 FT TRANSMEM 1655  
 FT TRANSMEM 1665  
 FT TRANSMEM 1675  
 FT TRANSMEM 1685  
 FT TRANSMEM 1695  
 FT TRANSMEM 1705  
 FT TRANSMEM 1715  
 FT TRANSMEM 1725  
 FT TRANSMEM 1735  
 FT TRANSMEM 1745  
 FT TRANSMEM 1755  
 FT TRANSMEM 1765  
 FT TRANSMEM 1775  
 FT TRANSMEM 1785  
 FT TRANSMEM 1795  
 FT TRANSMEM 1805  
 FT TRANSMEM 1815  
 FT TRANSMEM 1825  
 FT TRANSMEM 1835  
 FT TRANSMEM 1845  
 FT TRANSMEM 1855  
 FT TRANSMEM 1865  
 FT TRANSMEM 1875  
 FT TRANSMEM 1885  
 FT TRANSMEM 1895  
 FT TRANSMEM 1905  
 FT TRANSMEM 1915  
 FT TRANSMEM 1925  
 FT TRANSMEM 1935  
 FT TRANSMEM 1945  
 FT TRANSMEM 1955  
 FT TRANSMEM 1965  
 FT TRANSMEM 1975  
 FT TRANSMEM 1985  
 FT TRANSMEM 1995  
 FT TRANSMEM 2005  
 FT TRANSMEM 2015  
 FT TRANSMEM 2025  
 FT TRANSMEM 2035  
 FT TRANSMEM 2045  
 FT TRANSMEM 2055  
 FT TRANSMEM 2065  
 FT TRANSMEM 2075  
 FT TRANSMEM 2085  
 FT TRANSMEM 2095  
 FT TRANSMEM 2105  
 FT TRANSMEM 2115  
 FT TRANSMEM 2125  
 FT TRANSMEM 2135  
 FT TRANSMEM 2145  
 FT TRANSMEM 2155  
 FT TRANSMEM 2165  
 FT TRANSMEM 2175  
 FT TRANSMEM 2185  
 FT TRANSMEM 2195  
 FT TRANSMEM 2205  
 FT TRANSMEM 2215  
 FT TRANSMEM 2225  
 FT TRANSMEM 2235  
 FT TRANSMEM 2245  
 FT TRANSMEM 2255  
 FT TRANSMEM 2265  
 FT TRANSMEM 2275  
 FT TRANSMEM 2285  
 FT TRANSMEM 2295  
 FT TRANSMEM 2305  
 FT TRANSMEM 2315  
 FT TRANSMEM 2325  
 FT TRANSMEM 2335  
 FT TRANSMEM 2345  
 FT TRANSMEM 2355  
 FT TRANSMEM 2365  
 FT TRANSMEM 2375  
 FT TRANSMEM 2385  
 FT TRANSMEM 2395  
 FT TRANSMEM 2405  
 FT TRANSMEM 2415  
 FT TRANSMEM 2425  
 FT TRANSMEM 2435  
 FT TRANSMEM 2445  
 FT TRANSMEM 2455  
 FT TRANSMEM 2465  
 FT TRANSMEM 2475  
 FT TRANSMEM 2485  
 FT TRANSMEM 2495  
 FT TRANSMEM 2505  
 FT TRANSMEM 2515  
 FT TRANSMEM 2525  
 FT TRANSMEM 2535  
 FT TRANSMEM 2545  
 FT TRANSMEM 2555  
 FT TRANSMEM 2565  
 FT TRANSMEM 2575  
 FT TRANSMEM 2585  
 FT TRANSMEM 2595  
 FT TRANSMEM 2605  
 FT TRANSMEM 2615  
 FT TRANSMEM 2625  
 FT TRANSMEM 2635  
 FT TRANSMEM 2645  
 FT TRANSMEM 2655  
 FT TRANSMEM 2665  
 FT TRANSMEM 2675  
 FT TRANSMEM 2685  
 FT TRANSMEM 2695  
 FT TRANSMEM 2705  
 FT TRANSMEM 2715  
 FT TRANSMEM 2725  
 FT TRANSMEM 2735  
 FT TRANSMEM 2745  
 FT TRANSMEM 2755  
 FT TRANSMEM 2765  
 FT TRANSMEM 2775  
 FT TRANSMEM 2785  
 FT TRANSMEM 2795  
 FT TRANSMEM 2805  
 FT TRANSMEM 2815  
 FT TRANSMEM 2825  
 FT TRANSMEM 2835  
 FT TRANSMEM 2845  
 FT TRANSMEM 2855  
 FT TRANSMEM 2865  
 FT TRANSMEM 2875  
 FT TRANSMEM 2885  
 FT TRANSMEM 2895  
 FT TRANSMEM 2905  
 FT TRANSMEM 2915  
 FT TRANSMEM 2925  
 FT TRANSMEM 2935  
 FT TRANSMEM 2945  
 FT TRANSMEM 2955  
 FT TRANSMEM 2965  
 FT TRANSMEM 2975  
 FT TRANSMEM 2985  
 FT TRANSMEM 2995  
 FT TRANSMEM 3005  
 FT TRANSMEM 3015  
 FT TRANSMEM 3025  
 FT TRANSMEM 3035  
 FT TRANSMEM 3045  
 FT TRANSMEM 3055  
 FT TRANSMEM 3065  
 FT TRANSMEM 3075  
 FT TRANSMEM 3085  
 FT TRANSMEM 3095  
 FT TRANSMEM 3105  
 FT TRANSMEM 3115  
 FT TRANSMEM 3125  
 FT TRANSMEM 3135  
 FT TRANSMEM 3145  
 FT TRANSMEM 3155  
 FT TRANSMEM 3165  
 FT TRANSMEM 3175  
 FT TRANSMEM 3185  
 FT TRANSMEM 3195  
 FT TRANSMEM 3205  
 FT TRANSMEM 3215  
 FT TRANSMEM 3225  
 FT TRANSMEM 3235  
 FT TRANSMEM 3245  
 FT TRANSMEM 3255  
 FT TRANSMEM 3265  
 FT TRANSMEM 3275  
 FT TRANSMEM 3285  
 FT TRANSMEM 3295  
 FT TRANSMEM 3305  
 FT TRANSMEM 3315  
 FT TRANSMEM 3325  
 FT TRANSMEM 3335  
 FT TRANSMEM 3345  
 FT TRANSMEM 3355  
 FT TRANSMEM 3365  
 FT TRANSMEM 3375  
 FT TRANSMEM 3385  
 FT TRANSMEM 3395  
 FT TRANSMEM 3405  
 FT TRANSMEM 3415  
 FT TRANSMEM 3425  
 FT TRANSMEM 3435  
 FT TRANSMEM 3445  
 FT TRANSMEM 3455  
 FT TRANSMEM 3465  
 FT TRANSMEM 3475  
 FT TRANSMEM 3485  
 FT TRANSMEM 3495  
 FT TRANSMEM 3505  
 FT TRANSMEM 3515  
 FT TRANSMEM 3525  
 FT TRANSMEM 3535  
 FT TRANSMEM 3545  
 FT TRANSMEM 3555  
 FT TRANSMEM 3565  
 FT TRANSMEM 3575  
 FT TRANSMEM 3585  
 FT TRANSMEM 3595  
 FT TRANSMEM 3605  
 FT TRANSMEM 3615  
 FT TRANSMEM 3625  
 FT TRANSMEM 3635  
 FT TRANSMEM 3645  
 FT TRANSMEM 3655  
 FT TRANSMEM 3665  
 FT TRANSMEM 3675  
 FT TRANSMEM 3685  
 FT TRANSMEM 3695  
 FT TRANSMEM 3705  
 FT TRANSMEM 3715  
 FT TRANSMEM 3725  
 FT TRANSMEM 3735  
 FT TRANSMEM 3745  
 FT TRANSMEM 3755  
 FT TRANSMEM 3765  
 FT TRANSMEM 3775  
 FT TRANSMEM 3785  
 FT TRANSMEM 3795  
 FT TRANSMEM 3805  
 FT TRANSMEM 3815  
 FT TRANSMEM 3825  
 FT TRANSMEM 3835  
 FT TRANSMEM 3845  
 FT TRANSMEM 3855  
 FT TRANSMEM 3865  
 FT TRANSMEM 3875  
 FT TRANSMEM 3885  
 FT TRANSMEM 3895  
 FT TRANSMEM 3905  
 FT TRANSMEM 3915  
 FT TRANSMEM 3925  
 FT TRANSMEM 3935  
 FT TRANSMEM 3945  
 FT TRANSMEM 3955  
 FT TRANSMEM 3965  
 FT TRANSMEM 3975  
 FT TRANSMEM 3985  
 FT TRANSMEM 3995  
 FT TRANSMEM 4005  
 FT TRANSMEM 4015  
 FT TRANSMEM 4025  
 FT TRANSMEM 4035  
 FT TRANSMEM 4045  
 FT TRANSMEM 4055  
 FT TRANSMEM 4065  
 FT TRANSMEM 4075  
 FT TRANSMEM 4085  
 FT TRANSMEM 4095  
 FT TRANSMEM 4105  
 FT TRANSMEM 4115  
 FT TRANSMEM 4125  
 FT TRANSMEM 4135  
 FT TRANSMEM 4145  
 FT TRANSMEM 4155  
 FT TRANSMEM 4165  
 FT TRANSMEM 4175  
 FT TRANSMEM 4185  
 FT TRANSMEM 4195  
 FT TRANSMEM 4205  
 FT TRANSMEM 4215  
 FT TRANSMEM 4225  
 FT TRANSMEM 4235  
 FT TRANSMEM 4245  
 FT TRANSMEM 4255  
 FT TRANSMEM 4265  
 FT TRANSMEM 4275  
 FT TRANSMEM 4285  
 FT TRANSMEM 4295  
 FT TRANSMEM 4305  
 FT TRANSMEM 4315  
 FT TRANSMEM 4325  
 FT TRANSMEM 4335  
 FT TRANSMEM 4345  
 FT TRANSMEM 4355  
 FT TRANSMEM 4365  
 FT TRANSMEM 4375  
 FT TRANSMEM 4385  
 FT TRANSMEM 4395  
 FT TRANSMEM 4405  
 FT TRANSMEM 4415  
 FT TRANSMEM 4425  
 FT TRANSMEM 4435  
 FT TRANSMEM 4445  
 FT TRANSMEM 4455  
 FT TRANSMEM 4465  
 FT TRANSMEM 4475  
 FT TRANSMEM 4485  
 FT TRANSMEM 4495  
 FT TRANSMEM 4505  
 FT TRANSMEM 4515  
 FT TRANSMEM 4525  
 FT TRANSMEM 4535  
 FT TRANSMEM 4545  
 FT TRANSMEM 4555  
 FT TRANSMEM 4565  
 FT TRANSMEM 4575  
 FT TRANSMEM 4585  
 FT TRANSMEM 4595  
 FT TRANSMEM 4605  
 FT TRANSMEM 4615  
 FT TRANSMEM 4625  
 FT TRANSMEM 4635  
 FT TRANSMEM 4645  
 FT TRANSMEM 4655  
 FT TRANSMEM 4665  
 FT TRANSMEM 4675  
 FT TRANSMEM 4685  
 FT TRANSMEM 4695  
 FT TRANSMEM 4705  
 FT TRANSMEM 4715  
 FT TRANSMEM 4725  
 FT TRANSMEM 4735  
 FT TRANSMEM 4745  
 FT TRANSMEM 4755  
 FT TRANSMEM 4765  
 FT TRANSMEM 4775  
 FT TRANSMEM 4785  
 FT TRANSMEM 4795  
 FT TRANSMEM 4805  
 FT TRANSMEM 4815  
 FT TRANSMEM 4825  
 FT TRANSMEM 4835  
 FT TRANSMEM 4845  
 FT TRANSMEM 4855  
 FT TRANSMEM 4865  
 FT TRANSMEM 4875  
 FT TRANSMEM 4885  
 FT TRANSMEM 4895  
 FT TRANSMEM 4905  
 FT TRANSMEM 4915  
 FT TRANSMEM 4925  
 FT TRANSMEM 4935  
 FT TRANSMEM 4945  
 FT TRANSMEM 4955  
 FT TRANSMEM 4965  
 FT TRANSMEM 4975  
 FT TRANSMEM 4985  
 FT TRANSMEM 4995  
 FT TRANSMEM 5005  
 FT TRANSMEM 5015  
 FT TRANSMEM 5025  
 FT TRANSMEM 5035  
 FT TRANSMEM 5045  
 FT TRANSMEM 5055  
 FT TRANSMEM 5065  
 FT TRANSMEM 5075  
 FT TRANSMEM 5085  
 FT TRANSMEM 5095  
 FT TRANSMEM 5105  
 FT TRANSMEM 5115  
 FT TRANSMEM 5125  
 FT TRANSMEM 5135  
 FT TRANSMEM 5145  
 FT TRANSMEM 5155  
 FT TRANSMEM 5165  
 FT TRANSMEM 5175  
 FT TRANSMEM 5185  
 FT TRANSMEM 5195  
 FT TRANSMEM 5205  
 FT TRANSMEM 5215  
 FT TRANSMEM 5225  
 FT TRANSMEM 5235  
 FT TRANSMEM 5245  
 FT TRANSMEM 5255  
 FT TRANSMEM 5265  
 FT TRANSMEM 5275  
 FT TRANSMEM 5285  
 FT TRANSMEM 5295  
 FT TRANSMEM 5305  
 FT TRANSMEM 5315  
 FT TRANSMEM 5325  
 FT TRANSMEM 5335  
 FT TRANSMEM 5345  
 FT TRANSMEM 5355  
 FT TRANSMEM 5365  
 FT TRANSMEM 5375  
 FT TRANSMEM 5385  
 FT TRANSMEM 5395  
 FT TRANSMEM 5405  
 FT TRANSMEM 5415  
 FT TRANSMEM 5425  
 FT TRANSMEM 5435  
 FT TRANSMEM 5445  
 FT TRANSMEM 5455  
 FT TRANSMEM 5465  
 FT TRANSMEM 5475  
 FT TRANSMEM 5485  
 FT TRANSMEM 5495  
 FT TRANSMEM 5505  
 FT TRANSMEM 5515  
 FT TRANSMEM 5525  
 FT TRANSMEM 5535  
 FT TRANSMEM 5545  
 FT TRANSMEM 5555  
 FT TRANSMEM 5565  
 FT TRANSMEM 5575  
 FT TRANSMEM 5585  
 FT TRANSMEM 5595  
 FT TRANSMEM 5605  
 FT TRANSMEM 5615  
 FT TRANSMEM 5625  
 FT TRANSMEM 5635  
 FT TRANSMEM 5645  
 FT TRANSMEM 5655  
 FT TRANSMEM 5665  
 FT TRANSMEM 5675  
 FT TRANSMEM 5685  
 FT TRANSMEM 5695  
 FT TRANSMEM 5705  
 FT TRANSMEM 5715  
 FT TRANSMEM 5725  
 FT TRANSMEM 5735  
 FT TRANSMEM 5745  
 FT TRANSMEM 5755  
 FT TRANSMEM 5765  
 FT TRANSMEM 5775  
 FT TRANSMEM 5785  
 FT TRANSMEM 5795  
 FT TRANSMEM 5805  
 FT TRANSMEM 5815  
 FT TRANSMEM 5825  
 FT TRANSMEM 5835  
 FT TRANSMEM 5845  
 FT TRANSMEM 5855  
 FT TRANSMEM 5865  
 FT TRANSMEM 5875  
 FT TRANSMEM 5885  
 FT TRANSMEM 5895  
 FT TRANSMEM 5905  
 FT TRANSMEM 5915  
 FT TRANSMEM 5925  
 FT TRANSMEM 5935  
 FT TRANSMEM 5945  
 FT TRANSMEM 5955  
 FT TRANSMEM 5965  
 FT TRANSMEM 5975  
 FT TRANSMEM 5985  
 FT TRANSMEM 5995  
 FT TRANSMEM 6005  
 FT TRANSMEM 6015  
 FT TRANSMEM 6025  
 FT TRANSMEM 6035  
 FT TRANSMEM 6045  
 FT TRANSMEM 6055  
 FT TRANSMEM 6065  
 FT TRANSMEM 6075  
 FT TRANSMEM 6085  
 FT TRANSMEM 6095  
 FT TRANSMEM 6105  
 FT TRANSMEM 6115  
 FT TRANSMEM 6125  
 FT TRANSMEM 6135  
 FT TRANSMEM 6145  
 FT TRANSMEM 6155  
 FT TRANSMEM 6165  
 FT TRANSMEM 6175  
 FT TRANSMEM 6185  
 FT TRANSMEM 6195  
 FT TRANSMEM 6205  
 FT TRANSMEM 6215  
 FT TRANSMEM 6225  
 FT TRANSMEM 6235  
 FT TRANSMEM 6245  
 FT TRANSMEM 6255  
 FT TRANSMEM 6265  
 FT TRANSMEM 6275  
 FT TRANSMEM 6285  
 FT TRANSMEM 6295  
 FT TRANSMEM 6305  
 FT TRANSMEM 6315  
 FT TRANSMEM 6325  
 FT TRANSMEM 6335  
 FT TRANSMEM 6345  
 FT TRANSMEM 6355  
 FT TRANSMEM 6365  
 FT TRANSMEM 6375  
 FT TRANSMEM 6385  
 FT TRANSMEM 6395  
 FT TRANSMEM 6405  
 FT TRANSMEM 6415  
 FT TRANSMEM 6425  
 FT TRANSMEM 6435  
 FT TRANSMEM 6445  
 FT TRANSMEM 6455  
 FT TRANSMEM 6465  
 FT TRANSMEM 6475  
 FT TRANSMEM 6485  
 FT TRANSMEM 6495  
 FT TRANSMEM 6505  
 FT TRANSMEM 6515  
 FT TRANSMEM 6525  
 FT TRANSMEM 6535  
 FT TRANSMEM 6545  
 FT TRANSMEM 6555  
 FT TRANSMEM 6565  
 FT TRANSMEM 6575  
 FT TRANSMEM 6585  
 FT TRANSMEM 6595  
 FT TRANSMEM 6605  
 FT TRANSMEM 6615  
 FT TRANSMEM 6625  
 FT TRANSMEM 6635  
 FT TRANSMEM 6645  
 FT TRANSMEM 6655  
 FT TRANSMEM 6665  
 FT TRANSMEM 6675  
 FT TRANSMEM 6685  
 FT TRANSMEM 6695  
 FT TRANSMEM 6705  
 FT TRANSMEM 6715  
 FT TRANSMEM 6725  
 FT TRANSMEM 6735  
 FT TRANSMEM 6745  
 FT TRANSMEM 6755  
 FT TRANSMEM 6765  
 FT TRANSMEM 6775  
 FT TRANSMEM 6785  
 FT TRANSMEM 6795  
 FT TRANSMEM 6805  
 FT TRANSMEM 6815  
 FT TRANSMEM 6825  
 FT TRANSMEM 6835  
 FT TRANSMEM 6845  
 FT TRANSMEM 6855  
 FT TRANSMEM 6865  
 FT TRANSMEM 6875  
 FT TRANSMEM 6885  
 FT TRANSMEM 6895  
 FT TRANSMEM 6905  
 FT TRANSMEM 6915  
 FT TRANSMEM 6925  
 FT TRANSMEM 6935  
 FT TRANSMEM 6945  
 FT TRANSMEM 6955  
 FT TRANSMEM 6965  
 FT TRANSMEM 6975  
 FT TRANSMEM 6985  
 FT TRANSMEM 6995  
 FT TRANSMEM 7005  
 FT TRANSMEM 7015  
 FT TRANSMEM 7025  
 FT TRANSMEM 7035  
 FT TRANSMEM 7045  
 FT TRANSMEM 7055  
 FT TRANSMEM 7065  
 FT TRANSMEM 7075  
 FT TRANSMEM 7085  
 FT TRANSMEM 7095  
 FT TRANSMEM 7105  
 FT TRANSMEM 7115  
 FT TRANSMEM 7125  
 FT TRANSMEM 7135  
 FT TRANSMEM 7145  
 FT TRANSMEM 7155  
 FT TRANSMEM 7165  
 FT TRANSMEM 7175  
 FT TRANSMEM 7185  
 FT TRANSMEM 7195  
 FT TRANSMEM 7205  
 FT TRANSMEM 7215  
 FT TRANSMEM 7225  
 FT TRANSMEM 7235  
 FT TRANSMEM 7245  
 FT TRANSMEM 7255  
 FT TRANSMEM 7265  
 FT TRANSMEM 7275  
 FT TRANSMEM 7285  
 FT TRANSMEM 7295  
 FT TRANSMEM 7305  
 FT TRANSMEM 7315  
 FT TRANSMEM 7325  
 FT TRANSMEM 7335  
 FT TRANSMEM 7345  
 FT TRANSMEM 7355  
 FT TRANSMEM 7365  
 FT TRANSMEM 7375  
 FT TRANSMEM 7385  
 FT TRANSMEM 7395  
 FT TRANSMEM 7405  
 FT TRANSMEM 7415  
 FT TRANSMEM 7425  
 FT TRANSMEM 7435  
 FT TRANSMEM 7445  
 FT TRANSMEM 7455  
 FT TRANSMEM 7465  
 FT TRANSMEM 7475  
 FT TRANSMEM 7485  
 FT TRANSMEM 7495  
 FT TRANSMEM 7505  
 FT TRANSMEM 7515  
 FT TRANSMEM 7525  
 FT TRANSMEM 7535  
 FT TRANSMEM 7545  
 FT TRANSMEM 7555  
 FT TRANSMEM 7565  
 FT TRANSMEM 7575  
 FT TRANSMEM 7585  
 FT TRANSMEM 7595  
 FT TRANSMEM 7605  
 FT TRANSMEM 7615  
 FT TRANSMEM 7625  
 FT TRANSMEM 7635  
 FT TRANSMEM 7645  
 FT TRANSMEM 7655  
 FT TRANSMEM 7665  
 FT TRANSMEM 7675  
 FT TRANSMEM 7685  
 FT TRANSMEM 7695  
 FT TRANSMEM 7705  
 FT TRANSMEM 7715  
 FT TRANSMEM 7725  
 FT TRANSMEM 7735  
 FT TRANSMEM 7745  
 FT TRANSMEM 7755  
 FT TRANSMEM 7765  
 FT TRANSMEM 7775  
 FT TRANSMEM 7785  
 FT TRANSMEM 7795  
 FT TRANSMEM 7805  
 FT TRANSMEM 7815  
 FT TRANSMEM 7825  
 FT TRANSMEM 7835  
 FT TRANSMEM 7845  
 FT TRANSMEM 7855  
 FT TRANSMEM 7865  
 FT TRANSMEM 7875  
 FT TRANSMEM 7885  
 FT TRANSMEM 7895  
 FT TRANSMEM 7905  
 FT TRANSMEM 7915  
 FT TRANSMEM 7925  
 FT TRANSMEM 7935  
 FT TRANSMEM 7945  
 FT TRANSMEM 7955  
 FT TRANSMEM 7965  
 FT TRANSMEM 7975  
 FT TRANSMEM 7985  
 FT TRANSMEM 7995  
 FT TRANSMEM 8005  
 FT TRANSMEM 8015  
 FT TRANSMEM 8025  
 FT TRANSMEM 8035  
 FT TRANSMEM 8045  
 FT TRANSMEM 8055  
 FT TRANSMEM 8065  
 FT TRANSMEM 8075  
 FT TRANSMEM 8085  
 FT TRANSMEM 8095  
 FT TRANSMEM 8105  
 FT TRANSMEM 8115  
 FT TRANSMEM 8125  
 FT TRANSMEM 8135  
 FT TRANSMEM 8145  
 FT TRANSMEM 8155  
 FT TRANSMEM 8165  
 FT TRANSMEM 8175  
 FT TRANSMEM 8185  
 FT TRANSMEM 8195  
 FT TRANSMEM 8205  
 FT TRANSMEM 8215  
 FT TRANSMEM 8225  
 FT TRANSMEM 8235  
 FT TRANSMEM 8245  
 FT TRANSMEM 8255  
 FT TRANSMEM 8265  
 FT TRANSMEM 8275  
 FT TRANSMEM 8285  
 FT TRANSMEM 8295  
 FT TRANSMEM 8305  
 FT TRANSMEM 8315  
 FT TRANSMEM 8325  
 FT TRANSMEM 8335  
 FT TRANSMEM 8345  
 FT TRANSMEM 8355  
 FT TRANSMEM 8365  
 FT TRANSMEM 8375  
 FT TRANSMEM 8385  
 FT TRANSMEM 8395  
 FT TRANSMEM 8405  
 FT TRANSMEM 8415  
 FT TRANSMEM 8425  
 FT TRANSMEM 8435  
 FT TRANSMEM 8445  
 FT TRANSMEM 8455  
 FT TRANSMEM 8465  
 FT TRANSMEM 8475  
 FT TRANSMEM 8485  
 FT TRANSMEM 8495  
 FT TRANSMEM 8505  
 FT TRANSMEM 8515  
 FT TRANSMEM 8525  
 FT TRANSMEM 8535  
 FT TRANSMEM 8545  
 FT TRANSMEM 8555  
 FT TRANSMEM 8565  
 FT TRANSMEM 8575  
 FT TRANSMEM 8585  
 FT TRANSMEM 8595  
 FT TRANSMEM 8605  
 FT TRANSMEM 8615  
 FT TRANSMEM 8625  
 FT TRANSMEM 8635  
 FT TRANSMEM 8645  
 FT TRANSMEM 8655  
 FT TRANSMEM 8665  
 FT TRANSMEM 8675  
 FT TRANSMEM 8685  
 FT TRANSMEM 8695  
 FT TRANSMEM 8705  
 FT TRANSMEM 8715  
 FT TRANSMEM 8725  
 FT TRANSMEM 8735  
 FT TRANSMEM 8745  
 FT TRANSMEM 8755  
 FT TRANSMEM 8765  
 FT TRANSMEM 8775  
 FT TRANSMEM 8785  
 FT TRANSMEM 8795  
 FT TRANSMEM 8805  
 FT TRANSMEM 8815  
 FT TRANSMEM 8825  
 FT TRANSMEM 8835  
 FT TRANSMEM 8845  
 FT TRANSMEM 8855  
 FT TRANSMEM 8865  
 FT TRANSMEM 8875  
 FT TRANSMEM 8885  
 FT TRANSMEM 8895  
 FT TRANSMEM 8905  
 FT TRANSMEM 8915  
 FT TRANSMEM 8925  
 FT TRANSMEM 8935

RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. 651-2-5-7-4;  
 RA Singh S.P., van der Heide T., McKinney S., Green A.;  
 RT "Nucleotide sequence of a cDNA from *Brassica juncea* encoding a  
 RL microomal omega-6 desaturase."  
 CC (In) Plant Gene Register PGR95-107.  
 CC -1- FUNCTION: ER (microomal) omega-6 fatty acid desaturase introduces  
 CC the second double bond in the biosynthesis of 18:3 fatty acids;  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids (by similarity).  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sdb.cn/announce/>  
 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL; X91139; CAA62578.1; -;  
 CC InterPro; IPR005804; FA\_desat. fam.  
 CC Pfam; PF00487; FA\_desaturase; 1.  
 CC ProDom; PD001081; FA\_desat. fam. 2.  
 CC Oxidoreductase; fatty acid biosynthesis; Endoplasmic reticulum;  
 CC transmembrane.  
 CC KM TRANSMEM 56 76 POTENTIAL.  
 CC FT TRANSMEM 84 104 POTENTIAL.  
 CC FT TRANSMEM 117 137 POTENTIAL.  
 CC FT TRANSMEM 180 200 POTENTIAL.  
 CC FT TRANSMEM 226 246 POTENTIAL.  
 CC FT TRANSMEM 253 273 POTENTIAL.  
 CC FT DOMAIN 105 109 HISTIDINE BOX-1.  
 CC FT DOMAIN 141 145 HISTIDINE BOX-2.  
 CC FT DOMAIN 316 320 HISTIDINE BOX-3.  
 CC SQ SEQUENCE 384 AA; 44315 MW; 43AF77CE9861A492 CRC64;  
 CC -----  
 CC Query Match 63.6%; Score 1301; DB 1; Length 384;  
 CC Best Local Similarity 60.6%; Pred. No. 2e-97;  
 CC Matches 231; Conservative 60; Mismatches 84; Indels 6; Gaps 4;  
 CC -----  
 CC 1 MGAGGRMS-DESEK--NILERVVD-PPTLSLQKKAIFHCERSVIRSSYYVHDL 55  
 CC 1 MGAGGRMQVSPSPKSEETDTLKRVCETPPFVGLKKAIPPHCKRSISPSFYLWMDI 60  
 CC 56 IVAVFVYLTANTYPLITPLALAYLAWPYWFCQASILGLAWIIGHCCHNAFSDQLDD 115  
 CC 61 IVASCFYVATYPLPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPLPPL 120  
 CC 116 IVGFVLSALITLPEFSWKSRHNHANTNSLNDENVYIPKRSKYKISKLINPPGRVF 175  
 CC 121 TVGLIFHSFLVLPVFSWKSRHNSHNSGSLERDEVPFKKSDIKWIGKILNPLGTV 180  
 CC 176 TLVRLTLFPLLYLTINISGKKYGR-FANHPDPSPIFNDESRVOLLDFGLLAVFYAI 234  
 CC 181 MLTVQFTLGMPLPYMAFNVSGRPRYEGACHFHPNAPFYNDERLQIYVSDGIIAVCYGL 240  
 CC 235 KLVAAKAAAVINMYALPVGVSVFVLITLYLHHTHLSLPHYSTENMWIKGALSTIDR 294  
 CC 241 YRYAAQGVAVCVLCYGVPLLVANFLVLTLYLQHTHSLPHTYSSSEWDMRGALATADR 300  
 CC 295 DFGELNRFHVDVTHVLAHLISYIPHYAKARDAIPVAGEYKIKRTPIFKAMVREA 354  
 CC 301 DYGLINKFVHNITDTHVAHHLFSTMPKHYHAMEVTKAIRIIGDYQFPDGTWVYAMREA 360  
 CC 355 KECIYIEPDESEHKGVFWYN 375  
 CC -----

DB 361 KECIYIEPDESEHKGVFWYN 361  
 ID P66E\_ARATH STANDARD; PRT; 363 AA.  
 AC P46313;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)  
 DE (Delta-12 desaturase).  
 GN FAD2 OR AT3G12120 OR T23B7.6 OR T21B14.6 OR T21B14\_107.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OK NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=94176997; PubMed=7907506;  
 RX Okuley J., Lightner J., Feldmann K.A., Yadav N., Lark E., Browne J.;  
 RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for  
 RL polyunsaturated lipid synthesis."  
 RL Plant Cell 6:147-158(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20363099; PubMed=10907853;  
 RA Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;  
 RT "Structural analysis of the Arabidopsis thaliana chromosome 3. II.  
 RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC  
 RT and BAC clones."  
 RL DNA Res. 7:217-221(2000).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Anseorge W., Unseld M.,  
 RA Salanoubat M., Valle G., Bloecker H., Perez-Alonso M., Oberwälder B.,  
 RA Dalseny M., Bouty M., Grivell L.A., Maché R., Puigdomenech P.,  
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Broctier P.,  
 RA Wincker P., Catalicio L., Weisenbach J., Saurin W., Quelier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Mumbach R., Drzonek H., Erle H., Jordan N., Bandert P.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek G.,  
 RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,  
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,  
 RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,  
 RA de Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacubeta B.,  
 RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,  
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Wewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,  
 RA Crasy T.H., Haas B., Malet R., Wu D., Peterson J., Van Aken S.,  
 RA Paul G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
 RA Preuss D., Lin X., Nijman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis*  
 RT *thaliana*."  
 RL Nature 408:820-822(2000).  
 CC -1- FUNCTION: ER (microomal) omega-6 fatty acid desaturase introduces  
 CC the second double bond in the biosynthesis of 18:3 fatty acids;  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids.

CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, L26296; AAA32782.1; -;  
 CC EMBL, AP002063; BAB01960.1; -;  
 CC EMBL, AC069473; AAG51042.1; -;  
 CC InterPro: IPR005804; FA\_desat. fam.  
 CC Pfam: PF00487; FA\_desaturase; 1.  
 CC ProDom: PD001081; FA\_desat. fam; 2.  
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
 CC Transmembrane.  
 CC TRANSMEM 56 76 POTENTIAL.  
 CC TRANSMEM 117 137 POTENTIAL.  
 CC TRANSMEM 179 199 POTENTIAL.  
 CC TRANSMEM 225 245 POTENTIAL.  
 CC TRANSMEM 252 272 POTENTIAL.  
 CC DOMAIN 105 109 HISTIDINE BOX-1.  
 CC DOMAIN 141 145 HISTIDINE BOX-2.  
 CC DOMAIN 315 319 HISTIDINE BOX-3.  
 CC SEQUENCE 383 AA; 44047 MW; 8815ADD2D3B8C982 CRC64;

Query Match 63.5%; Score 1300.5; DB 1; Length 383;  
 Best Local Similarity 59.5%; Pred. No. 2.2e-97;  
 Matches 226; Conservative 65; Mismatches 84; Indels 5; Gaps 2;

QY 1 MGAGGRMDPSRCK---NILERVVD--PPTFLSDLKKAIPHCEERSVIRSYVVDL 55  
 DB 1 MGAGGRMPVPTSSKSEDTTKRVCCKEPFSPVSGDLKKAIPHCCKRSIPRPSFLISDI 60  
 QY 56 IVAVFFYLLANTYIPLIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLIDD 115  
 DB 61 IIAFCFYVATNYFLLPQLPSYLAIPYMAQCGVLTCIWIATHECGHAFSDYQLIDD 120  
 QY 116 IVFVLHALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKILNPPGVF 175  
 DB 121 TVGLTFHSHFLVFPYSWKYSHRHSHNTGSLERDEVFVPEKQSAIKWYGYLNPDLGRIM 180  
 QY 176 TLVPLTLTGFPYLTLNTISGKKYGRFANHPDMSPIFNDREVOYLDSFGILAVFAIK 235  
 DB 181 MLTVQFVLGMPLYLAFNVSGRPYDGPACHFPFNADPIYNDREYLQYLSDDAGILAVCFGLY 240  
 QY 236 LLVAAGAMVIMYAIPLVGVSEFVLITLYLHHTLSLPHYDSEMMNIGALSTIRD 295  
 DB 241 RYAAAGQAMASMTCLXGVPPLLYNATFLVLTLYQHHTPSLPHDSSSEMDLRGALATVDRD 300  
 QY 296 FGLNRFVHDVTHTVHLHLISYIPHYAKKARDAIKPVLAGYIKIDRTPIFKANYREAK 355  
 DB 301 YGILNKVFNHITDTVAHLFTSTMPHYNAMEATKAIKPLGDYQFQDGPWVYANVREAK 360  
 QY 356 ECIYEDEDESEHKGVFWH 375  
 DB 361 ECIYVEPRREGDKGVWYN 380

## RESULT 5

FD61\_SOYBN STANDARD; PRT; 387 AA.  
 AC P46630;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1

DE (EC 1.14.19.-).  
 GN FAD2-1.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Seed;  
 RX MEDLINE=96151506; PubMed=8587990;  
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;  
 RT "Developmental and growth temperature regulation of two different  
 RL microsomal omega-6 desaturase genes in soybeans";  
 RL Plant Physiol. 110:311-319(1996).  
 CC -1- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces  
 CC the second double bond in the biosynthesis of 18:3 fatty acids,  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Strongly expressed in developing seeds.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, L43920; AAB00859.1; -;  
 CC PIR, T07687; T07687.  
 CC InterPro: IPR005804; FA\_desat. fam.  
 CC Pfam: PF00487; FA\_desaturase; 1.  
 CC ProDom: PD001081; FA\_desat. fam; 2.  
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
 CC Transmembrane.  
 CC TRANSMEM 54 74 POTENTIAL.  
 CC TRANSMEM 87 107 POTENTIAL.  
 CC TRANSMEM 121 141 POTENTIAL.  
 CC TRANSMEM 183 203 POTENTIAL.  
 CC TRANSMEM 227 247 POTENTIAL.  
 CC TRANSMEM 251 271 POTENTIAL.  
 CC DOMAIN 109 113 HISTIDINE BOX-1.  
 CC DOMAIN 145 149 HISTIDINE BOX-2.  
 CC DOMAIN 319 323 HISTIDINE BOX-3.  
 CC SEQUENCE 387 AA; 44662 MW; 49068805C21A1C31 CRC64;

Query Match 60.5%; Score 1237.5; DB 1; Length 387;  
 Best Local Similarity 56.6%; Pred. No. 2.6e-92;  
 Matches 213; Conservative 70; Mismatches 90; Indels 3; Gaps 3;

QY 1 MGAGGRMDPS-EGKNILERP-VDPPTFLSDLKKAIPHCEERSVIRSYVVDLIVA 58  
 DB 9 MGGRGVAKAVQGGKPLSRVPNTKPPFTVQLKKAIPHCFQKSLTSPFVAVDLSFA 68  
 QY 59 YVFFYLLANTYIPLIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLIDDIVG 118  
 DB 69 FIF-YIATTFPHLLPQPSLLAMPYLVWLQCGLLTGLVWVIAHECGHAFSKYQWDDVVG 127  
 QY 119 FVLHSAITLPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKILNPPGVFVLV 178  
 DB 128 LTLHSTLLVLPYFSWKYSHRHSHNTGSLDRDEVFVPEKRSKYKYSKILNPPGLGAVSL 187  
 QY 179 FRLTLGFPYLTLNTISGKKYGRFANHPDMSPIFNDREVOYLDSFGILAVFAIKLY 238  
 DB 188 VTLTIGWMPYLAFNVSGRPYDGPASHYAPAIYSNRRLLIYSDVALFSVTYLSLYRVA 247

```

QY 239 AAKGAAMVANNYAIPVLGVSVEFLITLYLHHTLSLPHYDSTEMWIKALSTIDRDEGF 298
DB 248 TLKGIVMLLCYGVGFLILVNGFLVITLYLOHTHFALPHYDSEMDWLKALATMDRDYGI 307
QY 299 LNRVHDVTHVHLHLISYIPHYAKARDAIKRVGLGEYKIDTPIFKMYRAKACGI 358
DB 308 LNRVFNHTIDVHVAHLSFTMPHYAMETATNAIKPILEGYQFDDTPIFKALMREARBL 367
QY 359 YIEPDESEHKGVFWY 374
DB 368 YVEPDEGTSEKGVWY 383

RESULT 6
FD12 MORIS
ID _FD12 MORIS STANDARD; PRT; 400 AA.
AC P59668;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsids.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6-22;
RA Liu L., Li M., Xing L., Hu G.;
RL "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
CC to linoleic acid (delta9, delta12-18:2) (By similarity).
CC -1 PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -1 SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF417245; AALJ3301.1;
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
KM Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT DOMAIN 112 116 HISTIDINE BOX-1.
FT DOMAIN 148 152 HISTIDINE BOX-2.
FT DOMAIN 339 343 HISTIDINE BOX-3.
SQ SEQUENCE 400 AA; 46016 MW; F5512D3F8210BD2 CRC64;

Query March 38.2%; Score 782; DB 1; Length 400;
Best Local Similarity 39.8%; Pred. No. 1.2e-55;
Matches 156; Conservative 63; Mismatches 135; Indels 38; Gaps 6;
QY 10 PSEGNILERVVPPTLSDIKKAIPTHCERSVIRSSYYVVDLIVAVFYFLANYI 69
DB 22 PTKAKPAVERNYQPEFTIKERICIPAHCFERSGLRGCHVAIDLWTASLL-FLAAQI 80
QY 70 PLITPL-AYLAWYVYVQCASILTLGAVIGHGCGHAAPSYQYLDIVGVLSALITP 128
DB 81 DKFENPLIRYLAWPAYWIMOGIVCTGIWVLAHBCGHQSFTSKTLNNTVGMILHMLVP 140

```

```

QY 129 YFSWKYSHRNHANTNSLDNDEVYIPKRSKVIKYSKLNNPGR----- 173
DB 141 YHSWRISHSKHKHAKTGHMTKDQVFPKRSQVGL-----PKRSAAVAQEDMSVHL 193
QY 174 -----VFTLVRLITGFLYLLTNISGKKYGFANFPDMSTIFNDRERVQLLSDF 225
DB 194 DEBAPVTLFVWVVIQFLGWPAYVILMANSGDDYGRWSTHFTYSPIFPRRPFDDIISDL 253
QY 226 GLIAVFAVAILKLVAAKGAAMVANNYAIPVLGVSVEFLITLYLHHTLSLPHYDSTEMWI 285
DB 254 GVLNAGLITVYASQSLITVTKYIIPYLVNFWLVITLQHTDPLPHRYBSAAMFQ 313
QY 286 KQALSTIDRDEG-FLNRVHDVTHVHLHLISYIPHYAKARDAIKRVGLGEYKIDT 344
DB 314 RQALCTVDRSFGKFLDHFHFGIVTHVHNLFSQWPFHABEATYHLKLLGEYVYDPS 373
QY 345 PIFKMYRAKACGIYIEPDESEHKGVFWYHK 376
DB 374 PIVVAWRSFRCRFVE-----DHQDVVFPFK 400

RESULT 7
FD12 MORAP
ID _FD12 MORAP STANDARD; PRT; 400 AA.
AC Q9Y8H5; Q96TH3; Q9UVV4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=IS-4;
RA MEDLINE=99234062; PubMed=10215899;
RA Sakuradani E., Kobayashi M., Ashikari T., Shimizu S.;
RT "Identification of delta12-fatty acid desaturase from arachidonic
RT acid-producing Mortierella fungus by heterologous expression in the
RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae."
RL Eur. J. Biochem. 261:812-820(1999).
RN [2]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=ATCC 32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kitchner S.J., Mukerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."
RL Lipids 34:649-659(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 16256;
RA Liu L., Li M., Xing L., Hu G.;
RL "Delta 12 fatty acid desaturase gene of Mortierella alpina."
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
CC to linoleic acid (delta9, delta12-18:2).
CC -1 PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -1 SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

CC or send an email to license@ib-sib.ch).

CC -----

DR EMBL; AB020033; BAA81754.1; -

DR EMBL; AF110509; AAF08684.1; -

DR EMBL; AF117244; AAL13300.1; -

DR GO; GO:0016021; C: integral to membrane; NAS.

DR GO; GO:0016491; F: oxidoreductase activity; IDA.

DR GO; GO:0006633; P: fatty acid biosynthesis; IDA.

DR InterPro; IPR005804; FA\_desat. fam.

DR Pfam; PF00487; FA\_desaturase; 1.

DR ProDom; PD001081; FA\_desat. fam; 1.

KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.

FT TRANSMEM 91 111 POTENTIAL.

FT TRANSMEM 199 219 POTENTIAL.

FT TRANSMEM 245 265 POTENTIAL.

FT TRANSMEM 277 297 POTENTIAL.

FT DOMAIN 112 116 HISTIDINE BOX-1.

FT DOMAIN 148 152 HISTIDINE BOX-2.

FT DOMAIN 339 343 HISTIDINE BOX-3.

FT CONFLICT 17 19 STS -> TTT (IN REF. 3).

FT CONFLICT 21 23 APT -> PN (IN REF. 2).

FT CONFLICT 95 95 A -> V (IN REF. 2).

FT CONFLICT 107 107 I -> V (IN REF. 2).

FT CONFLICT 179 179 N -> S (IN REF. 3).

FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).

FT CONFLICT 261 261 A -> T (IN REF. 1).

FT CONFLICT 280 280 V -> I (IN REF. 3).

FT CONFLICT 358 358 Y -> H (IN REF. 1).

FT CONFLICT 392 392 H -> Q (IN REF. 2).

SC SEQUENCE 400 AA; 46001 MW; 40B2FCLC1E01E93F CRC64;

Query Match 38.2%; Score 781; DB 1; Length 400;

Best Local Similarity 40.3%; Pred. No. 1.5e-55;

Matches 156; Conservative 64; Mismatches 139; Indels 28; Gaps 6;

QY 10 PSEGNILERVVDPEFTLSDLKKAIPTHCFERSYIRSSYYVHDLIAYVYLYANTYI 69

DB 22 PLSAKPAERKRYOLPEFTIKETRECIAPACFERSGRGCHADLTWASL-FLAAIOTI 80

QY 70 PLIPPL-AYLAMPYVFCQASILGLWVIGHECGHAFSDYQIDIDIVGFVLSALYLP 128

DB 81 DKFENPLRLYLAMPVYVIMOGIVCTGIWVLANHECHQSGSTSKLTNNVGMILHSMILVP 140

QY 129 YFSWKYSRHNHANTNSLDNDEVYIPKRSKYKYSKLIIN-----P 170

DB 141 YHSWISHSKHKAKGHMTKQVFPVKTRSQGLPPK--ENAAVAVOEDMSVHLDEEAP 198

QY 171 PGRVETLVRLLTGLPFLYLITNLSGKKYGRFANHEDPMSPIFNDRERVOYLSDPGLAY 230

DB 199 IYTLTWMYIQLPFGPAPYLIMNASGQDYGRTSHHTYSPLEPPNPFDIITISDGLVLA 258

QY 231 FYAIFLVAAGAAVIMYAIPLVGVSVFVLYLYLHHTHLSLPHYDSTEMNWKIGALS 290

DB 259 LGAALVAMQSLVLTVTKYIYVPLVFNFWLTLIFLQHTDPKLPHYEGAMNPGRGALC 318

QY 291 TIDRDFG-FLNRVPHDVTHVTHLHLSIYIPHYAKKARDAIKPVLGSIYKIDRTPIKA 349

DB 319 TVDRFEGFALDMEFGIYVTHVAHHLFSGMPFYHAEEATYHLKLLGSEYVVDPSIYVA 378

QY 350 MYRAKECIYTERPDSEHKGVFWYHK 376

DB 379 VWRSEFRCRFEV-----DHGDVVFPEKK 400

RESULT 8

FD3C\_SESIN STANDARD; PRT; 447 AA.

AC P46620;

DT 01-FEB-1996 (Rel. 33; Created)

DT 01-FEB-1996 (Rel. 33; Last sequence update)

DT 28-FEB-2003 (Rel. 41; Last annotation update)

DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN PAD7.

OS Sesamum indicum (Oriental sesame) (gingelly).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiales; Pedaliaceae; Sesamum.

OC NCBI\_TaxID=4182;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. 4294; TISSUE=Cotyledon;

RA Shoji K.;

RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol.

CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; MEMBRANE-BOUND (PROBABLE).

CC -1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.

CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.itsb.ch/announce/> or send an email to license@ib-sib.ch).

CC -----

DR EMBL; U25817; AAA70334.1; -

DR InterPro; IPR005804; FA\_desat. fam.

DR Pfam; PF00487; FA\_desaturase; 1.

DR ProDom; PD001081; FA\_desat. fam; 2.

KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;

KW Transit peptide.

FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).

FT CHAIN 2 447 OMEGA-3 FATTY ACID DESATURASE.

FT DOMAIN 167 171 HISTIDINE BOX-1.

FT DOMAIN 203 207 HISTIDINE BOX-2.

FT DOMAIN 370 374 HISTIDINE BOX-3.

SC SEQUENCE 447 AA; 51116 MW; 4E76250DD6DA6B1 CRC64;

Query Match 31.4%; Score 642; DB 1; Length 447;

Best Local Similarity 38.2%; Pred. No. 2.5e-44;

Matches 132; Conservative 63; Mismatches 109; Indels 42; Gaps 10;

QY 4 GRRMSDPSEGNILERVVDPEFTLSDLKKAIPTHCFERSYIRSSYYVHDLIAYV---- 59

DB 88 GGEERDFG-----APPFTLSDLREAIPIKHCWKDWRKSGYVVRDVAVFGAL 137

QY 60 VFYLYANTYIPLIPTLALYAMPYVFCQASILGLWVIGHECGHAFSDYQIDIDIVGF 119

DB 138 VAAAYFN-----WVWVPLVWFASQSTFMALFVLGHDGCGHSPNDPKLSVVG 186

QY 120 VLHSAFLTTPYSWKSRHNHANTNSLDNDEVYIPKRSKYKYSKLIINPPGRVETLV 179

DB 187 ILHGSILVPGYIGWRISHETHNQNGHVENDSWPLSE--KIKYKIDTATKKLRFTLP 243

QY 180 RLTLGFLYLLTNISGKKYGRFANHEDPMSPIFNDRERVOYLSDP---GLAVFYAIKL 236

DB 244 PL-LAYPIYLSRSRGKQ---GSHFHDSDLPFVNEKDVITSTVCTATLALLVGLSF 298

QY 237 LVAAGAAVIMYAIPLVGVSVFVLYLYLH--THLSLPHYDSTEMNWKIGALSTDR 294

DB 299 VI---GVPQLLKXGIPYLGWVMMDLVLYLHHGHEDKLLPMYRGKEWSYLRGLTTLDR 355

QY 295 DPGFLNRVPHDVTHVTHLHLSIYIPHYAKKARDAIKPVLGSIYKIDRTPIKA 340

DB 356 DYGMNNIHDI-GTHVTHLDFQIPHYLLEATEAAKPVIGKYR 400

RESULT 9

FD3C\_RICCO



ID FD3C\_RICCO STANDARD; PRT; 460 AA.  
AC P4619;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).  
GN PAD7A-1.  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosoids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;  
OC Ricinus.  
OX NCBI\_TaxID=3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Baker 296; TISSUE=seed;  
RX MEDLINE=94302177; PubMed=8029360;  
RA van de Loo F.J., Somerville C.R.;  
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis";  
RL Plant Physiol. 105:443-444(1994).  
CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the  
CC third double bond in the biosynthesis of 16:3 and 18:3 fatty  
CC acids, important constituents of plant membranes. It is thought to  
CC use ferredoxin as an electron donor and to act on fatty acids  
CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.  
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).  
CC -1- DOMAIN: The histidine box domain may contain the active site  
CC and/or be involved in metal ion binding.  
CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: L25897; AAA73511.1; -.  
DR PIR: T10063; T10063.  
DR InterPro: IPR005804; FA\_desat\_fam.  
DR Pfam: PF00487; FA\_desaturase; 1.  
DR ProDom: PD001081; FA\_desat\_fam; 2.  
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
KM Transit peptide.  
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
FT CHAIN ? 460 OMEGA-3 FATTY ACID DESATURASE.  
FT DOMAIN 177 181 HISTIDINE BOX-1.  
FT DOMAIN 213 217 HISTIDINE BOX-2.  
FT DOMAIN 380 384 HISTIDINE BOX-3.  
SQ SEQUENCE 460 AA; 52561 MW; 8365929046F3C7B0 CRC64;

Query Match 31.2%; Score 639.5; DB 1; Length 460;  
Best Local Similarity 35.5%; Pred. No. 4.2e-44;  
Matches 134; Conservative 72; Mismatches 134; Indels 37; Gaps 9;

QY 12 EGGKILRVPVDPFTSLDKKAIPTGCFERSVRSYVVYVHDLIAV---VFYTLANT 67  
DB 96 EGKEEPDAGAPPTLADIPALPKQGVKNPMSKSYLRDVVVGGLAAVAAYFN- 154  
QY 68 YIPLIPLAYLAPVWFQASILITGLVIGHCCHAFSDYOLIDIVGFVLSALT 127  
DB 155 -----WVAAPLIVWFCQGTFFMALFVIGHOCGHSFNNPKLNSVGHLLHSLIV 204  
QY 128 PYFSWKYSHRNHNANTSLNDEVYIIPKSKVKIYSLKLNPPGRVFTLVRLTLGEP 187  
DB 205 PYHGMRIISHRTTHQNHGVNDESMHPLSE---KIFSLDVTYTLRPSLPFPM-LAYPF 260  
QY 188 YILTNISGKKYGRANHPDPSPIFNDREVOVLSDGGLAVFAIATLVAAGAAMVI 247  
DB 261 YLMSRSPEKK---GSHFHDPSGLFVPERKODITITSTACTMAALLVILNFSMGVOML 316

QY 248 NMTAIPVLGVSVFVLYITLYHH--THLSLPHYDSTENMWIKALSTIDRDGFLNRYFHD 305  
DB 317 KLYGIPYWIIFVWYLDFTYLLHHGHEDKLPYRGRKAWSYLGGTLTDRDYGWINNHHD 376  
QY 306 VTHHVLHHLISYVPHYAKERDAIKPVGEYKIDRT-----IFKAWYREKECY 359  
DB 377 I-GTHVHHLFPQILPHHLVLEATEAKPVMGKTYREPKSGPLPLHLGLSVRSKEDHY 435  
QY 360 IEPDESEHKGVFWYHK 376  
DB 436 VSDTGD-----VYTYOK 447

RESULT 10  
FD3E\_ARATH STANDARD; PRT; 386 AA.  
ID FD3E\_ARATH  
AC P46623;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).  
GN FAD3 OR AT2G39980 OR F3F1.10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Seedling;  
RX MEDLINE=94302147; PubMed=8029334;  
RA Yadav N.S., Wierzbicki A., Aegeer M., Caeter C.S., Perez-Grau L.,  
RA Kinney A.J., Hitz W.D., Booth J.R., Jr., Schweiger B., Stecca K.L.,  
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,  
RA Feldmann K.A., Pierce J., Browne J.;  
RT "Cloning of higher plant omega-3 fatty acid desaturases";  
RL Plant Physiol. 103:467-476(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;  
RA Wataniki M.C., Yamamoto K.T.;  
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=94345020; PubMed=8066143;  
RA Nishinchi T., Nishimura M., Aroniel V., Iba K.;  
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3  
RT fatty acid desaturase from Arabidopsis thaliana";  
RL Plant Physiol. 105:767-768(1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20083487; PubMed=10617197;  
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
RA Buell C.R., Kelchum K.A., Lee J.J., Ronning C.M., Koo H.L.,  
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,  
RA Talon L.J., Gill J.B., Adams M.D., Carrera A.J., Cressy T.H.,  
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,  
RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
RA Venter J.C.;  
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
RT thaliana";  
RL Nature 402:761-768(1999).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=22954850; PubMed=14593172;  
RA Yanada K., Lam J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Phan P.K., Cheuk R.F.,  
RA Katlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
 RA Arkawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
 RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,  
 RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
 RA Satou M., Tanabe R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,  
 RA Yuan S., Shinohara K., Davis R.W., Theologis A., Becker U.R.,  
 RT "Empirical analysis of transcriptional activity in the Arabidopsis  
 genome.";  
 RL Science 302:842-846(2003).  
 CC -1- FUNCTION: Microsomal (ER) omega-3 fatty acid desaturase introduces  
 the third double bond in the biosynthesis of 18:3 fatty acids,  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms are produced. According to EST  
 CC sequences;  
 CC Name=1;  
 CC IsoId=P48623-1; Sequence=Displayed.  
 CC -1- TISSUE SPECIFICITY: Abundant in leaves and seedlings. Barely  
 CC detectable in root tissue.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: L22931; AAA61778.1; -;  
 CC EMBL: D17579; BAA04505.1; -;  
 CC EMBL: D26508; BAA05514.1; -;  
 CC EMBL: AC004680; AAC11854.1; -;  
 CC EMBL: AY063966; AAL36322.1; -;  
 CC EMBL: AY096462; AAM20102.1; -;  
 CC PIR: JQ2335; JQ2335.  
 CC InterPro: IPR005804; FA\_desat\_fam.  
 CC Pfam: PF00487; FA\_desaturase; 1.  
 CC ProDom: PD001081; FA\_desat\_fam; 2.  
 CC K1: Fatty acid biosynthesis; Oxidoreductase; Endoplasmic reticulum;  
 CC Transmembrane; Alternative splicing.  
 CC FT TRANSMEM 63 83 POTENTIAL.  
 CC FT TRANSMEM 220 240 POTENTIAL.  
 CC FT TRANSMEM 242 262 POTENTIAL.  
 CC FT DOMAIN 101 105 HISTIDINE BOX-1.  
 CC FT DOMAIN 137 141 HISTIDINE BOX-2.  
 CC FT DOMAIN 304 308 HISTIDINE BOX-3.  
 CC SEQUENCE 386 AA; 44076 MW; 6A7EA2A692B85164 CRC64;  
 Query Match 30.3%; Score 620.5; DB 1; Length 386;  
 Best Local Similarity 34.6%; Pred. No. 11e-42;  
 Matches 135; Conservative 67; Mismatches 131; Indels 57; Gaps 12;

DB 119 GHILHSFLVYHGMKRIHRTNQHGVNDESMVLPPE---RVYKKLPHS-----TR 169  
 QY 178 VFRLT-----IGFPLYLTINISGGKYGRFANHPDMSPTFDRERVOVLSDFGLAVFY 232  
 DB 170 MLRTVPLPLMAYPLLYLCYRSPGKE-----GSHFNPYSLSFAPSRKLLATSTTCWSIMFV 225  
 QY 223 AIKLLVAKGAAMVYINWVAIPVLGVSVFVLTLYLHH--TLISPHYDSTEMNWKGLS 290  
 DB 226 SLIALSFVFGPLAVLKYGVGYIIFVWMLDAVTVLHHGHDEKLPWYRGKMSYLRGGLT 285  
 QY 291 TIIRDFGLNRFVFDVTHVTHLHLSYIPHYHAKKADAIKPVLGEEYKIDRT----- 344  
 DB 286 TIDBDYGFNNIHNDI-CTHYIHHLFPIRPHYHLVDATKAKHLYGRYRRPKSGALPI 344  
 QY 345 -----PIRKAMY-REAKECIYBDED 365  
 DB 345 HLVESLIVASIKDHYSDPTGDIVFETDPD 374  
 RESULT 11  
 ID F03E\_TOBAC STANDARD; PRT; 379 AA.  
 AC P48626;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).  
 GN PA33.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. SR1; TISSUE=leaf;  
 RX MEDLINE=95011632; PubMed=7926817;  
 RT Hanada T., Kodama H., Nishimura M., Iba K.;  
 RL "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";  
 RL Gene 147:293-294(1994).  
 CC -1- FUNCTION: ER (microsome1) omega-3 fatty acid desaturase introduces  
 CC the third double bond in the biosynthesis of 18:3 fatty acids,  
 CC important constituents of plant membranes. It is thought to use  
 CC cytochrome b5 as an electron donor and to act on fatty acids  
 CC esterified to phosphatidylcholine and, possibly, other  
 CC phospholipids.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: D26509; BAA05515.1; -;  
 CC PIR: JC2555; JC2555.  
 CC InterPro: IPR005804; FA\_desat\_fam.  
 CC Pfam: PF00487; FA\_desaturase; 1.  
 CC ProDom: PD001081; FA\_desat\_fam; 2.  
 CC K1: Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;  
 CC Transmembrane.  
 CC FT TRANSMEM 52 72 POTENTIAL.  
 CC FT TRANSMEM 213 233 POTENTIAL.  
 CC FT TRANSMEM 236 256 POTENTIAL.  
 CC FT DOMAIN 97 101 HISTIDINE BOX-1.  
 CC FT DOMAIN 133 137 HISTIDINE BOX-2.  
 CC FT DOMAIN 300 304 HISTIDINE BOX-3.

SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB02E1B2 CRC64;  
 Query Match 29.9%; Score 612; DB 1; Length 379;  
 Best local similarity 34.7%; Pred. No. 5.4e-42;  
 Matches 125; Conservative 73; Mismatches 128; Indels 34; Gaps 8;

QY 9 DPSEGNILERVDPPTLSDLKKAIPTHCFERSVIRSSYYVHDLVAVVYYLANTY 68  
 DB 23 DPS-----APPRLAIRNVIPKICWVDPRLSLSYVRDVI-----FVATL 65  
 QY 69 IPLIPLPLAYLAWVYVFCQASITGLWVIGHEGHAFFSYDOLIDIVGVLHSAITLP 128  
 DB 66 IGIHIDSDWFLYPLVMAIGCTFMWALFVLGHDCGHGSPSOLNNVVGIIHLSALIVP 125  
 QY 129 YFSKYSGRNHNATNSLDNDEVYIPKRSKVKIYKILNPPGVFTLVRLTGLPPLY 188  
 DB 126 YHGRIKSHKTHQHNQVETDESWMPE--KLNNKGYSTKRLRYKIPPL-LANPMY 181  
 QY 189 LLTNISGKXGRFANHPDPSPINRERVOVLLSDPGLAVFAIKLVAKAGAAVYN 248  
 DB 182 LMKSPGKS---GSHFVPYSDLFQPHRKRYVVTSLCWTMAALLVLCFAFGSLQWFK 237  
 QY 249 MYAIPVGVSPFLITLYLH--THLSLPHYDSTEMWIKALSTIRDPGLRVRFDV 306  
 DB 238 IYGAPLYIPVWMLDFVYLYLHHGYEKGLPMYRGKEMSYLRGGLTVDRDYGILFNNIHRDI 297  
 QY 307 THTVTLHLLISYIPHYAKEARDAIKPYLGEYKIDTRP-----IFKAWYREAKECYI 360  
 DB 298 -GTHVHHLFPQIHYHLREKTKAAKPVLGKTYRPFKPSGPIPHLVKDLTRSMKQDHY 356

RESULT 12  
 FD3C BRANA STANDARD; PRT; 404 AA.  
 ID PD3C BRANA STANDARD; PRT; 404 AA.  
 AC P46310;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-)  
 DE (Fragment).  
 GN PAD7.  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Seed;  
 RX MEDLINE=94302147; PubMed=8029334;  
 RA Yadav N.S., Wierzbicki A., Aegeer M., Caeter C.S., Perez-Grau L.,  
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweizer B., Stecca K.L.,  
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,  
 RA Feldman K.A., Pierce J., Browne J.;  
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";  
 RL Plant Physiol. 103:467-476(1993).  
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the  
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty  
 CC acids, important constituents of plant membranes. It is thought to  
 CC use ferredoxin as an electron donor and to act on fatty acids  
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 DR EMBL:J22963; AAA61774.1; ALT\_INIT.  
 DR PIR: P00812; P00812.  
 DR InterPro: IPR005804; FA\_desat\_fam.  
 DR Pfam: PF00487; FA\_desaturase\_1.  
 DR ProDom: PD001081; FA\_desat\_fam; 2.  
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
 KW Transf. peptide.  
 FT NON TER 1 1  
 FT TRANSIT 1 1  
 FT CHAIN 1 404  
 FT DOMAIN 121 125  
 FT DOMAIN 157 161  
 FT DOMAIN 324 328  
 FT DOMAIN HISTIDINE BOX-2.  
 FT DOMAIN HISTIDINE BOX-3.  
 SQ SEQUENCE 404 AA; 46617 MW; 4B58FB2F362ED54 CRC64;  
 Query Match 29.7%; Score 607; DB 1; Length 404;  
 Best local similarity 38.0%; Pred. No. 1.5e-41;  
 Matches 123; Conservative 58; Mismatches 115; Indels 28; Gaps 8;

QY 24 PPFTSLDKRAIPTHCFERSVIRSSYYVHDLVAVVYF---YLIANTYIPLIPLAYL 79  
 DB 52 PPFTSLDKRAIPTHCFERSVIRSSYYVHDLVAVVYF---YLIANTYIPLIPLAYL 100  
 QY 80 AMPYVFCQASITGLWVIGHEGHAFFSYDOLIDIVGVLHSAITLPYFSKYSGRNHN 139  
 DB 101 VMPLYWLAQGMFALVVLGHDCGHGSPSNDRLNSVGHILHLSILVPYGMWISIRTH 160  
 QY 140 HANTNSLDNDEVYIPKRSKVKIYKILNPPGVFTLVRLT-LGFPVLYLTNISGKY 198  
 DB 161 HQNHGHNENDESWHPE--KIYKSL--DKPTFFFTPLVLMVAFVYLMARSPGK- 214  
 QY 199 GRFANHPDPSPINRERVOVLLSDPGLAVFAIKLVAKAGAAVYNVATPVLGVS 258  
 DB 215 ---GSHVHPDSDLFPERNDVLTSTACWTMAALLVLCNFWKPMQWIKLYLIPYWINV 271  
 QY 259 VFPFLITLYLH--THLSLPHYDSTEMWIKALSTIRDPGLRVRFDVTHTVLHLLI 316  
 DB 272 MMLDFVYLYLHHGHEDLPMYRGKEMSYLRGGLTVDRDYGILNINHDI-GTHVHHLF 330  
 QY 317 SYIPHYAKEARDAIKPYLGEYK 340  
 DB 331 PQIPHYHLVEATEAKVPLGKYR 354

RESULT 13  
 FD3C ARATH STANDARD; PRT; 446 AA.  
 ID PD3C ARATH STANDARD; PRT; 446 AA.  
 AC P46310;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-)  
 GN PAD7 OR FADD OR AT3G1170 OR F9F8.4 OR F11B9.10.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;  
 RX MEDLINE=94302147; PubMed=8029334;  
 RA Yadav N.S., Wierzbicki A., Aegeer M., Caeter C.S., Perez-Grau L.,  
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweizer B., Stecca K.L.,  
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,  
 RA Feldman K.A., Pierce J., Browne J.;  
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";  
 RL Plant Physiol. 103:467-476(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia; TISSUE=Aerial parts;

RA MEDLINE=94043239; PubMed=8226956;  
 RA Iba K., Gibson S., Nishitani T., Fuse T., Nishimura M., Aronow V.,  
 RA Hugly S., Somerville C.R.;  
 RT "A gene encoding a chloroplast omega-3 fatty acid desaturase  
 RT complements alterations in fatty acid desaturation and chloroplast  
 RT copy number of the fad7 mutant of Arabidopsis thaliana.";  
 RU J. Biol. Chem. 268:24099-24105 (1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;  
 RA Watanabe M., Yamamoto K.;  
 RU Submitted (Nov-1993) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansgore W., Unsel M.,  
 RA Fattmann B., Valle G., Bloeker H., Peter-Alonso M., Obermair B.,  
 RA Delaney M., Bouty M., Griwell L.A., Mache R., Puigdomenech P.,  
 RA De Simone V., Cholme N., Artiguenave F., Robert C., Brothier P.,  
 RA Wincker P., Catolico L., Weisenbach J., Saurin W., Quetier F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Murbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nykatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
 RA Conrad A., Hornischer K., Kauer O., Loehner T.-H., Nordiek G.,  
 RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Clement J.,  
 RA Navarro P., Collado C., Perez-Perez A., Oltenswelder B., Duchemin D.,  
 RA Cooke R., Lande M., Berger-Llauro C., Purnelle B., Masuy D.,  
 RA de Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,  
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,  
 RA Cressy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
 RA Pal G., Mlischner J., Sellers P., Gill J.R., Feldblyum T.V.,  
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Friese C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Aamizu K.,  
 RA Saeguchi S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shimo S., Takeuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:820-822 (2000).  
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces  
 CC the third double bond in the biosynthesis of 16:3 and 18:3 fatty  
 CC acids, important constituents of plant membranes. It is thought  
 CC to use ferredoxin as an electron donor and to act on fatty acids  
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
 CC -1- TISSUE SPECIFICITY: Most abundant in leaves and seedlings.  
 CC -1- DOMAIN: The histidine box domain may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L2961; AAA61773.1; -;  
 DR EMBL; D14007; BAA03106.1; -;  
 DR EMBL; D26019; BAA05040.1; -;  
 DR EMBL; AC009991; AAF01508.1; -;  
 DR EMBL; AC073395; AAG50977.1; -;  
 DR PIR; J02336; J02336;  
 DR InterPro; IPR005804; FA\_desat\_fam.  
 DR Pfam; PF00487; FA\_desaturase; 1.

DR ProDom: PD001081; FA\_desat\_fam; 2.  
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;  
 KM Transyl peptide.  
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
 FT CHAIN ? 446 OMEGA-3 FATTY ACID DESATURASE.  
 FT DOMAIN 163 167 HISTIDINE BOX-1.  
 FT DOMAIN 199 203 HISTIDINE BOX-2.  
 FT DOMAIN 366 370 HISTIDINE BOX-3.  
 SQ SEQUENCE 446 AA; 51174 MW; 121125F634553D35 CRC64;  
 Query Match 29.6%; Score 606; DB 1; Length 446;  
 Best Local Similarity 34.7%; Pred. No. 2e-41;  
 Matches 135; Conservative 67; Mismatches 129; Indels 58; Gaps 13;  
 QY 16 ILERPVVD-----PPFTLSDKAIPTHCERSYIRSSYYVHDLIAYV-- 61  
 DB 74 IFESPLEEDNKKORFPCAPPENLADIRALIPKHCWKNPKWSLSYDVAVIFALAA 133  
 QY 62 --YLIANTYILPLPLAYLAMPYWPCASILGLWVIGECGHHASDQIDDIYGF 119  
 DB 134 GAAYLNN-----WIWPLPYWLAQGTMPALFVLGDCGHSFSDPKLSNVGH 182  
 QY 120 VHASALTPPYSMKYSRHHNANTNSLDNDEVYIPKRSKYISKLNPPGRVFTLVF 179  
 DB 183 LHSISILVPYGMKLSRTHTHQNGHVENDSMHPSMSE--KIINTL--DKPTFRFTL 237  
 QY 180 RLTLGPFLYLLTNIISCKKCYFRANHPDPMSPFNDRBRVOLLSDFGLLAVFAIKLV 238  
 DB 238 PLVWMLAYFYLMAWSPGK-----GSHVPSDPLFKPKRKVLTSTACMTMAALVCLN 293  
 QY 239 AAKGAAVINYALPVLGVSVFVLITYLHN--THLSIPHDSTEMWIKALSTIDDF 296  
 DB 294 FTIPFIOMLKLYGIPYWINVWMLDFVYLLHNGHEDKLPWRGKWSYLRGLTTLDYD 353  
 QY 297 GLRLRVFVDYVTHYVHLHLSIYIPYAKKEDADIKPAGSYKIDRT-----IF 347  
 DB 354 GLINNIHDI-GTHVYHLLFPQIRHYHLYVETRAKPLVGLTY--RPPDSGLPLHL 409  
 QY 348 KAMTREAKEYIIPDEDESEKGVFWYHK 376  
 DB 410 ELAKSIEDHYVS-DE-----GEVWYK 432  
 RESULT 14  
 PD3C\_SOYBN STANDARD; PRT; 453 AA.  
 AC P48621;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).  
 GN FAD7.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eusteroideae I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Seed;  
 RX MEDLINE=94302147; PubMed=8029334;  
 RA Yadav N.S., Wierzbicki A., Aegeerter M., Gaeter C.S., Perez-Grau L.,  
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,  
 RA Allen S.M., Blackwell M., Reltor R.S., Carlson T.J., Russell S.H.,  
 RA Feldmann K.A., Pierce J., Brower J.;  
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";  
 RL Plant Physiol. 103:467-476 (1993).  
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the  
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty  
 CC acids, important constituents of plant membranes. It is thought to  
 CC use ferredoxin as an electron donor and to act on fatty acids  
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL: L22965; AAA61776.1; -  
 DR PIR: J02339; J02339.  
 DR InterPro: IPR005804; FA\_desat\_fam.  
 DR Pfam: PF00487; FA\_desat\_fam; 2.  
 DR ProDom: PD001081; FA\_desat\_fam; 2.  
 DR Oxidoreductase; fatty acid biosynthesis; Chloroplast; Membrane;  
 KW Transact peptide.  
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
 FT CHAIN 1 ? OMEGA-3 FATTY ACID DESATURASE.  
 FT DOMAIN 171 175 HISTIDINE BOX-1.  
 FT DOMAIN 207 211 HISTIDINE BOX-2.  
 FT DOMAIN 374 378 HISTIDINE BOX-3.  
 SQ SEQUENCE 453 AA; 51362 MW; 9DC2FDB2852C018 CRC64;  
 Query Match 29.4%; Score 602.5; DB 1; Length 453;  
 Best Local Similarity 36.8%; Pred. No. 3.9e-41;  
 Matches 128; Conservative 64; Mismatches 117; Indels 39; Gaps 10;  
 QY 9 DPSEGNKLT--ERVV-----VDPPELTSLDKKAIPTGHEFSVSSYYVVDLI-----V 57  
 DB DLITNGTNEHEKLPDPGAPPPNADIRAIKHCWVDPMMSMRYVADVAVGL 139  
 QY 58 AYVYVYLYNTYVPLIPLTPLAYLAMPVPCQASITLGLMVGHECGHAFSDYQIIDIY 117  
 DB 140 AAAAYLYNN-----WLVWPLWYAAQCTFMALFVGLGDCGHSFNSKLNIV 188  
 QY 118 GFVLSALTPTFYFSKYSGRNHNANTSLDNDEVIIP--KRSKVKYISKLNPPGRV 174  
 DB 189 GHLHSSITLVYHGRISHRTHQHNGHAENDESNHPRKLFSLDTVTRLR----- 242  
 QY 175 FTLVRLTLGFPPLYLTLNISGKYGFANHPDPMSPINFDRERVVLSDGLAVFYAI 234  
 DB 243 FTAPEPL-LAFPVILFSSRSPKRT---GSHDPSSDLVPERKGVITSTACMAMLGL 297  
 QY 235 KLVAAKGAANVINYALPVLGVSFVLYLYLH--THLSLPHYDSTEMWIKGALSTI 292  
 DB 298 VGLGFVMPRIQLKLYGVVYVFWMLDLVTLVHGHGDKLPWYRGKEMSYLRGLTTL 357  
 QY 293 DRDGFGLNRVPHDVTHTVHLHLSYIPHYAKAKRDALKPYLGYYK 340  
 DB 358 DRDGYMINNIHDI-GTHVHHLPPQIPHYHLVETEAQVFGCYR 404  
 RESULT 15  
 FD3D\_ARATH STANDARD: PRT; 435 AA.  
 ID FD3D\_ARATH STANDARD: PRT; 435 AA.  
 AC P46622;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast  
 DE precursor (EC 1.14.19.-).  
 GN PAD8 OR ATSG05580 OR MOPI0.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucoside II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia; TISSUE=Aerial parts;  
 RA MEDLINE=95148742; PubMed=7846164;  
 RX Gibson S., Aronold V., Iba K., Somerville C.R.;  
 RT "Cloning of a temperature-regulated gene encoding a chloroplast  
 RT omega-3 desaturase from Arabidopsis thaliana";  
 RL Plant Physiol. 106:1615-1621 (1994).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;  
 RA Marahki M.C., Yamamoto K.T.;  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=97471969; PubMed=9330910;  
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,  
 RA Miyajima N., Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence  
 RT features of the 1.6 Mb regions covered by twenty physically assigned  
 RT pl clones";  
 RL DNA Res. 4:215-230 (1997).  
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the  
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty  
 CC acids, important constituents of plant membranes. It is thought to  
 CC use ferredoxin as an electron donor and to act on fatty acids  
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.  
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).  
 CC -1- INDUCTION: BY LOW TEMPERATURE.  
 CC -1- DOMAIN: The histidine box domains may contain the active site  
 CC and/or be involved in metal ion binding.  
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL: L27158; AAA65621.1; -  
 DR EMBL: U08216; AAB60302.1; -  
 DR EMBL: D17578; BAA04504.1; -  
 DR EMBL: AB005241; BAB11547.1; -  
 DR InterPro: IPR005804; FA\_desat\_fam.  
 DR Pfam: PF00487; FA\_desat\_fam; 2.  
 DR ProDom: PD001081; FA\_desat\_fam; 2.  
 DR Oxidoreductase; fatty acid biosynthesis; Chloroplast; Membrane;  
 KW Transact peptide.  
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).  
 FT CHAIN 1 ? TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID  
 FT DOMAIN 156 160 DESATURASE.  
 FT DOMAIN 192 196 HISTIDINE BOX-1.  
 FT DOMAIN 359 363 HISTIDINE BOX-2.  
 SQ SEQUENCE 435 AA; 50136 MW; 3D7A8035A6214E1 CRC64;  
 Query Match 29.2%; Score 598.5; DB 1; Length 435;  
 Best Local Similarity 34.9%; Pred. No. 7.8e-41;  
 Matches 126; Conservative 67; Mismatches 127; Indels 41; Gaps 9;  
 QY 24 PPFTSLDKKAIPTGHEFSVSSYYVVDLIYAY-----VFYIANTYILIPPLAYL 79  
 DB 87 PPFNLADIRAIIPHGWKPNMMSYVVRVAIVFGLAAVAAYFNN-----WL 135  
 QY 80 AMPVWPCQASITLGLMVGHECGHAFSDYQIIDIYGFVLSALTPTFYFSKYSGRNHN 139  
 DB 136 LMPLYWFGQGMFPAFLVGLGDCGHSNSDRINLSVAGHLHSSITLVPHYGMIRSHRTH 195  
 QY 140 HANTSLDNDEVIIPKRSKVKYISKLNPPGRVFTLVPLTLGFPPLYLTLNISGKYG 199  
 DB 196 HONHGHVNDSESNHPLDES---LYKNLEKTYOMRFTLPPFM-LAYPVYLMNRSFGKO-- 249



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 14:43:29 ; Search time 372 Seconds  
(without alignments)  
4305.298 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEKNTLERY.....ITYEPDESHKGVFWYHKM 377

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 212409041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+p2n.model -DEV=x1h  
-O=/cgn2\_1/uspro.spool/US10069772/runat.18062004.145511.5274/app.query.fasta.1.519  
-DB=N.geneeq.297an04 -OPMT=faactac -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNIT=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MTN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US10069772 @CGN 1.1 352 @runat.18062004.145511.5274 -NCPU=6 -ICPU=3  
-NO MAMP -LAREQIDBRY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LNGLOOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneeq.297an04:\*  
1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002s:\*  
7: geneeqn2003as:\*  
8: geneeqn2003bs:\*  
9: geneeqn2003cs:\*  
10: geneeqn2004s:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	1285	4	AAF88311
2	1636	79.9	1128	2	AAT95688
3	1592.5	77.8	1312	2	AAV63102
4	1589.5	77.7	1358	2	AAV63101
5	1578.5	77.1	1364	2	AAV72550
6	1337.5	65.3	1398	9	AD640488
7	1332.5	65.1	1422	5	AAD22380
8	1323.5	64.7	1411	6	AAI69486

9	1318	64.4	1155	2	AAV84676	AAV84676 Wild-type
10	1318	64.4	1155	2	AAV84676	AAV84676 Wild-type
11	1318	64.4	1155	2	AAV84676	AAV84676 Wild-type
12	1317	64.3	1464	2	AAV84676	AAV84676 Wild-type
13	1317	64.3	1464	2	AAV84676	AAV84676 Wild-type
14	1313	64.1	1155	2	AAV84676	AAV84676 Wild-type
15	1312	64.1	1155	2	AAV84676	AAV84676 Wild-type
16	1312	64.1	1155	2	AAV84676	AAV84676 Wild-type
17	1312	64.1	1155	2	AAV84676	AAV84676 Wild-type
18	1312	64.1	1155	2	AAV84676	AAV84676 Wild-type
19	1312	64.1	1155	2	AAV84676	AAV84676 Wild-type
20	1311	64.0	1155	2	AAV84676	AAV84676 Wild-type
21	1311	64.0	1155	2	AAV84676	AAV84676 Wild-type
22	1311	64.0	1155	2	AAV84676	AAV84676 Wild-type
23	1311	64.0	1155	2	AAV84676	AAV84676 Wild-type
24	1311	64.0	1155	2	AAV84676	AAV84676 Wild-type
25	1310	64.0	1155	2	AAV84676	AAV84676 Wild-type
26	1310	64.0	1155	2	AAV84676	AAV84676 Wild-type
27	1308	63.9	1155	2	AAV84676	AAV84676 Wild-type
28	1308	63.9	1155	2	AAV84676	AAV84676 Wild-type
29	1307	63.8	1155	2	AAV84676	AAV84676 Wild-type
30	1307	63.8	1155	2	AAV84676	AAV84676 Wild-type
31	1307	63.8	1155	2	AAV84676	AAV84676 Wild-type
32	1307	63.8	1155	2	AAV84676	AAV84676 Wild-type
33	1305	63.8	1155	2	AAV84676	AAV84676 Wild-type
34	1305	63.8	1155	2	AAV84676	AAV84676 Wild-type
35	1302.5	63.6	1411	3	AAV84676	AAV84676 Wild-type
36	1301	63.6	1155	2	AAV84676	AAV84676 Wild-type
37	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
38	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
39	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
40	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
41	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
42	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
43	1300.5	63.5	1155	2	AAV84676	AAV84676 Wild-type
44	1299	63.5	1155	2	AAV84676	AAV84676 Wild-type
45	1299	63.5	1155	2	AAV84676	AAV84676 Wild-type

ALIGNMENTS

RESULT 1	AAV88311 standard; DNA; 1285 BP.
XX	AAV88311;
AC	AAV88311;
DT	22-AUG-2001 (first entry)
XX	
DE	C. officinalis calendulic acid desaturase encoding DNA.
XX	
KW	Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
KW	triglyceride; transgenic plant; ds.
XX	
OS	Calendula officinalis.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	42..1175
FT	/*tag= a
FT	/product= "calendulic acid desaturase"
XX	
XX	DE19941609-AI.
XX	
PD	08-MAR-2001.
XX	
XX	01-SEP-1999; 99DE-01041609.
XX	
XX	01-SEP-1999; 99DE-01041609.
XX	
PA	(IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX	
XX	Feussner I, Hornung E, Fritzsche K, Peitzsch N, Renz A;
PI	
XX	

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

```
FT /product= "Crepis alpina delta 12 acetylase"
```

XX 17



PD 09-OCT-1997.  
 XX 14-FEB-1997; 97WO-SE000247.  
 XX 29-MAR-1996; 96SE-00001236.  
 XX (BAFO/) BAFOR M.  
 PA (BANA/) BANAS A.  
 PA (DAHL/) DAHLQVIST A.  
 PA (GUM/) GUMMESON P.  
 PA (LEEM/) LEE M.  
 PA (LENN/) LENNAN M.  
 PA (SUOE/) SJOEDAHN S.  
 PA (STYM/) STYME S.  
 PI Bator M, Banas A, Dahlqvist A, Gummeson P, Lee M, Lenman M,  
 PI Sjoedahl S, Stymme S;  
 DR WPI; 1997-503117/46.  
 DR P-PSDB; AAM36793.  
 XX New acetylase used for production of crepenynic acid from linoleic acid -  
 PT derived from Crepis alpina; used for production of acetylenic fatty acids  
 PT suited for the production of coatings, plastics and lubricants.  
 XX Claim 7; Page 21; 33pp; English.  
 XX This DNA encodes the Crepis alpina delta 12 acetylase. This is used in  
 CC the production of acetylenic compounds. The process comprises treating  
 CC C18 fatty acids having a double bond at position delta 12 with an  
 CC acetylase to form 12-ynolic acids. The acetylenic compounds can be  
 CC produced by organisms such as oilseed plants, yeast and fungi which are  
 CC transformed with this acetylase DNA. These organisms can accumulate  
 CC these acetylenic compounds which are chemical feedstocks, particularly  
 CC for coatings, plasticisers and lubricants. The process enables the  
 CC production of these acetylenic compounds from a renewable resource with  
 CC high purity and at reasonable cost. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX Sequence 1128 BP; 270 A; 308 C; 237 G; 313 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No: 1.18e-167 Length: 1128  
 Score: 1636.00 Matches: 289  
 Percent Similarity: 87.50% Conservative: 40  
 Best Local Similarity: 76.86% Mismatches: 45  
 Query Match: 79.92% Indels: 2  
 DB: Gaps: 1  
 US-10-069-772-2 (1-377) x AAT95688 (1-1128)  
 QY 1 MetGlyAlaGlyArgMetSerAspProSerGluGlyValSerAlaLeuGluArgVal 20  
 DB 1 ATGGAGTGGCGGTGGCCGT-----GTCGCGACTTCGCAAAACCCCTCATGGAACGTGTC 54  
 QY 21 ProValAspProPheThrLeuSerAspLeuValValAlaLeuProThrHisCysPhe 40  
 DB 55 TCAATTATCAACCTTCACCGTAGATGATCTCAAGCAAGCAATCCCTCCCATTTGCTTC 114  
 QY 41 GluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyrVal 60  
 DB 115 AAGCATCTGTAATCCGTTCTTACTACATAGTCACGATGCGATATATATGCGCTACATC 174  
 QY 61 PheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeuAla 80  
 DB 175 TTCTACTCTCTGCGCAAAATATTCGATTCCTCCCTGCGCTTATGCTTACTCTGCT 234  
 QY 81 TrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGlyHis 100  
 DB 235 TGGCCCTTACTAGTCTGTGTCAAGCTAGCATCTCCACCGGCTTATGGGTATCGGTAC 294  
 QY 101 GluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAlaIleValGlyPheVal 120

DB 295 GAATGGCGTACCAATGCCCTTCAGCGACTACCAATGCGGTGACGACACTGTGGCTTCATC 354  
 QY 121 LeuHisSerAlaLeuLeuThrProTyrPheSerTrpValSerHisArgAsnHis 140  
 DB 355 CTCACCTGTCTTCATGACCCCGTATTTCTCTCGAAATACAGCCACCGAACCAT 414  
 QY 141 AlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLysVal 160  
 DB 415 GCCAAACCAATTCGCTTGACACGATGATGATTACATCCCAAAAGCAAGGCCAAAGTC 474  
 QY 161 LysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180  
 DB 475 GCGCTTACTATTAAGTTCTCAACACCCACCTGCGCATGTGATTTATTCATCAC 534  
 QY 181 LeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysLysTyrGlyArg 200  
 DB 535 TTCAACCTAGGCTTCCTCTTATCTCTTTACCAATATTTCCGGCAAGATAGAAAGG 594  
 QY 201 PheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGlnVal 220  
 DB 595 TTTCGCAACCATTTGACACCCCATGATGTCGATTTTCAAGAAGCGGAGCGGTTCCAGTTC 654  
 QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuValAlaAla 240  
 DB 655 TTGCTATCGAATCTTGCGCTTCTGTGCTGTACGAGATTAACTTGCCTGACAGCG 714  
 QY 241 LysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe 260  
 DB 715 AAAGCGCCGCTGCGTAGCGATGATTTACGGAATTTCCAGTTTATGGCGTGTATCTTT 774  
 QY 261 PheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSerThr 280  
 DB 775 TTGCATATCATCATCTGCTTGCACCAACCCATGCTGCTGCTCATATGATCATCT 834  
 QY 281 GluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300  
 DB 835 GAATGGAACCTGCGCAAGGCGCTTTGTCAACAATCGATGAGGACTTGGGTTCCTGAT 894  
 QY 301 ArgValPheHisAspValThrHisThrHisValLeuHisIleLeuSerTyrIlePro 320  
 DB 895 AGTGTCTCATGATGATTTACACACATCACTGATGCAATGCTTTTACATATCA 954  
 QY 321 HisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyrHis 340  
 DB 955 CACTATCATGGAAGGAGGAGGAGGATGATCAACACAGCTTGGGCACTTTATATAG 1014  
 QY 341 IleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGlyLysIleTyrIle 360  
 DB 1015 ATCGATAGACTCCCAATTCGAAAGCAATGAGAGGCGCAAGATGATCATCTTCATC 1074  
 QY 361 GluProAspGluAspSerGluHisLysGlyValPheTrpTyrHisLys 376  
 DB 1075 GAGCTTAATAAAGGTAGGAGTCCAAAGGTGTATATGTAACAATAA 1122  
 RESULT 3  
 ID AAV63102 standard; cDNA; 1312 BP.  
 AC AAV63102;  
 XX 02-FEB-1999 (first entry)  
 DB Crepis sp. delta-12-epoxygenase cDNA clone Crepx.  
 XX Fatty acid epoxygenase; Crepx; delta-12-epoxygenase;  
 KW mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;  
 KW vegetable oil; oilseed; ss.  
 OS Crepis sp.  
 XX Key Location/Qualifiers  
 FH 26.1150  
 FT CDS /\*tag= a

XX MO9846762-A1.  
 XX 22-OCT-1998.  
 XX  
 PR 09-APR-1998; 98WO-AU000246.  
 XX  
 PR 15-APR-1997; 97AU-00006223.  
 PR 15-APR-1997; 97AU-00006226.  
 PR 16-APR-1997; 97US-0043706P.  
 PR 20-JUN-1997; 97US-0050403P.  
 XX  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (STM/) STYME S.  
 PI Styhme S, Green A, Singh S, Lemman M;  
 XX  
 DR MPI: 1998-568734/48.  
 DR P-PSDB; AAM79743.  
 XX  
 PT New isolated fatty acid epoxigenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.  
 XX  
 PS Claim 16, Page 84-86; 150pp; English.

XX This cDNA clone, designated Crepx, codes for a novel epoxigenase (see  
 CC AAM79743) of a Crepis sp. (not Crepis palaestina) that has a high  
 CC verholc acid content. The Crepx gene shows a high degree of homology to  
 CC the novel Cpai2 delta-12-epoxigenase gene (see AAV63101) of C.  
 CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using  
 CC a Crepis alpha acetylenase partial gene sequence (see AAV63104) as  
 CC probe. The invention relates generally to novel genetic sequences (see  
 CC AAV63101-03) encoding fatty acid epoxigenases (see AAV79742-44),  
 CC especially delta-12-epoxigenases or mixed function monooxygenases. These  
 CC provide the means by which fatty acid metabolism can be manipulated in  
 CC e.g. yeast, mould, bacteria, insects, birds, mammals and plants  
 CC (especially oilseed plants such as flax), in particular to convert  
 CC unsaturated fatty acids to epoxigenated fatty acids. The invention  
 CC extends to genetically modified oil-accumulating organisms and to the  
 CC oils derived from them. These oils can be used in production of coatings,  
 CC resins, glues, plastics, surfactants or lubricants

XX SQ Sequence 1312 BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;

# Alignment Scores:

Pred. No.: 7,79e-163 Length: 1312  
 Score: 1592.50 Matches: 285  
 Percent Similarity: 86.24% Conservative: 41  
 Best Local Similarity: 75.40% Mismatches: 47  
 Query Match: 77.80% Indels: 5  
 Gaps: 3

US-10-069-772-2 (1-377) x AAV63102 (1-1312)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyValSerLeuLeuGluArgVal 20  
 Db 26 ATGGGTGCGCGCGCGCGT-----GGTCGACATCGCAAAAGTCGTCATCGTCAACGTGTC 79  
 QY 21 ProValAspPro---ProPheThrLeuSerAspLeuValSerAlaLeuProThrHisGly 39  
 Db 80 TCAGTGTATCCAGTAACCTTCTCACTGAGTATTTGAAGCAAGCAATCCCTCCACATTGC 139  
 QY 40 PheGluArgSerValIleArgSerSerValTyrValValIleAspLeuIleValAlaTyr 59  
 Db 140 TTCACGCACTGTGATCGCTTCACTTATTAAGTTGTCAGATCATATATTCCTAC 199  
 QY 60 ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrIleu 79  
 Db 200 ATCTTCTATCTTCCTTGGCAACATATATCCCTATTCCTCCATCCCTGAGCTACTTA 259  
 QY 80 AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99

Db 260 GCTTGGCGCGCTTACGTGCTTCGCAAGCTACGCTCCTCACTGGGTTATGATCCTCGGC 319  
 QY 100 HisGluCysGlyHisIleAlaPheSerAspTyrGlnLeuIleAspAlaIleValGlyPhe 119  
 Db 320 CATGATATGTGGTACCATGCTTATGACATCAACATGATGTCAGACACTGGGGCTTC 379  
 QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpValSerHisArgAsnHis 139  
 Db 380 ATCATCAATTCATTTCTCCACCCCGTATTTCTTGGAAATACAGTCACCGGAATCAC 439  
 QY 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLys 159  
 Db 440 CATTCACACACACAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATG 499  
 QY 160 ValLysIleTyrSerLysLeuLeuAsnAsnProGlyArgValPheThrLeuValPhe 179  
 Db 500 CTCAAGCGTATCTATTAACCTTAAACACCCACCTGTCGACGTGGTTGGTTATTC 559  
 QY 180 ArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrLeuIleSerGlyValGlyTyrGly 199  
 Db 560 ATGTTCACCCCTAGGATTTCTTAACTTTCGCAAAATATTTCCGCAAGAAATACGAT 619  
 QY 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219  
 Db 620 AGGTTTCCCAACCACTTCGACCCCATGATCATTTTCAAGAACGTCAGCGGTTTCAG 679  
 QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAla 239  
 Db 680 GTCTTCCTTCCTGATCTTGCTTCTTGCTGTTTATGAAATTAAGTCTGTCGTGACA 739  
 QY 240 AlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProValLeuGlyValSerVal 259  
 Db 740 AATTAAGAGAGCTGGTGGTGCGCTGATGATGAGTCCGATGCTAGGCGTATTTACC 799  
 QY 260 PhePheValLeuIleThrTyrLeuHisIleThrIleSerLeuPheProHisTyrAspSer 279  
 Db 800 TTTTTCATGTGATCAGCTTTCATCACCACCACTGATGTCGCTCATTAATGATTTCA 859  
 QY 280 ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299  
 Db 860 ACTGAATGGAATCGATCAGAGGGGCTTTCGACCAATTCGATAGCATTTGGGCTTCGTG 919  
 QY 300 AsnArgValPheHisAspValThrHisThrIleValLeuHisIleSerTyrIle 319  
 Db 920 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979  
 QY 320 ProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyr 339  
 Db 980 CCACACTATCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1039  
 QY 340 LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGlyCysIleTyr 359  
 Db 1040 ATGATCGATGAGCTCCCAATTTTAAAGCAATGTGAGAGAGCGGCAATGATGATGATG 1099  
 QY 360 IleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrHisLysMet 377  
 Db 1100 ATTCAGGCT-----GATAGCAAGCTCAAAAGGTGTTATGATGATCAATTAATG 1147  
 Db AAV63101 standard; cDNA; 1358 BP.  
 XX AAV63101;  
 XX  
 DT 02-FEB-1999 (first entry)  
 XX  
 DE Crepis palaestina delta-12-epoxigenase cDNA clone Cpai2.  
 XX Fatty acid epoxigenase; Cpai2 gene; mixed function monooxygenase;  
 KW delta-12-epoxigenase; epoxigenated fatty acid; transgenic plant;  
 KW vegetable oil; oilseed; se.  
 XX  
 OS Crepis palaestina.

XX Key Location/Qualifiers  
 FH CDS 30..1154  
 FT /\*tag= a  
 XX MO9846762-A1.  
 XX 22-OCT-1998.  
 XX 09-APR-1998; 98MO-AU000246.  
 XX 15-APR-1997; 97AU-00006223.  
 XX 15-APR-1997; 97AU-00006226.  
 XX 16-APR-1997; 97US-0043706P.  
 XX 20-JUN-1997; 97US-0050403P.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA (STM/ ) STYME S.  
 XX Styrene S, Green A, Singh S, Lenman M;  
 XX MPI; 1998-568734/48.  
 DR P-PSDB; AAW79742.  
 XX New isolated fatty acid epoxigenase gene - used particularly for  
 PT transforming plants for producing modified oils for use in, e.g.  
 PT coatings, resins, glues, plastics, surfactants or lubricants.  
 XX Claim 15; Page 78-81; 150pp; English.  
 XX This full-length cDNA clone, designated Cpa12, codes for a novel mixed  
 CC function monooxygenase (see AAW79742) of Crepis palaestina that is  
 CC characterized as having delta-12-epoxigenase activity. It was isolated  
 CC from a C. palaestina cDNA library using a Crepis alpha acetylase  
 CC partial gene sequence (see AAW63104) as probe. The encoded protein  
 CC contains His-rich motifs (see AAW79752-54) that are characteristic of  
 CC mixed function monooxygenases. The Cpa12 gene was shown to be highly  
 CC expressed in developing seeds, with no expression detectable in leaves.  
 CC The invention relates generally to novel genetic sequences (see AAW63101-  
 CC 03) encoding fatty acid epoxigenases (see AAW79742-44), especially delta-  
 CC 12-epoxigenases or mixed function monooxygenases. These provide the means  
 CC by which fatty acid metabolism can be manipulated in e.g. yeast, mould,  
 CC bacteria, insects, birds, mammals and plants (especially oilseed plants  
 CC such as flax), in particular to convert unsaturated fatty acids to  
 CC epoxigenated fatty acids. The invention extends to genetically modified  
 CC oil-accumulating organisms and to the oils derived from them. These oils  
 CC can be used in production of coatings, resins, glues, plastics,  
 CC surfactants or lubricants  
 CC  
 XX SQ Sequence 1358 BP; 358 A; 308 C; 278 G; 414 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.73e-162 Length: 1358  
 Score: 1589.50 Matches: 285  
 Percent Similarity: 85.98% Conservative: 40  
 Best Local Similarity: 75.40% Mismatches: 48  
 Query Match: 77.65% Indels: 5  
 DB: Gaps: 3  
 US-10-069-772-2 (1-377) x AAV63101 (1-1358)  
 QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20  
 Db 30 ATGGGTGCGGCGGCGT-----GTCGACATCGGAAATCGGTACAGACGTGTC 83  
 QY 21 ProValaAspPro--ProPheThrIeuSerAspLeuLysValaIleProThrHisCys 39  
 Db 84 TCAGTTGATCCAGTAACCTTCTCACTGAGTAAATGGAAGCAAGCAATCCCTCCATTGC 143  
 QY 40 PheGluArgSerValIleArgSerSerTyrTyrValIleValHisAspLeuIleValaIleTyr 59  
 Db 144 TTCAGAGATCTGTAAATCCGCTCATCTAATGTTGTTCAAGATCATTAATGCCATAC 203

QY 60 ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeu 79  
 Db 204 ATCTTCTACTCTCTTGGCAACATATATCCCTACTCTTCTACTAGTACCTACTACTTA 263  
 QY 80 AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlnLeuTrpValIleGly 99  
 Db 264 GCTTGGCCCGTTTACTGTTCTGTCAGCTAGCTGCTCAGCTGCTTATGATCTCGGC 323  
 QY HisGluCysGlyHisIleAlaPheSerAspTyrGlnLeuIleAspAspIleValaIlePhe 119  
 Db 324 CACGAATGTGTACCAATGCTCTTACCACTACACATGTTGACGACACCTGTGGCTTC 383  
 QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrLysSerHisArgAsnHis 139  
 Db 384 ATCTCCACATATTTCTCTCCTCACCCCGATATTTCTTGGAATATTCAGCACCGGAATCAC 443  
 QY 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLys 159  
 Db 444 CATTCCAAACACAAATTCATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
 QY ValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPhe 179  
 Db 504 CTCGCGCGTATCTTAAATCTTAAACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563  
 QY 180 ArgLeuThrIeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysTyrGly 199  
 Db 564 ATGTTCACCTTAAGATTTCTTTTACTCTTGAACAATATTTCCGGCAAGAAATACGAC 623  
 QY 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219  
 Db 624 AGGTTTGCACACACCTTCGACCCCATGATGATCAATTTTCAAGAACGACCGGTTTCAG 683  
 QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuValaIle 239  
 Db 684 GTCTTCCTTGGATCTTGGCTTCTTCTTGGCGGTGTTTATGGAATTAAGTTCCTGACCA 743  
 QY 240 AlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProValLeuGlyValSerVal 259  
 Db 744 AATTAAGAGAGCTGTTGGTGGATGCGTGAATGATGATGATGATGATGATGATGATGATGAT 803  
 QY 260 PhePheValLeuIleThrTyrLeuHisIleThrIleSerLeuProHisTyrAspSer 279  
 Db 804 TTTTTCATGTGATCACCTTCTTGCACACACCATCATGATGATGATGATGATGATGATGAT 863  
 QY 280 ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299  
 Db 864 ACTGAATGAACTGATGAGGGGCTTGTGACCAATCGATAGGAGCTTGTGATCTCTG 923  
 QY 300 AsnArgValPheHisAspValThrHisThrIleValLeuHisIleLeuIleSerTyrIle 319  
 Db 924 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983  
 QY 320 ProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyLysTyr 339  
 Db 984 CCACACTATCATGCAAGAGGCAAGGATCAATCAACCAATCTTGGCGGACCTTTAT 1043  
 QY 340 LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr 359  
 Db 1044 ATGATCGACAGACTCCAAATTTAAAGCAATGTGAGAGGGGAGGAGGAGTGCATGAC 1103  
 QY 360 IleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrHisLysMet 377  
 Db 1104 ATCGAGCT-----GATAGCAACTCAAGGTGTTTATGTTATCAATTAATG 1151  
 RESULT 5  
 AAV72550 standard; cDNA; 1364 BP.  
 ID AAV72550 standard; cDNA; 1364 BP.  
 XX AAV72550;  
 AC  
 XX 27-AUG-2003 (revised)  
 DT 10-FEB-1999 (first entry)  
 XX

DE Vernonia galamensis fatty acid epoxidising enzyme encoding cDNA.  
XX  
XX Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;  
KW expression; chimeric gene; recombinant enzyme; ss.  
OS Vernonia galamensis.  
XX  
FH Key Location/Qualifiers  
FT CDS 103..1257  
FT /tag=a  
XX  
XX US5646784-A.  
XX  
XX 08-DEC-1998.  
XX  
XX 11-JUN-1997; 97US-00872302.  
XX  
XX 11-JUN-1997; 97US-00872302.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Hitz WD;  
XX  
XX MPI, 1999-059065/05.  
XX  
XX P-85DB; AAM83354.  
XX  
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid  
PT epoxidising enzyme - used to alter levels of expression of the enzymes in  
PT transformed host cells or to produce recombinant enzymes.  
XX  
XX  
XX Claim 6; Col 25-29; 21pp; English.  
XX  
XX The present sequence encodes Vernonia galamensis fatty acid epoxidising  
CC enzyme. The present invention also describes: (i) Vernonia galamensis  
CC fatty acid desaturase; (ii) chimeric genes comprising the fragments  
CC linked to regulatory sequences; and (iii) transformed host cells  
CC containing the chimeric genes. The DNA's from the present invention can  
CC be used to alter levels of expression of the enzymes in transformed host  
CC cells or to produce the recombinant enzymes by transformation of  
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)  
XX  
XX Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;  
SQ  
  
Alignment Scores:  
Pred. No.: 2.73e-161 Length: 1364  
Score: 1578.50 Matches: 280  
Percent Similarity: 87.16% Conservative: 39  
Best Local Similarity: 76.50% Mismatches: 44  
Query Match: 77.11% Indels: 3  
DB: Gaps: 2  
  
US-10-069-772-2 (1-377) x AAV72550 (1-1364)  
QY 15 AenileuGluarValProValASP---ProProPheThrLeuSerAspLeuIys 33  
DB 157 AATATTAACGAAAGCGACCGGTTATGCGGACCACTTCTGTTAAGCATTTAAGAAA 216  
QY 34 AAlaileProThrHisCyaspheGluarSerValIleargSerSerTyrrValValHis 53  
DB 217 GCAATCCCTCCGCGATTCCTTCAGGATCCGATCCGTTATCTGTGCTAGCTTTGAG 276  
QY 54 AspLeuIleValAlaTyrrValPheTyrrTyrrLeuAlaSerThrTyrrIleProLeuIlePro 73  
DB 277 GATTCATATTACCTTCCTTTTATACAGCGTCGCAACTCTTACATTCCTTCCTCT 336  
QY 74 ThrProLeuAlaTyrrLeuAlaThrProValTyrrTPPheCyaspGluAlaSerIleLeuThr 93  
DB 337 CCTCTCTACCTTACTTACGATGCGCTGTTCGTTTGGCAATCTTCGATCTCACT 396  
QY 94 GlyLeuTPValIleGlyHisGluCyaspGlyHisIleAlaPheSerAspTyrrGlnLeuIle 113  
DB 397 GGTATTATGGGTCATTGGCGCATGATGTGGCCATCATGCTTATAGAGTACCAAGGGATT 456

QY 114 AspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrrPheSerTrpLys 133  
DB 457 GATTAACACCGTTGATTCATCTCTTCCTTCCTTCACACCTTACTTTCTTGAAA 516  
QY 134 TyrrSerHisArgAsnHisIleAlaAsnThrAsnSerLeuAspAspGluValTyrrIle 153  
DB 517 TACAGCCATCGAAGACACCATCCACAGATTCACATCGAAGGAGAGGTTTACTT 576  
QY 154 ProLysArgLysSerLysValLysIleTyrrSer-----LysLeuLeuAsnProPro 171  
DB 577 CCTAAGCCAGATCCCGACCTCAGAAATTAATTCATTTCAATTTCTTGACAAACCCCT 636  
QY 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrrLeuThr 191  
DB 637 GGTCAATCTTCAATTTGCTTATCATGTGACCTTGAGCTTCTTCTTATACCTTGACC 696  
QY 192 AenileSerGlyLysLysTyrrGlyArgPheAlaAsnHisPheAspProMetSerProIle 211  
DB 697 AATATTTACGCGAAGAAATACCAAGTTTCCCAACCACTTGATCCGTTAGCCCATC 756  
QY 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaPhe 231  
DB 757 TTCAGTAGCGGTGAACGATCCAGTGCCTATCGATGCGGTCTCATGCTGCTGTTT 816  
QY 232 TyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaIleAlaTPValIleAsnMetTyrrAla 251  
DB 817 TACGGCTTAAGTTTCTTGTAAGCAAAAGGTTGCGTTGGTTAAGCGCATGACCA 876  
QY 252 IleProValLeuGlyLysSerValPhePheValLeuIleThrTyrrLeuHisIleThrHis 271  
DB 877 GCCCAGTGGTTGGGCTGAATGCTTCATATATATGATCATTTATTCACACACCCAT 936  
QY 272 LeuSerLeuProHisTyrrAspSerThrGluTrpAsnTrpIleLysGlyAlaLysSerThr 291  
DB 937 CTGCTTCGCTCATTTACGATTCGACCGAATGGAATCGAATGGAAGACCTTGACTCA 996  
QY 292 IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleVal 311  
DB 997 ATCGATAGAGATTCGGCTCTCGAATAGGGTGTTCATGACGTCATCACAACACAGCTG 1056  
QY 312 LeuHisIleLeuIleSerTyrrIleProHisTyrrHisAlaLysGluAlaArgAspAlaIle 331  
DB 1057 TTGCATCATTTGTTCCGCTACATTCACATATATGCAAGAGGCGAGCGCAATA 1116  
QY 332 LysProValLeuGlyGluTyrrTyrrLysIleAspArgThrProIlePheLysAlaMetTyrr 351  
DB 1117 AAGCGGCTTAAGGAGGATATCGATGATCGATGAGACTCCGTTTTCMAAGCAATGTGG 1176  
QY 352 ArgGluAlaLysGluCyaspIleTyrrIleGluProAspGluAspSerGluHisLysGlyVal 371  
DB 1177 AGAGAGCGGAAGAAATGATTCATTCAGCGCAATGAGATGAAGTAAAGACCAAGGTGTA 1236  
QY 372 PheTrpTyrrHisLysMet 377  
DB 1237 TATTGGTACCAATAAATG 1254  
  
RESULT 6  
ADE40488  
ID ADE40488 standard; DNA; 1398 BP.  
XX  
XX ADE40488;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX P. granatum delta-12-desaturase PufAD12 DNA.  
XX  
XX desaturase; transgenic; plant; oil; triglyceride; unsaturated fatty acid;  
KW food; animal feed; cosmetic; pharmaceutical; pomegranate; der; gene;  
XX  
XX delta-12-desaturase; PufAD12.  
XX  
XX Punica granatum.  
XX  
XX  
FH Key Location/Qualifiers

[illegible]

Db	394	CTCAGGGGTGCTGGGTGATGAGCCACGAGTGGGGGACCATGGTTTAGGCACTACAG	453
Oy	112	LeuIleAspApIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSer	131
Db	454	TGGGTGGACGACTGTGTCGGCTGGTACTGCACTCAGCGCTCTGTCCCTACTCTCC	513
Oy	132	ThrIleTyrSerThrIleArgAsnHisIleAlaAsnThrIleAsnSerLeuAspAspGluVal	151
Db	514	TGGAAATACAGCCACCGCGGACCACTCCAAACGGGCTCGATTGAGCGGTGAAGCGTGAAGGTT	573
Oy	152	TyrIleProLysArgLysSerLysValIleTyrSerLysLeuLeuAsnProPro	171
Db	574	TTTCGTCCCAAGCCCAAGTCCAAATGCCGTGGTCTTCCAAGTACCTGAACAACCCGCA	633
Oy	172	GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThr	191
Db	634	GGCGAAGTCATGACGCTGATGTGACCTTGACCTTGCGGCTGGCGGTGTGATGGCATTTG	693
Oy	192	AsnIleSerGlyLysLysTyrGlyValArgPheAlaAsnHisPheAspProMetSerProIle	211
Db	694	AACGCTCTGGCTGGCCCTTAGACAGGTTCGCTTGCCACTTTGACCCGTATGGCCGATG	753
Oy	212	PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe	231
Db	754	TACACCGACGAGGAGCGCTACATGATCACTACATTTCTGTATGTAGGATCATATGCGCCAGC	813
Oy	232	TyrAlaIleLysLeuLeuValAlaAlaLysGlyValAlaAlaTyrValIleAsnMetTyrAla	251
Db	814	TACACGCGGTGACAAAGATGCAGCAGACCGCGTGGCTGGCTGGTGGTTGTGTATATGCT	873
Oy	252	IleProValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrHis	271
Db	874	GTCCCTCTCCGATCGTGAAGCAATTCCTGTGTCAGATCACTACCTCCAGCAACCCAC	933
Oy	272	LeuSerLeuProHisTyrAspSerThrGluTyrAsnThrIleLysGlyAlaLeuSerThr	291
Db	934	CCGGCCCTTCCCACTATGACTGTCGGAATGGAGTGGCTCAGGGGGGCACTGGACACA	993
Oy	292	IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleVal	311
Db	994	GCGACGACGAGCTACGGGATCTCAACAAGTCTTCACAACAAATACGACACCAATGTC	1053
Oy	312	LeuHisIleLeuIleSerTyrIleProHisIleTyrHisIleValLysGlyValAspArgAlaIle	331
Db	1054	GCCCAACCACTCTTCTCCACATGCCGACCTACCAACCGATGAGGCTTACCAAGCCGATC	1113
Oy	332	LysProValLeuGlyLysTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyr	351
Db	1114	AAGCGATACCTAGGAGACTACTACACTGACGAGGACTCCGGATATCAAGAGCAATGGG	1173
Oy	352	ArgGluAlaLysGlyLysTyrIleGluProAspGluAspSerGluHisIleGlyVal	371
Db	1174	AGAGAGGCTAAGGAGTGCCTGTACTGTGAAGCCCAACAGCGGGGCCAACGTAAGGGGTT	1233
Oy	372	PheTyrTyrHisLys 376	
Db	1234	TTCTGGTACAGAGAG 1248	
RESULT 7			
ID	AAD22380	standard; cDNA, 1422 BP.	
XX	AC	AAD22380;	
DT	12-FEB-2002	(first entry)	
DE	Cotton oleoyl-PC delta12-desaturase (gFAD2-2) protein cDNA.		
XX	XX		
KM	Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;		
KM	linoleic acid; stearic acid; oleic acid; transgenic plant;		
XX	cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2; ss.		

OS *Gossypium hirsutum*.  
 XX Key Location/Qualifiers  
 FH CDS 98..1249  
 FT /\*tag=a  
 FT /product="Cotton gHFD2-2 protein"  
 EN MO200179499-A1.  
 XX PD 25-OCT-2001.  
 XX 18-APR-2001; 2001MO-AU000436.  
 XX 18-APR-2000; 2000US-0198124P.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX PA Green A, Singh S, Liu Q;  
 XX PI WPI; 2001-602932/68.  
 DR P-PSDB; AAE13421.  
 XX PT Modifying endogenous oil of cotton plants, to produce cotton seed oil  
 PT with reduced palmitic and/or linoleic acid content, involves producing  
 PT transgenic plants containing a fatty acid biosynthesis gene in a  
 PT construct.  
 XX PS Example 8; Fig 6; 201pp; English.  
 XX CC The invention relates to a method for modifying the endogenous oil of a  
 CC cotton plant, to produce cotton seed oil. The method comprises producing  
 CC a transgenic cotton plant having a gene construct which includes a fatty  
 CC acid biosynthesis gene operably linked to a promoter sequence capable of  
 CC conferring expression of the delta9-desaturase (delta9 stearyl-ACP  
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-  
 CC desaturase) gene, in the seed of a cotton plant. The invention is useful  
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid  
 CC content, and increased stearic and/or oleic acid content. The present  
 CC sequence is cotton oleoyl-PC delta12-desaturase (gHFD2-2) protein cDNA  
 CC related to the invention  
 XX SQ Sequence 1422 BP; 358 A; 335 C; 307 G; 422 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.56e-134 Length: 1422  
 Score: 1332.50 Matches: 230  
 Percent Similarity: 79.16% Conservative: 70  
 Best Local Similarity: 60.69% Mismatches: 74  
 Query Match: 65.10% Indels: 5  
 DB: Gaps: 2  
 US-10-069-772-2 (1-377) x AAD22380 (1-1422)  
 QY 1 MetGyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16  
 DB 98 ATGGGTGCTGGAGGAGGAATGCGGTTCACAAAGCAAAAACCGAATTCACCTCA 157  
 QY 17 LeuGluATGValProValAsp---ProProPheThrLeuSerAspLeuLysAlaIle 35  
 DB 158 CTGAAGCGAGTTCCTACTCAAGCCACCTTCATCTGAGGAAATCAAGAAACCTTC 217  
 QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55  
 DB 218 CCACCACTACTGTTCCAGGCGCTCCGTTTACCGCTCATTCATCTCCTTACGACTTT 277  
 QY 56 IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75  
 DB 278 ATATTGGCTCTCTTTTACCATATGGCCACCAATTCCTCCCAACCTTCTAGGCT 337  
 QY 76 LeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95  
 DB 338 CTCCTCAACGTCGCTTGCGCTCTTATTATGGGCAATGCAAGATTGCACTTTACCGGCTT 397

QY 96 TrpValIleGlyHisGluCysGlyHisAlaPheSerAspTyrGlnLeuIleAspAsp 115  
 DB 398 TGGGTCAATAGCCCATGAATGTGGCCACCATGCTTTCAGTATATCAATGGCTGACAC 457  
 QY 116 IleValGlyPheValIleuHisSerAlaLeuLeuThrProTyrPheSerTyrLysSer 135  
 DB 458 ACCGTGGGCTTATCCCTCCACTCTTCTCTTACTTATTCATATTTCTGTGAAATATAGC 517  
 QY 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLys 155  
 DB 518 CACCGCGCTCACCATTCATTAACACCGGTTCCTCCAAAGGAGTGAAGTGTGCCCAAG 577  
 QY 156 ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProGlyArgValPhe 175  
 DB 578 AAAAAATCGTGTAAAGTGGTGGCCCAACACTTCAACATTCACCGGCTGCTTCG 637  
 QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195  
 DB 638 TCATTCACCATTCACACTTACCTTGTTGGCGGCTTTACTTACGTTCAACGTTGCCGCG 697  
 QY 196 LysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215  
 DB 698 CGGCTTACGACAGGTTGCGTTGCCACTATGACCTTACCGGCCCATATTTTCCGACCGG 757  
 QY 216 GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235  
 DB 758 GAACGACCTCAAACTATATCTGTGACCGCGCGCTCTGCTGCTATGCGCTTAC 817  
 QY 236 LeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValLeu 255  
 DB 818 CGTCTCGTGGTGGCCAAAGGGGTAGGTTGGTTATTCGTTATGGGTCCTTATTTG 877  
 QY 256 GlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuPro 275  
 DB 878 GTGGTTAAAGCCCTCTTATGATATGATACGATTTGGCAACACACTCCCATCTTTGCGG 937  
 QY 276 HisTyrAspSerThrGlnTyrAsnThrIleGlyAlaLeuSerThrIleAspArgAsp 295  
 DB 938 CACTATGATTTCTCGAGTGGAGCTGATGAGAGAGCTTTATCAACTGTGACAGAGAT 997  
 QY 296 PheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHisLeu 315  
 DB 998 TATGGGATTTTAAACAGGTTTTCATTAACATTAACCGACATCATGTGCGCTCATTTTG 1057  
 QY 316 IleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeu 335  
 DB 1058 TTTTCGAAGAATGCTCATCATCATGCGATGCGGCCAACAGGCGATTAAGCCCATATTTG 1117  
 QY 336 GlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLys 355  
 DB 1118 GGGGAATACATATCAGTTCCGATGGAGATGCTGTCTATTAAGCGGATATGAGGAGCGAAG 1177  
 QY 356 GluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrTyr 374  
 DB 1178 GAGTGTCTTACGTTGAACCAATGAGGCGCAACAAGATTAAGGTGTCTTTGGTTT 1234  
 RESULT 8  
 AA169486  
 ID AA169486 standard; cDNA; 1411 BP.  
 XX AA169486;  
 AC AA169486;  
 XX 08-MAR-2002 (first entry)  
 DT C. officinalis Cofad2 cDNA.  
 XX C. officinalis Cofad2 cDNA.  
 XX Cofad2, linoleic acid; conjugated fatty acid; plant; cosmetic;  
 KM pharmaceutical; lubricant; ss.  
 XX Calendula officinalis.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 89..1240  
 FT

```
FT      /*tag= a
FT      /product= "Cofad2"
XX      MO200185968-A2.
XX      15-NOV-2001.
XX      09-MAY-2001; 2001WO-IB001059.
XX      09-MAY-2000; 2000US-0203027P.
XX      (BIOR-) BIORIGINAL FOOD & SCI CORP.
XX      Qiu X;
XX      MPI: 2002-089796/12.
XX      P-PSDB; AMG80695.
XX      Nucleic acids which encode a conjugase and its related enzyme a delta
XX      PT desaturase to be used for the large scale production of conjugated
XX      PT linoleic acid and linolenic acid in plants.
XX      PS      Claim 3; Fig 1; 49pp; English.
XX      CC      This invention describes a novel polypeptide, Cofad2, capable of
XX      CC catalyzing the formation of two conjugated double bonds. The products of
XX      CC the invention can be used for the large scale production of conjugated
XX      CC linoleic acids. The composition may be used for cosmetic or
XX      CC pharmaceutical purposes. The conjugated linoleic acids may be used for
XX      CC coating, painting or cold weather ester-type lubricant purposes. There is
XX      CC not a natural source which is rich in conjugated linoleic acids and
XX      CC chemical processes result in a mixture of several isomers. Plant
XX      CC biotechnology is cost-effective and renewable with little side effects.
XX      CC This sequence encodes the Calendula officinalis Cofad2 protein
XX      SQ      Sequence 1411 BP; 360 A; 374 C; 311 G; 366 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,466-133      Length:      1411
Score:          1323.50      Matches:      233
Percent Similarity: 76.32%      Conservative: 57
Best Local Similarity: 61.32%      Mismatches: 83
Query Match:      64.66%      Indels:      7
DB:              Gaps:      2

US-10-069-772-2 (1-377) x AA169486 (1-1411)
QY      1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20
DB      89 ATGGGTGCAAGCGGTGCAATGCAGATCCCAACGCGTGGCAACAAACGAGCCGAA 148
QY      21 ProValAsp-----ProProPheThrLeuSerAspLeuLysLeuAla 34
DB      149 CCAATCCACGCGTCCACATGAAACACCCCATTCACAGTTGAGACATCAAGAAACCG 208
QY      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAsp 54
DB      209 ATCCCACTCATTTGTTTCAACCGATCGTAATTCGTTCAATTTTCAATGCTTTTACAC 268
QY      55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74
DB      269 CTCACAAATCGCGTCAATCTGTACATGCAATGCAACATTTACATCTACACCTCCATGC 328
QY      75 ProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGly 94
DB      329 CCGCTCGCTCTAGCGGACATGCGCCGTTTACCTGGCCGCTCAAGGGGTGCTTAAACCGG 388
QY      95 LeuTyrValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAsp 114
DB      389 GTGGGTGATCAAGCCACCAATGCGCATCATGCTTTTACGACACCAATGGCTCAT 448
QY      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleTyr 134
```

```
DB      449 GACACCGTGGTCTGCTTGCTGACTCGTTCCTACTCGTGCCCTTATCTTCGTGAAATAT 508
QY      135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIlePro 154
DB      509 AGCCACCGTAGGACACCACTGCAACAGGGCTCGATTCAGACACGATGAGTTTGTCTCCG 568
QY      155 LysArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProProGlyArgVal 174
DB      569 AAGTTGAATATCGGCGTCCGTCACACCGCCGCTACCTTAACAAACCAACCGCCGCGAATC 628
QY      175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSer 194
DB      629 TTGACCCCTACCTGTAACCCCTTAACCTCGTGGCTCTTATACCTCACGCTTCAACGTTTCG 688
QY      195 GlyLysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
DB      689 GGCGGTACTAGACACCGGTGCGTCCATTTTCACCCGAAATAGCCGATCTTACTCCGAG 748
QY      215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234
DB      749 CGGACAGCGGCTCAAACTTTCATATCCGACCGCGGATCTTAGCCGTACTGCTACTC 808
QY      235 LysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProVal 254
DB      809 TTCCGACTCGCAATGACCAAGGCGCTCACGCGGTCTTACCAACGATGCGTGGCCGTTA 868
QY      255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274
DB      869 CTCGTGTCACAGGTTTCTTACTTGTATTCATCTTCAACACACTCACCTTCCTGCTC 928
QY      275 ProHisTyrAspSerThrGluTyrAsnTyrIleLysGlyAlaLeuSerThrIleAspArg 294
DB      929 CCGACATATGACTCAACGAAATGAGATGTTGTTAGCTGGGGCCCTCACCAATGCACCGT 988
QY      295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
DB      989 GATTACGGGATCTTAAACAAAGTGTCTCATTAACATTAACGACACTGAGTGGCCACCAT 1048
QY      315 LeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProVal 334
DB      1049 TTGTTCTTACAAAGCCCTCATATTCATGCAATGAGACGACGAAAGTGAATCAACCGATT 1108
QY      335 LeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla 354
DB      1109 TTGGGCAATTATTTATCACTTGTGACGAGCACTTCATTTTAAGCGAGTATTCGGGAAACA 1168
QY      355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrTyr 374
DB      1169 AAGGATGCAATTATTTGTTAATGATGAGATGAGAGGTGAAA--GATGGTGTATTATGGTAT 1225

RESULT 9
AAV84676
ID      AAV84676 standard; DNA; 1155 BP.
AC      AAV84676;
XX      04-MAR-1999 (first entry)
DE      Wild-type Fad2 gene F form coding sequence.
XX      Brassica, recombinant; microsomal; delta-12 fatty acid desaturase; oil;
XX      KM delta-15 fatty acid desaturase; seed; fatty acid; oleic acid; Fad3;
XX      KM erucic acid; canola; rapeseed; linolenic acid; oxidative; Fad2; ss.
XX      Brassica napus.
OS
XX      Key
XX      CDS
XX      Location/Qualifiers
XX      FT      1..1155
XX      FT      /*tag= a
XX      FT      /gene= "Fad2"
XX      FT      /product= "Wild-type Fad2 F form"
XX      PN      US5850026-A.
```





XX 17-DEC-1998.  
 PD 11-JUN-1998; 98WO-US012332.  
 XX PF 12-JUN-1997; 97US-00874109.  
 XX PR (CRGI) CARGILL INC.  
 XX PA Debonte LR, Zhegong F, Loh WH, Shorosh BS;  
 XX PI WPI: 1999-059929/05.  
 XX DR P-PSDB; AAM94053.  
 XX PT New isolated mutant fatty acid desaturase genes - obtained by mutation of  
 XX PT Brassicaceae or Helianthus plants, used for producing plants or seeds  
 XX PT having altered fatty acid compositions.  
 XX PS Example; Page 73-75; 116pp; English.  
 XX CC The invention relates to fatty acid desaturases (FAD) from Brassicaceae  
 CC or Helianthus, where the FAD gene comprise at least one mutation in  
 CC their sequences. The mutation is in a region encoding the His-Xaa-Xaa-Xaa  
 CC His motif of the delta-12 or delta-15 fatty acid desaturases. The  
 CC invention also provides methods for producing the FAD mutant genes and  
 CC gene products. The products can be used for producing plants and seeds  
 CC which have altered fatty acid compositions, e.g. an elevated oleic acid  
 CC content, a decreased, stabilised linoleic acid content, both elevated  
 CC oleic acid and decreased, stabilised linoleic acid content or a  
 CC decreased, stabilised level of alpha-linolenic acid and increased level  
 CC of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower,  
 CC safflower, castor bean or corn. The present sequence represents the DNA  
 CC sequence of the coding region of the Brassica wild-type FAD2-F gene  
 XX SQ Sequence 1155 BP; 246 A; 361 C; 275 G; 273 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,36e-133 Length: 1155  
 Score: 1318.00 Matches: 233  
 Percent Similarity: 77.17% Conservative: 61  
 Best Local Similarity: 61.15% Mismatches: 81  
 Query Match: 64.39% Indels: 6  
 DB: 2 Gaps: 4

US-10-069-772-2 (1-377) x AAX06619 (1-1155)

QY 1 MetGlyValGlyValGlyMet-----SerAspProSerGluGlyLys-----AsnIle 16  
 Db 1 ATGGGTGCAAGGTGGAAGATGCAAGTGTCTCTCCCTCCAGAAAGTGTGAAACGACACC 60

QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValLeuAlaIle 35  
 Db 61 ATCAAGCGCGTACCTCGGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCAATC 120

QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55  
 Db 121 CCACCGCACTGTTCACAAAGCTGATCCCTGCTTCTCTCACTGATGCGAGATC 180

QY 56 IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75  
 Db 181 ATCATAGCT 240

QY 76 LeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95  
 Db 241 CT 300

QY 96 TyrValIleGlyHisGlyCysGlyHisIleAlaPheSerAspTyrGlnLeuIleAspAsp 115  
 Db 301 TGGGTCAATAGCCCAAGATGGCGCACACGCTTCAAGCACTACAGAGTGGCTTGAGAC 360

QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleTyrSer 135  
 Db 361 ACCGTGGTCTCATCTTCACT 420

QY 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgValTyrIleProLys 155  
 Db 421 CATCGACGCCACCATTCACACTGCTCCCTCGAGAGAGACGAAGTGTGTCCTCCCAAG 480

QY 156 ArgLysSerLysValIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPhe 175  
 Db 481 AAGAAGTCAGCAATCAATGTGTACGGCAGCAAGTCAACCTTGGGCGGACCGCTG 540

QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195  
 Db 541 ATGTTAACGTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 196 LysLysTyr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214  
 Db 601 AGACCTTACGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234  
 Db 661 CGCAGGCGTCCAGAAATATCATCTCCGACGCTGCAATCCCTGCGCTGCTGCTGCTGCTG 720

QY 235 LysLeuLeuValAlaIleLysGlyAlaIleTyrValIleAsnMetTyrAlaIleProVal 254  
 Db 721 TTCGTTACCGCCGCGCGGAGGTGCGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrHisLeuSerLeu 274  
 Db 781 CTGATGTGCAATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 275 ProHisTyrAspSerThrGluTyrAsnThrIleLysGlyAlaLeuSerThrIleAspArg 294  
 Db 841 CCTCATACAGATTCGCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleThrHisValLeuHis 314  
 Db 901 GACTACGGAATCTTGAACAAGTCTTCCACAATATTCACAGACAGCGGCGCATCAT 960

QY 315 LeuIleSerTyrIleProHisIleTyrHisAlaLysGluAlaArgAspAlaIleLysProVal 334  
 Db 961 CTGTTTCCACGAGCGCGCATTTATCAGCGATGAGAACTCCAGAGCGGATTAACCGATA 1020

QY 335 LeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla 354  
 Db 1021 CTGGAGAGATATATCATGTTGATGAGCGCGGCTGTTAAGCGATGAGAGGAGCGG 1080

QY 355 LysGluCysIleTyrIleGluProAspGluAspSerLysIleLysGlyValIlePheThrTyr 374  
 Db 1081 AAGGAGGTATCTATGTGAACCGGACGAGCGAGCGAAGTGAAGAAAGGTGTGTGTGATC 1140

QY 375 His 375  
 Db 1141 AAC 1143

RESULT 11  
 AA251120 standard; DNA; 1155 BP.  
 XX ID AA251120;  
 AC AA251120;  
 XX 05-JUN-2000 (first entry)  
 DE B. napus Delta-12 fatty acid desaturase-F (Fad2-F) wild type gene.  
 XX XX Long chain monounsaturated fatty acid; erucic acid; oleic acid;  
 KM delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable oil;  
 KM industrial oil; lubricant; hydraulic oil; delta-12 fatty acid desaturase;  
 XX Fad2; Fad2-F; rapeseed; de.  
 OS Brassica napus.  
 XX XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1155  
 FT /\*tag= a

FT		/product="Pad2-F"
XX		
XX	MO200007433-A1.	
PN		
XX	17-FEB-2000.	
PD		
XX		
XX	03-AUG-1999;	99MO-US017645.
PF		
XX	03-AUG-1998;	98US-00128602.
PR		
XX		
XX	(CRGI ) CARGILL INC.	
PA		
XX	Kodall D, Fan Z, Debonte LR;	
PI		
XX	WPI; 2000-223937/19.	
DR	P-PSDB; AAY70114.	
DR		
XX	New Brassica plants and seeds having elevated long chain monounsaturated	
PT	fatty acid content, for industrial uses, e.g. engine lubricants.	
PT		
XX		
XX	Disclosure; Page 102-104; 117pp; English.	
PS		

CC The patent discloses Brassica plants and seeds having a long chain  
CC monounsaturated fatty acid (PA) content of at least 8% and an erucic  
CC acid content of at least 15% based on total PA composition. The patent  
CC further relates to genes encoding delta-12 and delta-15 fatty acid  
CC desaturases (Pad2 and Pad3 respectively). Mutations in these genes result  
CC in useful alterations in the fatty acid compositions of the seed oil e.g.  
CC mutation in Pad2 gene confers elevated oleic acid content and decreased  
CC linoleic acid content. The Brassica seeds are useful source for vegetable  
CC oil and industrial oils such as engine lubricants, transmission fluids  
CC for diesel engines and hydraulic oil. The present sequence is that of a  
CC wild type gene encoding Brassica napus microsomal Delta-12 fatty acid  
CC desaturase-F (Pad2-F)

FT /product= "microsomal delta-12 desaturase"  
 XX US6372965-B1.  
 XX 16-APR-2002.  
 XX 14-AUG-1998; 98US-00133962.  
 XX 17-NOV-1992; 92US-00977339.  
 PR 15-OCT-1993; 93WO-US009987.  
 PR 20-JUN-1994; 94US-00262401.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 XX Lightner JE, Okuley JU, Hitz W, Kinney AJ, Perez-Grau L;  
 PI Yadav NS;  
 XX WPI: 2002-392229/42.  
 DR P-PSDB; ABB80028.  
 XX New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or  
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and  
 PT producing seed oil with altered levels of unsaturated fatty acids.  
 XX Claim 1; Col 71-74; 54pp; English.  
 XX The invention relates to an isolated nucleic acid fragment encoding or  
 CC comprising a sequence encoding a plant enzyme that is a delta-12  
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.  
 CC Chimeric genes comprising nucleic acids of the invention are used to  
 CC create transgenic plants with altered levels of unsaturated fatty acids,  
 CC and can modify plant lipid composition. Nucleic acids of the invention  
 CC can be used as hybridisation probes to isolate or amplify nucleotide  
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-  
 CC related enzymes. They can also be used in restriction fragment length  
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in  
 CC seed oil of oil producing plant species. They can also be used to produce  
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic  
 CC acids of the invention can combine the high oleate trait of transformed  
 CC seeds with mutations for altered fatty acid compositions to obtain new  
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in  
 CC total saturates and high in monounsaturates would provide significant  
 CC health benefits to consumers (reduced risk of coronary heart disease) as  
 CC well as economic benefits to oil processors. The current sequence  
 CC represents a rape microsomal delta-12 desaturase cDNA  
 XX  
 SQ Sequence 1423 BP; 320 A; 405 C; 333 G; 365 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.53e-133 Length: 1423  
 Score: 1317.00 Matches: 234  
 Percent Similarity: 76.44% Conservative: 58  
 Best Local Similarity: 61.26% Mismatches: 82  
 Query Match: 64.34% Indels: 8  
 DB: 6 Gaps: 4  
 US-10-069-772-2 (1-377) x ABL58600 (1-1423)  
 QY 1 MEGGVLVLAAGLYGVAAGMCT-----SERRAPPROSERGLINGLYLVAAH 15  
 DB 129 ATGGGTCCAGGTGGAAGATGCAAGTGTCTCTCCCTCCAAAAGTGGAAACCGACAC 188  
 QY 16 LLEUGLVARGVALPROVALASP---PROPHRPHRTHLEUSERAPLLEUVALA 34  
 DB 189 ATC---AAGCCGTCACCTCGAGACACCGCCCTTCACTGCGAGAACTCAAGAACCA 245  
 QY 35 LLEPHRTHRHSYSPHEGLVARGSERVALLEARGSERVYTYVALVALHISAP 54  
 DB 246 ATCCACCGCACTGTTCAACGCTCGATCCCTGCTTCTCTCACTCATCTGGGAC 305  
 QY 55 LEULLEVALVALTYRVALPHEVYTYRLEUVALASANTHYTYRLEPROLEILPROTHR 74  
 DB 306 ATCATCATVAGCTCTGCTCTTACTAGCTGCGACCACTTACTTCCCTCTCCAC 365

QY 75 PROLEUALTYRLEUALATPPTROVALTYRTTPHRCYSGINALASERILEUETHGLY 94  
 DB 366 CCTCTCTCTTACTCTGCGCTGCTCTACTAGGGCGTCCGACGGGTGCTCTTAACCGGC 425  
 QY 95 LEUTPVALLIEGLYHIEGLUCYGLYHISIALAPHESERRAPTYRGLNLEULASP 114  
 DB 426 GTCGGGTCATAGCCACAGATGGGCGCACCGCCCTTACGCACTACAGTGGTGGAC 485  
 QY 115 ASPILLEVALGYPHEVALLEUHSERALEUETHRPROTYRPHESERTPLRYSTYR 134  
 DB 486 GACACCGTGGCTTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 545  
 QY 135 SERHISARGAENHISIALASANTHRASNSERLEUASPAENAPGLVALTYRILEPRO 154  
 DB 546 AGTCATGAGCGCCACCATTCACACATCGGCTCCCTCGAGAGACGAAGTGTGTCGCC 605  
 QY 155 LYSARGLYSERLYSVALVLYLTYSERTYRLEUASNAANPROFGLYARGVAL 174  
 DB 606 AAGAAGAAGTCAGACATCAAGTGTACGGCAAGTACCTCAACACCTTTGGAGCGCAC 665  
 QY 175 PHETHRLEUVALPHEARGLEUTHRLEUGLYPHEPROLEUTHRLEUETHRASNLESER 194  
 DB 666 GTGATGTTACGGTTCACTTCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725  
 QY 195 GLYLYSLYSTYR---GLYARGPHEALASNHISAPHEASPPROMESERPROILEPHEASN 213  
 DB 726 GGGAGACCTTACGACGGGCGGCTTGCCTTGCATTTCCACCCCAACGCTCCCATACAC 785  
 QY 214 ASPARGGLVARGVALGINVALLEUUSERASPPHEGLYLEUVALVALPHERYALA 233  
 DB 786 GACCGTAGCGCTCCAGATATACATCTCCGACCTGCGCATCTCGCGCTGCTACCGGT 845  
 QY 234 ILEYSLEUVALAIALALYGLYALALATPVALLEAMETTYRVALILEPRO 253  
 DB 846 CTTCACCGCTACGCTGCTCCAGAGGTTGCTCGAATGCTCTCTTACGAGTTCCT 905  
 QY 254 VALLEUGLYVALSERVALPHEPHEVALLEUETHRTYRLEUHSISTHRISLEUSER 273  
 DB 906 CTTCGATGTGCAACGGGTTCTTATGTTATCACTTACGACACACCATCTTCC 965  
 QY 274 LEUPROHISTYRASPSETHRTGILTPASANTPILYSEGLYALALEUSERTHIRLEASP 293  
 DB 966 CTGCGCTACATATGACTGCTGAGTGGAGATGTTGAGGGAGCTTTGGCACCGTTGAC 1025  
 QY 294 ARGSPHREGLYPHELEUASARGVALPHEHISAPVALTHRHSITHRISVALLEUHS 313  
 DB 1026 AGAGACTACGGAATCTTGAACAAAGTCTTCCAAATATCAAGACACGACGTGGCGAT 1085  
 QY 314 HISLEULESERTYRILEPROHISTYRHSIALALYSGLVLAARGAPALALEYERPRO 333  
 DB 1086 CACTCTGTTTCGACACATCGCCGATTAATCAATGAGTGAAGTGAAGCGATTAAGCGC 1145  
 QY 334 VALLEUGLYGTYRITYRYSILASPARGTHRPROILEPHELYSALAMEITYRARGGLU 353  
 DB 1146 ATACTGGAGAGATATATCATGTTGATGAGACCGCGGTTAGCGAATGTGAGGAG 1205  
 QY 354 ALALYSEGLUCYSILETYRILEGLUPROASPLUASERGLUNHSYSGLYVALPHERTP 373  
 DB 1206 GCGAAGGAGGTATCTATGTGGAACCGACAGCGCAAGGTGAGAAAGGTGTTCTCG 1265  
 QY 374 TYRHS 375  
 DB 1266 TACAAAC 1271  
 RESULT 13  
 ID AAX91076 standard; cDNA; 1464 BP.  
 XX AAX91076;  
 AC AAX91076;  
 XX 15-NOV-1999 (first entry)  
 DT

DE	B. napus delta-12 fatty acid desaturase 2 (FAD2) D form encoding cDNA.
XX	
Kw	Fatty acid, delta-12 desaturase; fatty acid desaturase; FAD; enzyme;
Kw	linoleic acid; alpha-linolenic acid; mutant; nutritional value;
Kw	genetic mapping; plant breeding; ss.
XX	
OS	Brassica napus.
XX	
FH	Key
FT	location/Qualifiers
FT	130..1284
FT	/*tag= a
FT	/product= "FAD2 D-form"

PN EP945514-A1.  
 XX  
 PD 29-SEP-1999.  
 XX  
 PF 26-MAR-1998; 98EP-00302322.  
 XX  
 PR 26-MAR-1998; 98EP-00302322.  
 XX  
 PA (DUBO ) DU PONT DE MEMOURS & CO E I.  
 XX  
 XX Brogdie RM, Miao G, Debonte LR, Reiter RS, Hitz WD;  
 PI WPI; 1999-530050/45.  
 XX P-PsDB; AAY27329.  
 DR  
 XX  
 PT Altering fatty acid profiles in plant seeds, useful for changing  
 PT nutritional value of seeds.

The invention relates to a method for altering the fatty acid composition in plant seeds and comprises transforming a plant with a nucleic acid construct (I) comprising a seed-specific regulatory sequence linked to either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene encoding a protein with a mutation in a His-(Asp/Glu)-Cys-(Ala)-His amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15 FAD. Expression of this construct in plants decreases the level of activity of these enzymes in the cells of the plant i.e. the construct acts as a dominant negative. The construct comprising a mutant delta-12 gene is used to decrease the level of linoleic acid in the seeds of plants to (isobean, rapeseed, sunflower, oil palm, coconut palm, flax, caenor and peanut). Similarly a construct comprising a mutant delta-15 gene is used to decrease the levels of alpha-linolenic acid in the seeds of plants, especially Brassica carola. The new method may also be used to transform a plant with both (I) comprising DNA encoding mutant delta-12 and (I) comprising DNA encoding mutant delta-15 FAD genes, to decrease the levels of both linoleic and alpha-linolenic acid simultaneously in their seeds. These methods alter the nutritional value of the seeds of plants which have been transformed. (I) may also be used as DNA diagnostic markers in plant genetic mapping and plant breeding programs. In addition (I) may be used to isolate other related FAD genes. The present sequence represents a Brassica napus cDNA which encodes the wild type D form of microsomeal delta-12 fatty acid desaturase 2 (FAD2)

```

Db      1267 TACNAC 1272
RESULT 14
AAK91077
ID      AAK91077 standard; cDNA; 1155 BP.
XX
AC      AAK91077;
XX
DT      15-NOV-1999 (first entry)
XX
DE      B. napus mutant D-form of delta-12 FAD2 encoding cDNA.
XX
KM      Fatty acid; delta-12 desaturase; fatty acid desaturase; FAD; enzyme;
KW      linoleic acid; alpha-linolenic acid; mutant; nutritional value;
        genetic mapping; plant breeding; mutant; ss.
OS      Brassica napus.
OS      Synthetic.
XX
FH      Key
FT      CDS
        location/Qualifiers
        1..1155
        /*tag= a
        /product= "mutant FAD2 D-form"
        316
        /*tag= b
        /note= "G to A transversion mutation of the D-form"
FT      mutation
XX
XX      EP945514-A1.
XX
XX      29-SEP-1999.
XX
XX      26-MAR-1998; 98EP-00302322.
XX
XX      26-MAR-1998; 98EP-00302322.
XX
XX      26-MAR-1998; 98EP-00302322.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Brogile RM, Miao G, Debonte LR, Reiter RS, Hitz WD;
XX
XX      WPI; 1999-530050/45.
XX
XX      P-PSDB; NAY27330.
XX
XX
XX      Altering fatty acid profiles in plant seeds, useful for changing
XX      nutritional value of seeds.
XX
XX      Example 1; Page 23-25; 44p; English.
XX
XX      The invention relates to a method for altering the fatty acid composition
XX      in plant seeds and comprises transforming a plant with a nucleic acid
XX      construct (I) comprising a seed-specific regulatory sequence linked to
XX      either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene
XX      encoding a protein with a mutation in a His-(Asp/Glu)-Cys-(Gly/Ala)-His
XX      amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15
XX      FAD. Expression of this construct in plants decreases the level of
XX      activity of these enzymes in the cells of the plant i.e. the construct
XX      acts as a dominant negative. The construct comprising a mutant delta-12
XX      gene is used to decrease the level of linoleic acid in the seeds of
XX      plants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax,
XX      castor and peanut) Similarly a construct comprising a mutant delta-15
XX      gene is used to decrease the levels of alpha-linolenic acid in the seeds
XX      of plants, especially Brassica canola. The new method may also be used to
XX      transform a plant with both (I) comprising DNA encoding mutant delta-12
XX      and (I) comprising DNA encoding mutant delta-15 FAD genes, to decrease
XX      the levels of both linoleic and alpha-linolenic acid simultaneously in
XX      their seeds. These methods alter the nutritional value of the seeds of
XX      plants which have been transformed. (I) may also be used as DNA
XX      diagnostic markers in plant genetic mapping and plant breeding programs.
XX      In addition (I) may be used to isolate other related FAD genes. The
XX      present sequence represents a Brassica napus cDNA which encodes the
XX      mutant D form of microsomal delta-12 fatty acid desaturase 2 (FAD2)
XX
XX      Sequence 1155 BP; 250 A; 357 C; 273 G; 275 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 1.52e-132 Length: 1155
Score: 1313.00 Matches: 233
Percent Similarity: 76.44% Conservatve: 59
Best Local Similarity: 60.99% Mismatches: 82
Query Match: 64.14% Indels: 8
Gaps: 2
DB: 4

US-10-069-772-2 (1-377) x AAK91077 (1-1155)

QY      1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db      1 ATGGGTGACAGGTGGAAGAATGCAAGTGTCTCTCCCTCCCAAAAAGTGGAAACCGACAAAC 60
QY      16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAla 34
Db      61 ATC---AAGCGGTACCCCTGCGAGACACCGCCCTTCACTGTGGAAGAACTCAAGAAAGCA 117
QY      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAsp 54
Db      118 ATCCACCGGACACTTTTCAACAGCTCATCCCTGCTCTTCTCTCACTCATCTGCGGAC 177
QY      55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74
Db      178 ATCATCATAGGCTCTGCTCTTCTACTACGTCGACACCACTTACTTCTCTCTCTCTCTCAC 237
QY      75 ProLeuAlaTyrLeuAlaIleTyrProValTyrTyrPheCysGluAlaSerIleLeuThrGly 94
Db      238 CCTCTCTCTTACTTCTGCGCTGCTCTTCTTACTTCTGCGCTGCGCTGCTCTTACTACCGGC 297
QY      95 LeuTyrValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlyLeuIleAsp 114
Db      298 GTCTGGGTCAATGAGCCCAAGATGCGGCCACCAACCTTACAGCACTACAGTGGTGGAC 357
QY      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleTyr 134
Db      358 GACACCGTGGCGCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY      135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIlePro 154
Db      418 AGTCATGACCGCCACCACTTCCACACATGCGCTCTCTGACAGAGCAAGATGTTGTTGCC 477
QY      155 LysArgLysSerLysValIleTyrSerLysLeuLeuAsnAsnProGlyArgVal 174
Db      478 AAGAGAGATGATGACATCAAGTGTACGCAAGTACCTTCAACACCTTTGGAGCGCAC 537
QY      175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSer 194
Db      538 GTGATGTTTAACGGTTCAGTTCACTCTGCGCTGCGCTTGTACTTAGCTTCAAGCTTCG 597
QY      195 GlyLysLysTyr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
Db      598 GGGGACCTTACGACGCGGCGCTTGTGCTTGCATTTTCCACCCCAACGCGCTCCCATCTAC 657
QY      214 AspArgGluArgValGlnValIleLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233
Db      658 GACCGGAGCGCTCTCCAGATTTACATCTCCAGCGCTGACATCTCGCGCTCTGCTGAGCT 717
QY      234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrIleLeuAsnMetTyrAlaIlePro 253
Db      718 CTTCACCGCTACGGCTGCTGCTCAAGAGAGTTGCTCGATGCTGCTCTTACGAGATTCG 777
QY      254 ValLeuGlyLysValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSer 273
Db      778 CTTCATGATGTCATGAGTCTTCTTGTGTTGATCTACTTATGACGACACCACTTCCTTCC 837
QY      274 LeuProHisTyrAspSerThrGluTyrAsnTyrIleLysGlyAlaLeuSerThrIleAsp 293
Db      838 CTGCTCACTTATGACTGCTGTGATGGATTTGTAGGGAGACTTTGGCCACCGTTTAC 897
QY      294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313

```

DB 898 AGAGACTAGCATCTTGAACAAGGTCTTCCACATATCAGGACACCGACGTGGCGAT 957  
QY 314 HisLeuIleSerTyrIleProHisIleTyrHisIleValLeuArgAspAlaIleLeuPro 333  
DB 958 CACCTGTTCTGCACATGCCGATCATATCATCGATGAGGCTAACAAGCGATAAAGCCG 1017  
QY 334 ValLeuGlyValTyrTyrIleLeuSerArgThrProIlePheLeuAlaMetTyrArgGlu 353  
DB 1018 ATACTGGAGAGATATATCATCTTCATGGAGCGCGGTAAAGCCATGTGGAGGAG 1077  
QY 354 AlaLysGluCysIleTyrIleGluProAspGluAspSerGluHisIleGlyValPheThr 373  
DB 1078 CGAAGAGATGATATATGTGACACCGACGACGAGGAGAGAAAGTGTGTCTCG 1137  
QY 374 TyrHis 375  
DB 1138 TACAAC 1143  
RESULT 15  
AAT85848  
ID AAT85848 standard; DNA; 1155 BP.  
AC AAT85848;  
XX  
XX 17-OCT-2003 (revised)  
DT 14-JAN-1998 (first entry)  
XX  
XX Microsomal delta-12 fatty acid desaturase (F form) gene.  
DE  
XX  
XX Delta-12 fatty acid desaturase; oleic acid; rapeseed oil; seed oil;  
KW vegetable oil; canola; sunflower; Helianthus, ss.  
XX  
XX Brassica napus; cv Westar.  
OS  
XX  
XX WO9721340-A1.  
XX  
XX 19-JUN-1997.  
PD  
XX  
XX 13-DEC-1996; 96WO-US020090.  
PF  
XX  
XX 14-DEC-1995; 95US-00572027.  
PR  
XX  
XX (CRGI ) CARGILL INC.  
PA  
XX  
XX Debonite RL, Fan Z, Loh HT;  
PI  
XX  
XX WPI; 1997-33248/30.  
DR  
XX  
XX P-PSDB; AAM24997.  
PT  
XX  
XX Mutated Brassica or Helianthus delta-12 or -15 fatty acid desaturase  
PT genes - and plants containing them, having altered fatty acid content of  
PT seed oil, especially low saturates but high oleic acid content.  
XX  
XX  
XX Example 12; Page 71-72; 88pp; English.  
PS  
XX  
XX This DNA sequence codes for canola microsomal delta-12 fatty acid  
CC desaturase (FAD) F form (see AAM24997). Plants are claimed that contain a  
CC mutation in the delta-12 FAD gene. A preferred mutation is in the region  
CC encoding a conserved motif (see AAM24994) of delta-12 FADs. A T to A  
CC transversion at nucleotide 515 of the canola delta-12 FAD gene (see  
CC AAT85849) results in a Leu to His amino acid substitution that  
CC inactivates the enzyme and alters the fatty acid composition of the seed  
CC oil (see AAM24998). Mutant plants, preferably canola and sunflower, that  
CC contain the mutation are obtained by conventional mutagenesis of plant  
CC cells and plant regeneration. Further mutations may be introduced into  
CC another conserved motif (see AAM24996) of delta-12 FAD and also into  
CC delta-15 FAD. The mutant plants produce oils of low saturated fatty acid  
CC content (maximum 5%, with not over 2% erucic acid), high oleic acid  
CC content (at least 71%) and low linoleic acid content. The content of  
CC palmitic acid may be high or low. The vegetable oils can be used in food  
CC production and should help to reduce the incidence of coronary heart  
CC disease and atherosclerosis. (Updated on 17-OCT-2003 to standardise OS  
CC field)

XX  
SQ Sequence 1155 BP; 249 A; 357 C; 274 G; 275 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,95e-132 Length: 1155  
Score: 1312.00 Matches: 233  
Percent Similarity: 76.44% Conservative: 59  
Best Local Similarity: 60.99% Mismatches: 82  
Query Match: 64.09% Indels: 8  
DB: 2 Gaps: 4  
US-10-069-772-2 (1-377) x AAT85848 (1-1155)  
QY 1 MetGlyAlaGlyValArgMet-----SerAspProSerGluGlyLysAsn 15  
DB 1 ATGGGTGACGGTGGAGAAATGCAAGTGTCTCTCTCCATCAAAAAGTGTGAACCGACAC 60  
QY 16 IleLeuGluArgValProValAsp---ProPheThrLeuSerAspLeuIleLysAla 34  
DB 61 ATC--AAGCCGCTACCTCGGACACACCGCCTTCACTGTCGAGAACTCAAGAAACA 117  
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValAlaHisAsp 54  
DB 118 ATCCACCGCACTGTTTCAAAAGCTCGATCCCTGCTCTTCTCTACCTCATCGTGGAC 177  
QY 55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74  
DB 178 ATCATCATAGGCTCTCGCTTACTACTGCTCCACACCATCTACTCTCCCTCTCTAC 237  
QY 75 ProLeuAlaTyrLeuAlaIleProValIleTyrPheCysGluAlaSerIleLeuThrGly 94  
DB 238 CCTCTCTCTACTCTCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297  
QY 95 LeuTyrValIleGlyHisGluCysGlyHisIleAlaPheSerAspTyrGluLeuIleAsp 114  
DB 298 GTCTGGGTCAATAGCCCAAGAGTGGGGCCACACCGCTTCAAGCACTACAGAGCTGGAC 357  
QY 115 AspIleValIleGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyr 134  
DB 358 GACACCGTGGCTCTCATCTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417  
QY 135 SerHisArgAsnHisIleAlaAsnThrAsnSerLeuAspAspGluValTyrIlePro 154  
DB 418 AGTCATGACGCCACCATTCACACCTGCTCTCTCGAAGAGACAGAAAGTGTGTCTCCC 477  
QY 155 LysArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProProGlyArgVal 174  
DB 478 AAGAAGAGTCAAGCATCAAGTGAAGGCAAGTACCTCAACAACCTTTGGAGACGACC 537  
QY 175 PheThrLeuValPheArgLeuThrIleuGlyPheProLeuTyrLeuLeuThrAsnIleSer 194  
DB 538 GTGATGTTAAGGTTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 597  
QY 195 GlyLysLysTyr---GlyArgPheAlaAsnHisIlePheAspProMetSerProIlePheAsn 213  
DB 598 GGGAGACCTTACGACGGGCGCTGCTTCCATTTCCACCCCAAGCTTCCATCTACAC 657  
QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233  
DB 658 GACCGCGAGCTCTCCAAATATATCATCTCCGACGCTGCACTGCGCTGCTGCAAGGT 717  
QY 234 IleLysLeuLeuValAlaAlaLysGlyValAlaTyrValIleAsnMetTyrAlaIlePro 253  
DB 718 CTTCACCGCTACGCTGCTGCTCAAGAGTCTCTCGATGCTGCTTACGAGTTCG 777  
QY 254 ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrHisLeuSer 273  
DB 778 CTTCGATTTGATAGGCTTTTGTAGTTTGTACTTTCAGCAACGACACGATCTCTCC 837  
QY 274 LeuProHisTyrAspSerThrGluTyrPheAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293  
DB 838 CTGCTCTACTATGACTGCTGATGAGGATGTTGAGGAGACTTGGCCACCGTTAC 897



**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 15:43:26 ; Search time 77 Seconds  
(without alignments)  
2717.097 Million cell updates/sec

Title: US-10-069-772-2

Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEGNILERV.....IYIEPDDSEKHGVFWYHKM 377

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Xgapop 6.0 , Xgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh  
-Q/cgnt\_1/USFTO.spool/US10069772/runat.18062004.145513.5313/app.query.fasta.1.519  
-DB=usdb.patent.patent -OP=fastcap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0  
-LIST=45 -DOCL=1 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USFR=US10069772 @CGN 1.1 54 @runat.18062004.145513.5313 -NCPL=6 -ICPU=3  
-NO\_MMAP -IARBEQUARY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

1: /cgnt\_6/ptodata/2/ina/5A.COMB.seq:\*\n2: /cgnt\_6/ptodata/2/ina/5B.COMB.seq:\*\n3: /cgnt\_6/ptodata/2/ina/6A.COMB.seq:\*\n4: /cgnt\_6/ptodata/2/ina/6B.COMB.seq:\*\n5: /cgnt\_6/ptodata/2/ina/PTUS.COMB.seq:\*\n6: /cgnt\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	79.9	1128	4	US-09-161-994A-1
2	1592.5	77.8	1312	4	US-09-059-769-3
3	1589.5	77.7	1358	4	US-09-059-769-1
4	1578.5	77.1	1364	2	US-08-872-302-1
5	1318	64.4	1155	2	US-09-354-231B-13
6	1318	64.4	1155	4	US-09-128-602B-13
7	1318	64.4	1155	4	US-09-995-297-13
8	1317	64.3	1155	4	US-09-128-602B-9
9	1317	64.3	1155	4	US-09-354-231B-9
10	1317	64.3	1155	4	US-09-128-602B-9
11	1317	64.3	1155	4	US-09-995-297-9
12	1317	64.3	1426	4	US-09-133-962A-3

13	1313	64.1	1155	4	US-09-354-231B-11	Sequence 11, Appli
14	1313	64.1	1155	4	US-09-128-602B-11	Sequence 11, Appli
15	1313	64.1	1155	4	US-09-995-297-11	Sequence 11, Appli
16	1312	64.1	1155	3	US-08-907-608-5	Sequence 5, Appli
17	1312	64.1	1155	4	US-09-354-231B-5	Sequence 5, Appli
18	1312	64.1	1155	4	US-09-128-602B-5	Sequence 5, Appli
19	1312	64.1	1155	4	US-09-482-287-5	Sequence 5, Appli
20	1312	64.1	1155	4	US-09-966-888-5	Sequence 5, Appli
21	1312	64.1	1155	4	US-09-995-297-5	Sequence 5, Appli
22	1311	64.0	1155	2	US-08-675-650B-5	Sequence 5, Appli
23	1311	64.0	1155	4	US-09-354-231B-15	Sequence 15, Appli
24	1311	64.0	1155	4	US-09-128-602B-15	Sequence 15, Appli
25	1311	64.0	1155	4	US-09-995-297-15	Sequence 15, Appli
26	1310	64.0	1155	4	US-09-354-231B-17	Sequence 17, Appli
27	1310	64.0	1155	4	US-09-128-602B-17	Sequence 17, Appli
28	1310	64.0	1155	4	US-09-995-297-17	Sequence 17, Appli
29	1308	63.9	1155	3	US-08-907-608-3	Sequence 3, Appli
30	1308	63.9	1155	4	US-09-482-287-3	Sequence 3, Appli
31	1308	63.9	1155	4	US-09-966-888-3	Sequence 3, Appli
32	1307	63.8	1155	2	US-08-675-650B-3	Sequence 3, Appli
33	1305	63.8	1155	4	US-09-354-231B-7	Sequence 7, Appli
34	1305	63.8	1155	4	US-09-128-602B-7	Sequence 7, Appli
35	1305	63.8	1155	4	US-09-995-297-7	Sequence 7, Appli
36	1300.5	63.5	1372	4	US-09-133-962A-1	Sequence 1, Appli
37	1300.5	63.5	2973	4	US-09-133-962A-15	Sequence 15, Appli
38	1299	63.5	1155	3	US-08-907-608-1	Sequence 1, Appli
39	1299	63.5	1155	4	US-09-354-231B-1	Sequence 1, Appli
40	1299	63.5	1155	4	US-09-128-602B-1	Sequence 1, Appli
41	1299	63.5	1155	4	US-09-482-287-1	Sequence 1, Appli
42	1299	63.5	1155	4	US-09-966-888-1	Sequence 1, Appli
43	1299	63.5	1155	4	US-09-995-297-1	Sequence 1, Appli
44	1295	63.3	1155	4	US-09-354-231B-3	Sequence 3, Appli
45	1295	63.3	1155	4	US-09-128-602B-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-161-994A-1  
Sequence 1, Application US/09161994A  
Patent No. 6333448  
GENERAL INFORMATION:  
APPLICANT: BAFOR, Maureen  
APPLICANT: BANAS, Antoni  
APPLICANT: DAHLQVIST, Anders  
APPLICANT: GUMMELSON, Per-Olov  
APPLICANT: LEE, Michael  
APPLICANT: SJODAL, Stefan  
APPLICANT: STYRNE, Sten  
APPLICANT: LENMAN, Marie  
TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF  
FILE REFERENCE: BAFOR-1  
CURRENT APPLICATION NUMBER: US/09/161.994A  
CURRENT FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 9601236.4  
PRIOR FILING DATE: 1996-03-29  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 1128  
TYPE: DNA  
ORGANISM: Crepis alpina  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1125)  
US-09-161-994A-1  
Alignment Scores:  
Pred. No.: 2.27e-195  
Score: 1636.00  
Percent Similarity: 87.50%  
Best Local Similarity: 76.86%  
Query Match: 79.92%  
Length: 1128  
Matches: 289  
Conservative: 40  
Mismatch: 45  
Indels: 2

DB: 4 Gaps: 1

US-10-069-772-2 (1-377) x US-09-161-994A-1 (1-1128)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAlaIleLeuGluArgVal 20  
 DB 1 ATGGGTGGCGGGGGCGGT-----GCTGGACCTTGGCAAAACCCCTCAAGAACGTCGTC 54

QY 21 ProValAspProPheThrLeuSerAspLeuGlyValAlaIleProThrHisCysPhe 40  
 DB 55 TCAGTTGATCCACCCCTTACCGGTGATGATCTCAAGCAAGAAATCCCTCCCATTTGCTTC 114

QY 41 GluArgSerValIleArgSerSerTyrTyrValAlaHisAspLeuIleValAlaTyrVal 60  
 DB 115 AAGGATCTGTAATCCGTTCTTACTACATAGTCCAGATGCTATTAATGCGCTTACATC 174

QY 61 PheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeuAla 80  
 DB 175 TTCTACTCTCTTGGCGCAAAATACATTCGATTCCTCCCTGCGCTTACCTGCTGCT 234

QY 81 TrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGlyHis 100  
 DB 235 TGGCCCTTACTGCTTGTGTCAGCTAGCATCCACCGGCTTATGGGTATCGGTGTCAC 294

QY 101 GluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPheVal 120  
 DB 295 GAATGCGGTGACCATGCTTACGACATCACAGTGGGTGTCAGACATGTTGGGCTTACATC 354

QY 121 LeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleTyrSerHisArgAsnHisHis 140  
 DB 355 CTCACCTGTTTCTATGATACCCCGTATTTCTCTGAAATATACAGCCACCGGACCAACAT 414

QY 141 AlaAsnThrAsnSerLeuAspAspAspGluValTyrIleProLysArgLysSerLysVal 160  
 DB 415 GCCAACACAAATGCTGCTGACACAGATGAAGTTTATCCCAAAAGAACGCCCAAGC 474

QY 161 LysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180  
 DB 475 GCGCTTATCTAATAAGTCTCAACACCCACCGACGCTGATGATTATGTCATCACCC 534

QY 181 LeuThrLeuGlyPhePheProLeuTyrLeuLeuThrAsnIleSerGlyLysLysTyrGlyArg 200  
 DB 535 TTACACCTTAGGCTTCTCTATACCTCTTACCAATATTTCCGGCAAGAAATGATAAGG 594

QY 201 PheAlaAsnHisAspAspProMetSerProIlePheAsnAspGluArgValGlnVal 220  
 DB 595 TTGGCAACCAATTTGACCCCATGATCGAATTTCAAAAGCGGAGCGGTTCAAGTTC 654

QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAlaVal 240  
 DB 655 TTGCTATCGGATCTTGGGCTTCTTCTGCTGCTTTCACGATTAACCTTGGCGGTACACG 714

QY 241 LysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe 260  
 DB 715 AAAGGCGCGGCTGGGTACGTCATTAAGGAATTCAGATTGAGGGGTGTTATCTTT 774

QY 261 PheValIleLeuThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSerThr 280  
 DB 775 TTTCATATCATCATCTTATGACCAACCATCTGCTGGTCCCATTAATGATTCATCT 834

QY 281 GluTrpAsnTrpIleLysGlyValAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300  
 DB 835 GAATGGAATGCTGACAGGGGCTTTGTCACAAATCGATAGGACCTTGGGTCTCTGAT 894

QY 301 ArgValIlePheHisAspValThrHisThrHisValLeuHisHisIleLeuIleSerTyrIlePro 320  
 DB 895 AGTGTGCTCATGATGTTTACACACTCACTCATGCTTATCTTTTTCATACATTTCCA 954

QY 321 HisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValLeuGlyGluTyrTyrLys 340  
 DB 955 CACTATCATGCGAAGAGCAAGGATGATCAACACAGCTTTGGGACCTTTATATAG 1014

QY 341 IleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGlyLysIleTyrIle 360

DB 1015 ATCGATAGACTCCCAATCTGAAAGCAATGTGAGAGGCCCAAGAAATGATCTTCATC 1074

QY 361 GluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLys 376  
 DB 1075 GAGCTGAAAAGGATGAGGATCCAGGCTGTATATGTCATTAATAA 1122

RESULT 2

US-09-059-769-3

Sequence 3, Application US/09059769

Patent No. 6329518

GENERAL INFORMATION:

APPLICANT: Green, Allan

APPLICANT: Singh, Surinder

APPLICANT: Lemman, Marcit

APPLICANT: Stymme, Sten

TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses

TITLE OF INVENTION: Therefore

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,769

FILING DATE: April 14, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06223

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06226

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043706

FILING DATE: 16-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/050403

FILING DATE: 20-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Fetber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1312 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: *Crepis* sp.

FEATURE:

NAME/KEY: CDS

LOCATION: 26..1147

US-09-059-769-3

Alignment Scores:

Pred. No.: 8.46e-190 Length: 1312

Score: 1592.50 Matches: 285

Percent Similarity: 86.24% Conservative: 41

Best Local Similarity: 75.40% Mismatches: 47

Query Match: 77.80% Indels: 5

DB: 4 Gaps: 3

US-10-069-772-2 (1-377) x US-09-059-769-3 (1-1312)

Qy 1 MetGlyAGIYGLYArgMetSerAspProSerGIUGLYLysAsnIleLeuGIUArgVal 20  
 Db 26 ATGGGTGCGGGGGCGGT-----GGTCGGACATCGGAAAAGTCGGTACATGAGAGTGTTC 79

Qy 21 ProValAspPro---ProPheThrLeuSerAspLeuLysValIleProThrHisCys 39  
 Db 80 TCAGTGTATCCAGTAACCTTCTCACTGAGTATTTGAAAGCAAGCAATCCCTCCACATTTGC 139

Qy 40 PheGIUArgSerValIleArgSerSerTYrTYrValValHisAspLeuIleValAlaTYr 59  
 Db 140 TTCGAGCATGTGTCATCCGTCATCTTATTAAGTTGTCAGGATCTCATATATGCTTAC 199

Qy 60 ValPheTYrTYrLeuAlaAsnThrTYrIleProLeuIleProThrProLeuAlaTYrLeu 79  
 Db 200 ATCTTCACTTCCTTCGCAACACATATATCCCTATCCCTCCATCCCTGACCTTACTTA 259

Qy 80 AlaTPProValTYrTYrPheCysGlnAlaSerIleLeuThrGlyLeuTYrValIleGly 99  
 Db 260 GCTTGCGCGCTTACTGCTTCTGTACAGTACGCTCTCACTGAGTTATGATCTCGGC 319

Qy 100 HisGlyCysGlyHisHisAlaPheSerAspTYrGlnLeuIleAspAspIleValGlyPhe 119  
 Db 320 CATGAAATGTGTACATCATGCTATAGCAATACATGAGGTGACGACATGTTGGGCTTC 379

Qy 120 ValLeuHisSerAlaLeuLeuThrProTYrPheSerTYrTYrSerHisArgAsnHis 139  
 Db 380 ATCATTCATTCATTTCTCTCAACCCGATATTTCTTGGAAATACAGTACCGGATAC 439

Qy 140 HisAlaAsnThrAsnSerLeuAspAsnAspGIUValTYrIleProLysArgLysSerLys 159  
 Db 440 CATTCACACACAAAGTTCATGATACATGATGATTTTCATTTCCAAAAGCAAGTCCAAA 499

Qy 160 ValLysIleTYrSerLysLeuLeuAsnAsnProProGIUArgValPheThrLeuValPhe 179  
 Db 500 CTCAGGCTATCTTAACCTTCTTAACACACCTGTCGAGCTGTGGTTTGGTTATC 559

Qy 180 ArgLeuThrLeuGlyPheProLeuTYrLeuLeuThrAsnIleSerGIULysLysTYrGly 199  
 Db 560 ATGTTCACCTTACGATTTCTTTTAACTTCTTGAACAAATATTTCCGGACAGAAATACAT 619

Qy 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219  
 Db 620 AGGTTTGCACACACTTCGACCCCATGAGTCCAAATTTCCAAACGAGGAGGTTTACG 679

Qy 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTYrAlaIleLysLeuLeuValAla 239  
 Db 680 GTCTTCCTTTCGATCTTGTCTTCTTCTGTTTATGGAATTTAAAGTTGCTGTTACCA 739

Qy 240 AlaLysGlyAlaAlaTPValIleAsnMetTYrAlaIleProValLeuGlyValSerVal 259  
 Db 740 AATAAAGAGCTGCTGGTGGTGCATGATGAGTTCGCGTCTGAGGAGTATTTAC 799

Qy 260 PhePheValLeuIleThrTYrLeuHisHisThrHisLeuSerLeuProHisTYrAspSer 279  
 Db 800 TTTTTCATGTATCATCTTCTTACACACACCTCATCGTGTGCTTCATTATGATTTCA 859

Qy 280 ThrGIUTrpAsnTPTrIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299  
 Db 860 ACTGATATGAGTATGAGAGGGGCTTTGTTCAGCAATCGATAGGACTTTGGTCTCTG 919

Qy 300 AsnArgValPheHisAspValThrHisValLeuHisHisLeuIleSerTYrIle 319  
 Db 920 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979

Qy 320 ProHisTYrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTYrTYr 339  
 Db 980 CCACATCATCATGACAAAGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 1039

Qy 340 LysIleAspArgThrProIlePheLysValMetTYrArgGluAlaLysGlyCysIleTYr 359

Db 1040 ATGATTCGATAGACTCCCAATTTTAAAGCAATGTGAGAGAGGCGGCAATGATGTAC 1099

Qy 360 IleGIUProAspGIUAspSerGIUHisIleGlyValPheTPTYrHisIleYMet 377  
 Db 1100 ATCGAGCT-----GATGCAAGCTCAAGAGTGTATTGTGATATCAATAATG 1147

RESULT 3

US-09-059-769-1

Sequence 1, Application US/09059769

Patent No. 6329518

GENERAL INFORMATION:

APPLICANT: Green, Allan

APPLICANT: Singh, Surinder

APPLICANT: Lemman, Maric

APPLICANT: Stymne, Sten

TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,769

FILING DATE: April 14, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06223

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06226

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043706

FILING DATE: 16-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/050403

FILING DATE: 20-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Feider, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1358 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 30..1151

US-09-059-769-1

Alignment Scores:

Pred. No.: 2,13e-189

Score: 1589.50

Percent Similarity: 85.98%

Best Local Similarity: 75.40%

Query Match: 77.65%

DB: 4

Length: 1358

Matches: 285

Conservative: 40

Mismatches: 48

Indels: 5

Gaps: 3



Db	337	CGTCCTACCTTACTTGAAGCATGGCCTGTTTACTGATGTTTGGCAATCTTGATCCGACT	396
Qy	94	GLYLEUTHRPVALILEGLYHISGLUCYSEGLYHISGLAPHESEASPTRYGLINLEULE	113
Db	397	GGTTTATGGGCATATGGCCATGAATGGCCATCATGCTTAAAGAGAACCAAGGGGTT	456
Qy	114	ASPAPRIEVALGLYPHEVALLEUTHISESERALALEUTHPROTYRPHSEERTPLYS	133
Db	457	GAATACACCGGTGGATCATCTCCATATCTCTTCTTCTACACCTTACTTCTTTGGAAA	516
Qy	134	TYRSEERHISARGASNHISHSIALAANTHRANSEERLEUASPASAPGLUVALTYRILE	153
Db	517	TACAGCCATCGAAGAACCATCCCAACAGATTTCACTCGAAGAACGAGAGGTTTACAT	576
Qy	154	PROLYBALGLYSERLYSEVALYSLILETYRSEER-----LYSELEULEUASNAENPRO	171
Db	577	CTTAAAGCCAAAGTCCACAGCTCAGAAATTACTCAATTTCAATTTCTTGACAACACCCCT	636
Qy	172	GLYARGVALPHETHRLEUVALPHEARGLEUTHLEUGLYPHEPROLEUTHYLEUTHR	191
Db	637	GGTCGAATCTTCATTTTGCTTATCATAGTTGACCTTGCGGCTTTCCTTTAATCTCTTGACC	696
Qy	192	ASNIIESEERGLYLYSELYSTYRGLYARGPHEALANENHISPHESPROMCESERPROILE	211
Db	697	AATATTTGAGCGAAGAAATACCAAGGTTTGCCAAACCACTTGATCCGTGAGCCCATC	756
Qy	212	PHENANAPARGLUARGVALGINVALLEULEUSEERASPHEGLYLEULEUHALVALPHE	231
Db	757	TTTCAGTGGCGGTAACGAAATCGAATCGAGTCGCTATCGAATGTCGCTCATCTCGTGT	816
Qy	232	TYRALAILELYSELEULEUVALAALALAYSGLYAALATRPVALILEASMETTYRALA	251
Db	817	TACGGGCTTAAGTTTCTGTAGCGAAAAAGGGTTCCGTTGGGTAAAGGCATGTACGGA	876
Qy	252	ILEPROVALILEUGLYVALISERVALPHEPHEVALLEULEUTHTYRLEUTHISHTHRHS	271
Db	877	GCCCAAGTGGTTGGGCTGAATCCCTTCAATAATATGATCATCTTAATCTCCACCAACCCAT	936
Qy	272	LEUSERLEUPROHISTRYRASPSEERTHRGUTRPAENTRPILEYEGLYVALAUSEERTHR	291
Db	937	CTGTCTTGCGCCTCATTTACGATTCGACCGAATGGAATCGGATCAAGAGAGCCTTGACTCA	996
Qy	292	ILEASPARGAPRHEGLYPHELEUASNAARGVALPHEHISAPRVALTHRHSITHRHSVAL	311
Db	997	ATCGATAGAGATTCGCTCTCCGTGAATGGGGTTCCATGACGTCACTCACACACACGCTG	1056
Qy	312	LEUTHSHISLEULIESEERTYRILEPROHISTRYRHSIALAYSGLYAALARGSPALALE	331
Db	1057	TTTGCAATCATTTGTTCCCGTACATTCACATTTATCATGCAAGAGAGCGAGCCACCAATTA	1116
Qy	332	LYSPROVALILEUGLYGLUTYRTRYRHSILEASPARGTHRPROILEPHELYSALMETTYR	351
Db	1117	AAGCCGGTGTAGGGGAGATCCGATGATGATGATGATGATGATGATGATGATGATGATGATG	1176
Qy	352	ARGGLUALYVGLUCYSLILETYRILEGLUPROASPGLUASPSEERGLUHSILEYSGLYVAL	371
Db	1177	AGAGGGGGAAGGATGATCATTCATCGAGCCAGATGAAGTAAGTAAGCAACAAAGGTGTA	1236
Qy	372	PHERTPTPTYRHSILEYSEMET 377	
Db	1237	TATGTGTACCATTAATAATG 1254	

RESULT 5  
US-08-675-650B-1  
; Sequence 1, Application US/08675650B  
; Patent No. 5850026  
; GENERAL INFORMATION:  
; APPLICANT: DeBonte, L. et al.  
; TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND  
; TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C., P.A.

[illegible]

```

QY 136 HisArgAsnHisAlaAsnThrAsnSerLeuAspAspGluValTyrIleProlys 155
Db 421 CATGAGCGCCACACATTCACACTGGCTCCCTCGAGAGACGAAAGTGTGTGCCCAAG 480
QY 156 ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnProGlyArgValPhe 175
Db 481 AAGAGTCAGACATCACTGGACCGCAAGTACCTCAACACCTTTGGAGCGACCGTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db 541 ATGTTAAGCTTCACTGCTCCGCTGGCGCTGTGCTTGAAGCTTCAAGCTCCGGA 600
QY 196 LysLysTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db 601 AGACCTTACGACGGGGCTTGGCTTGCATTTCCACCCCAAGCTCCCATCACAACGAC 660
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234
Db 661 CGCGAGCTCTCCAGATATACATCTCCGACGCTGGCATCTTCGCTGCTACCGGTTC 720
QY 235 LysLeuLeuValAlaAlaLysGlyValAlaTyrValIleAsnMetTyrAlaIleProVal 254
Db 721 TTCCTTACGGCGCGCGCGAGAGTGGCTTGCATGTCTGCTTACGAGTCCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274
Db 781 CTGATGTCAATGCTTCTCGTGTGATCACTTACCTTGCAGACACCGCATCTCCCTG 840
QY 275 ProHisTyrAspSerThrGluTyrAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
Db 841 CCTACTACGATTCCTCGAGTGGAGTGGTGGAGGAGCTTTGGTACCGTTACGACA 900
QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
Db 901 GACTACGGAATCTTAAACAAGTCTTCCACATATATACGACACCGACGTGGCGATCAT 960
QY 315 LeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProVal 334
Db 961 CTGTTCTCAGCATGCCCATATATCAGCGATGAGTACCAAGCGCATTAAGCGATA 1020
QY 335 LeuGlyGlyTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla 354
Db 1021 CTGGAGAGATATATCAGTTCGATGGAGCGCGGTGGTAAAGCATGTGGAGGAGCG 1080
QY 355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrPyr 374
Db 1081 AAGAGTGTATCTATGTGAACCGACGACGCAAGTGAAGAAGAAGTGTCTGTGTAAC 1140
QY 375 His 375
Db 1141 AAC 1143

```

```

; NAME/KEY: CDS
; LOCATION: (1) ... (1152)
US-09-354-231B-13

Alignment Scores:
Pred. No.: 2.03e-155 Length: 1155
Score: 1318.00 Matches: 233
Percent Similarity: 77.17% Conservative: 61
Best Local Similarity: 61.15% Mismatches: 81
Query Match: 64.39% Indels: 6
DB: 4 Gaps: 4

US-10-069-772-2 (1-377) x US-09-354-231B-13 (1-1155)
QY 1 MetGlyAlaGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
Db 1 ATGGGTGAGGTGGAGAAATGCAAGTGTCTCTCCCTCCCAAGAAAGTGAACCAACACACC 60
QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAlaIle 35
Db 61 ATCAAGCGCGTACCTCGGAGACACCGCTTCACTGCGAGAACTCAAGAAAGCAATC 120
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisLeu 55
Db 121 CACCGCATCTTTCAACACGCTCATCCCTGCTCTTCTCTACTCATCTGAGCATC 180
QY 56 IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75
Db 181 ATCATAGCTCTGCTTCTTACTACGTCGACCACTTACTTCCCTCCCTCACCT 240
QY 76 LeuAlaTyrLeuAlaTyrProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95
Db 241 CTCTCTTACTTCCGCTGCTCTCTACTACGTGGCTCCCAAGGAGTGTCTTAAACGGCGTC 300
QY 96 TrpValIleGlyHisLysGlyCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAsp 115
Db 301 TGGGTATAGCCCAACGAGTGGCGCACCAACCTTACAGCATACACAGTGGCTTGAACAC 360
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer 135
Db 361 ACCGTGGTCTCATCTTCCATCTCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspGluValTyrIleProlys 155
Db 421 CATGAGCGCCACACATTCACACTGGCTCCCTCGAGAGACGAAAGTGTGTGCCCAAG 480
QY 156 ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnProGlyArgValPhe 175
Db 481 AAGAGTCAGACATCACTGGACCGCAAGTACCTCAACACCTTTGGAGCGACCGTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db 541 ATGTTAAGCTTCACTGCTCCGCTGGCGCTGTGCTTGAAGCTTCAAGCTCCGGA 600
QY 196 LysLysTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db 601 AGACCTTACGACGGGGCTTGGCTTGCATTTCCACCCCAAGCTCCCATCACAACGAC 660
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234
Db 661 CGCGAGCTCTCCAGATATACATCTCCGACGCTGGCATCTTCGCTGCTACGAGTCCGCTC 720
QY 235 LysLeuLeuValAlaAlaLysGlyValAlaTyrValIleAsnMetTyrAlaIleProVal 254
Db 721 TTCCTTACGGCGCGCGCGAGAGTGGCTTGCATGTCTGCTTACGAGTCCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274
Db 781 CTGATGTCAATGCTTCTCGTGTGATCACTTACCTTGCAGACACCGCATCTCCCTG 840
QY 275 ProHisTyrAspSerThrGluTyrAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
Db 841 CCTACTACGATTCCTCGAGTGGAGTGGTGGAGGAGCTTTGGCTACCGCTTACACAGA 900

```

Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314  
 Db 901 GACTACGGAATCTTGAACAAGTCTTCCACAATATATACGACACGACGATGGCGCATCAT 960  
 Qy 315 LeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProVal 334  
 Db 961 CTGTCTCCACAGATCCCGCATTTATCAACCGATGAGACCTACCAAGCGATTAAGCCGATA 1020  
 Qy 335 LeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla 354  
 Db 1021 CTGGAGAGATATATACGATTTGATGAGACGCGGATGTTAAAGCGATGAGAGGAGCG 1080  
 Qy 355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrPyr 374  
 Db 1081 AAGAGGTATCTATGTGTAACCGGACAGGACGATGAGAAAGAGTGTCTCGTAC 1140  
 Qy 375 His 375  
 Db 1141 AAC 1143

RESULT 7

US-09-128-602B-13  
 ; Sequence 13, Application US/09128602B  
 ; Patent No. 6414223  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kodali, Dharna  
 ; APPLICANT: Fan, Zhong  
 ; APPLICANT: Debonite, Lorin R.  
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
 ; FILE REFERENCE: 07148-07201  
 ; CURRENT APPLICATION NUMBER: US/09/128,602B  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SOFTWARE: FASTSEQ For Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 1155  
 ; TYPE: DNA  
 ; ORGANISM: Brassica napus  
 ; NAME/KEY: CDS  
 ; LOCATION: (1) ... (1152)  
 ; US-09-128-602B-13

Alignment Scores:

Pred. No.: 2,03e-155 Length: 1155  
 Score: 1318.00 Matches: 233  
 Percent Similarity: 77.17% Conservative: 61  
 Best Local Similarity: 61.15% Mismatches: 81  
 Query Match: 64.39% Indels: 6  
 Gaps: 4

US-10-069-772-2 (1-377) x US-09-128-602B-13 (1-1155)

Qy 1 MetGlyAlaGlyValArgMet-----SerAspProSerGluGlyLys-----AsnIle 16  
 Db 1 ATGGGTGACAGGTGGAGAGATCAAGTGTCTCTCCCTCCAAAGAACTCGAAACCGACACC 60  
 Qy 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAlaIle 35  
 Db 61 ATCAAGGCGGTACCTCGGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCATC 120  
 Qy 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55  
 Db 121 CCACCGCACCTGTTTCAACGCTCATCCCTCTTCTCTCTCACTCATCTGGGACATC 180  
 Qy 115ValAlaTyrValPheTyrTyrLeuAlaAsnHisThrIleProLeuIleProThrPro 75  
 Db 181 ATCAATAGCTCTCTGCTTCTACTACGCGCACCACTTACCTCCCTCTCCCTACCCCT 240  
 Qy 76 LeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95

Db 241 CTCTCCATCTTGGCGCTCTCTACTAGGCGCTGCCAAGGAGTGGCTTCAACCGGCGTC 300  
 Qy 96 TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGluLeuIleAspAsp 115  
 Db 301 TGGGTATAGCCCAAGATGCGGCGGACCAACCGCTTACAGCATACCAATGAGCTTACACAC 360  
 Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrLysTyrSer 135  
 Db 361 ACCGTGGTCACTTCTTCACT 420  
 Qy 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLys 155  
 Db 421 CATGACCGCACCAATTCACACATGCGCTCTCTCGACAGACAGAGTGTGTGCCCCAAG 480  
 Qy 156 ArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProProGlyArgValPhe 175  
 Db 481 AAGAGTACATCACTACGTGTGAGGACAGTAACTCAACAACTTTGGAGACGACGCTG 540  
 Qy 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195  
 Db 541 ATGTTAAGGTTCACTTCACTCTCGGCTGCGGCTGTGTACTTACCTTCAAGCTTCCGGA 600  
 Qy 196 LysLysTyr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214  
 Db 601 AGACCTTACAGACGCGCGCTTCCATTTCCACCCCAACGCTCCCATCTTACAAACAC 660  
 Qy 215 ArgGluArgValGluValLeuLeuSerAspPheGlyLeuAlaValPheTyrAlaIle 234  
 Db 661 CGCAGGCTCTCCAGATATACATCTCCAGCCTGCGATCTTGGCGGTGCTTACGCTTC 720  
 Qy 235 LysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProVal 254  
 Db 721 TTCGGTTAAGCGCGCGGAGAGAGTGGCCCGATGATGCTGCTTACAGAGTCCCGCTT 780  
 Qy 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274  
 Db 781 CTGATGTCAATAGGTTCTCTGTTGATCACTTATGTCGACACACGATCTTCCCTG 840  
 Qy 275 ProHisTyrAspSerThrGluTyrAsnThrIleLysGlyAlaLeuSerThrIleAspArg 294  
 Db 841 CCTACCTACAGATGTCGAGATGAGATGTTGAGGAGGCTTGGCTTACCGTTGACACA 900  
 Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314  
 Db 901 GACTACGGAATCTTGAACAAGTCTTCCACAATATATACGACACGACGATGGCGCATCAT 960  
 Qy 315 LeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProVal 334  
 Db 961 CTGTCTCCACAGATCCCGCATTTATCAACCGATGAGACCTACCAAGCGATTAAGCCGATA 1020  
 Qy 335 LeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla 354  
 Db 1021 CTGGAGAGATATATACGATTTGATGAGACGCGGATGTTAAAGCGATGAGAGGAGCG 1080  
 Qy 355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrPyr 374  
 Db 1081 AAGAGGTATCTATGTGTAACCGGACAGGACGATGAGAAAGAGTGTCTCGTAC 1140  
 Qy 375 His 375  
 Db 1141 AAC 1143

RESULT 8

US-09-995-297-13  
 ; Sequence 13, Application US/09995297  
 ; Patent No. 6649782  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kodali, Dharna  
 ; APPLICANT: Fan, Zhong  
 ; APPLICANT: Debonite, Lorin R.  
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
 ; FILE REFERENCE: 07148-072002

```

; CURRENT APPLICATION NUMBER: US/09/995,297
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
; US-09-995-297-13

Alignment Scores:
Pred. No.: 2,036-155          Length: 1155
Score: 1318.00              Matches: 233
Percent Similarity: 77.17%    Conservative: 61
Best Local Similarity: 61.15% Mismatches: 81
Query Match: 64.39%          Indels: 6
DB: 4                        Gaps: 4

US-10-069-772-2 (1-377) x US-09-995-297-13 (1-1155)

QY 1 MetGlyAlaGlyYArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
DB 1 ATGGGTGAGGTGGAGAAATGCAAGTGTCTCTCCCTCCAGAAAGTCTGAACCGACACC 60
QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 35
DB 61 ATCAAGCGCGTACCTGGCAGACACCGCCCTTCACTGTGGAGAACTCAAGAAACCAATC 120
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerYrYrValValHisAspLeu 55
DB 121 CCACCGCACTGTTTCAAAGCTCAGATCCCTGCTCTTCTCTACTACTGAGACATC 180
QY 56 IleValAlaYrValPheYrYrLeuAlaAsnThrYrIleProLeuIleProThrPro 75
DB 181 ATCATAGCTCTGCTGCTTACTAGCTGCGCACCACTACTTCCCTCCTCCTCACCCT 240
QY 76 LeuAlaYrLeuAlaIleProValYrYrPheGlyGlnAlaSerIleLeuThrGlyLeu 95
DB 241 CTCTCTCTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 96 TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspYrYrGlnLeuIleAsp 115
DB 301 TGGGTCAATAGCCCAAGTGGCGGCAACGCGCTTCAAGGACTTACCAAGTGGCTTAC 360
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProYrYrPheSerYrYrSer 135
DB 361 ACCGTGGGTGCTCATCTTCCACTCTTCCCTGCTGCTTCTTCTTCTTCTTCTTCTT 420
QY 136 HisAlaGlnHisHisAlaAsnThrAsnSerLeuAspAsnAspGlnValYrIlePro 155
DB 421 CATCGACCGCCACCATCTCAACACTGCTCCCTCCGAGAGACGAAGTGTGTCTCCCA 480
QY 156 ArgLysSerLysValIleYrYrSerLysLeuAlaAsnProProGlyArgValPhe 175
DB 481 AAGAAAGTCAAGATCAAGTGGTACCGCAAGTACTTCAACACCTTGGGACGCACTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuYrYrLeuLeuThrAsnIle 195
DB 541 ATGTTAAGCGTTCAGTCTGCTGCGGCTGCGCTGTGTACTTACCTTCAAGCTTCG 600
QY 196 LysLysYrYr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 214
DB 601 AAGACCTTACGAGCGGCGCTTCCCTTGCATTTCCACCCCAAGCTCCATCTACACG 660
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheYrVal 234
DB 661 CGCGAGCGTCTCAAGATATACATCTCCGAGCGCTGGCATCTCTGCGGTCTGCTAC 720
```

```

QY 235 LysLeuLeuValAlaAlaLysGlyAlaAlaIleProValIleAsnMetYrAlaIleProVal 254
DB 721 TTCCGTTCAGCGCCGCGCGAGAGAGTGGCTCGATGATCTCTCTTCTTACGAGTCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrYrYrLeuHisHisThrHisLeuSerLeu 274
DB 781 CTGATTTGCAATGGTCTTCTGCTGTGTATCACTTACTTGGCAGACACCACTCTCCCTG 840
QY 275 ProHisYrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
DB 841 CTTCACTACGATTTGCTCGAGTGGATGTTGTGAGGGAGCTTGTGCTACCGTTACAGAGA 900
QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
DB 901 GACTACGGAATCTTGAAACAGGTCTTCCACATATTTACGACACCGACAGTGGCGCATAT 960
QY 315 LeuIleSerYrIleProHisIleYrHisAlaLysGluAlaArgAspAlaIleAspProVal 334
DB 961 CTGTTCTCAGAGTCCCGCATTTATACCGCATGAGACCTACCAAGCCATTAAGCCGAT 1020
QY 335 LeuGlyGluYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 354
DB 1021 CTGGAGAGTATTTATCAGTTGATGAGACGCGCGGTGTAAAGCGATGTGAGGAGGCG 1080
QY 355 LysGluCysIleYrYrIleGluProAspGluAspSerGluHisLysGlyValPheTrpYr 374
DB 1081 AAGAGTGTATCTATGTGAACCGGACAGGACGAGTGAAGAAAGTGTGTCTGTATC 1140
QY 375 His 375
DB 1141 AAC 1143

RESULT 9
US-09-354-231B-9
; Sequence 9, Application US/09354231B
; Patent No. 6342658
; GENERAL INFORMATION:
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063002
; CURRENT APPLICATION NUMBER: US/09/354,231B
; CURRENT FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
; US-09-354-231B-9

Alignment Scores:
Pred. No.: 2,716-155          Length: 1155
Score: 1317.00              Matches: 234
Percent Similarity: 76.44%    Conservative: 58
Best Local Similarity: 61.26% Mismatches: 82
Query Match: 64.34%          Indels: 8
DB: 4                        Gaps: 4

US-10-069-772-2 (1-377) x US-09-354-231B-9 (1-1155)

QY 1 MetGlyAlaGlyYArgMet-----SerAspProSerGluGlyLysAsn 15
DB 1 ATGGGTGAGGTGGAGAAATGCAAGTGTCTCTCCCTCCAAAAGTCTGAACCGACAAAC 60
QY 16 IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 34
DB 61 ATC---AAGCGGTACCTTGGAGACACCGCCCTTCACTGTGAGAACTCAAGAAAGCA 117
```



OY	35	IIlePrOthHisCyePheleuIuArgSerValIIleArgSerSerTyrrTyrrValValHisAsp	54
Db	118	ATCCACCGCAGCTGTTTCAAAGCGCTGCATCCCTCGCTCTTCTCTCACTCATCTGGAGAC	177
OY	55	LeuIIleValAlaTyrrValPheTyrrTyrrLeuAlaAsnThrTyrrIIleProleuIIleProthr	74
Db	178	ATCATCATATGCTCTCCGCTTCTACTATACGTCGCCACACACTTACTCTCTCCCTCCAC	237
OY	75	ProIleuAlaTyrrLeuAlaTrpProValTyrrTrpPheCysGlnAlaSerIIleLeuThrgly	94
Db	238	CCTCTCTCTACTTGGCTGGCCCTCTCTACTGGGCGTCGACAGGCGTCGCGCTTACCGG	297
OY	95	LeuTrpValIIleGlyHisGluCysGlyHisIleAlaPheSerAspTyrrGlnLeuIIleAsp	114
Db	298	GCTCGGGCATGCGCCACACAGTGGCGGCCACACGCTTCAGGCATACCAAGTGGCTGGAC	357
OY	115	AspIIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrrPheSerTrpIleTyrr	134
Db	358	GACACCGTCGGGCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	417
OY	135	SerHisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnAspGlnValTyrrIIlePro	154
Db	418	AGTATCGACCGCCACCATTCACAACCTGGCTCCCTGAGAGAGACGAAGTGTGTGCC	477
OY	155	LybArgIleSerIleValIleTyrrSerIleValLeuAsnAsnProGlyArgVal	174
Db	478	AAGAAGAAAGTCAGATCATAGGTGTAACGCAAGTACCTCAACAACCTTTGGAGCCGAC	537
OY	175	PheThrIleuValPheArgIleuThrIleuGlyPheProLeuTyrrIleuThrIleuThrIleuSer	194
Db	538	GTGATGTTTACGGTTCAGTTCATCTCGGCTGGCCCTTGTACTTACCTTCAACGCTCG	597
OY	195	GlyIleValTyrr--GlyArgPheAlaAsnHisPheAspProMetSerProIIlePheAsn	213
Db	598	GGGAGACCTTACGAGCGGGCGCTTCGGTCCATTTCCACCCACAGCTCCCATCTAACAC	657
OY	214	AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrrAla	233
Db	658	GACCGTCGAGCGCTCCAGATATACATCTCCGACGCTGGCATCTCCGCTGCTGCTACGGT	717
OY	234	IleIleValLeuLeuValAlaAlaIleGlyAlaAlaTrpValIIleAsnMetTyrrAlaIIlePro	253
Db	718	CTTACCGGTACGTCGCTGTCCAGAGAGTGGCTCGATGGTCTGCTTACGAGAGTCTCT	777
OY	254	ValIleuGlyValSerValPhePheValIleuIleThrTyrrLeuHisIleThrHisIleuSer	273
Db	778	CTTCGATGTTGCAACGGGTTCTTAATTTGATTCACACTTACTTGCAGACACGCACTCTCC	837
OY	274	LeuProHisTyrrAspSerThrGluTrpAsnTrpIleIleGlyAlaLeuSerThrIleAsp	293
Db	838	CTGGCTCACTATGACTCGTCTGAGTGGGATGTGGTGGAGGACTTTGGCCACCGTTGAC	897
OY	294	ArgArgPheGlyPheLeuAsnArgValPheHisAspValThrHisValValLeuHis	313
Db	898	AGAGACTACGGAACTTGAAACAAGGCTTCCACATATACACGACACGCGAGTGGCGCAT	957
OY	314	HisIleuIleSerTyrrIIleProHisTyrrHisAlaIleValGluAlaArgAspAlaIleIlePro	333
Db	958	CACCTGTTCTGCACCACTCCGCAATTTACATGCGATGAAAGCTACGAAAGCGAATAAGCCG	1011
OY	334	ValIleuGlyGluTyrrTyrrIleAspArgThrProIlePheValAlaMetTyrrArgGlu	353
Db	1018	ATATCGGGAGAGTATTATATCAAGTTCATGGAGTGGACGCGGTGGTTAAGCGCATGTGGAGGAG	107
OY	354	AlaIleValGluCysIleTyrrIIleGluProAspGluAspSerGlnHisIleIleGlyValPheTrp	373
Db	1078	GCGAAGAGGTGATATGATGTGAACCGGACAGGCAAGGCTGAGAAAGAAAGTGTGTTCTGG	113
OY	374	TyrrHis	375
Db	1138	TTCAAC	1143

```

RESULT 10
US-09-128-602B-9
; Sequence 9, Application US/09128602B
; Patent No. 6414223
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharm
; APPLICANT: Pan, Zhegong
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE OF INVENTION: FATTY ACID CONTENT
; FILE REFERENCE: 07148-072001
; CURRENT APPLICATION NUMBER: US/09/128,602B
; CURRENT FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-128-602B-9

Alignment Scores:
Pred. No.: 2,71e-155 Length: 1155
Score: 1317.00 Matches: 234
Percent Similarity: 76.44% Conservative: 58
Best Local Similarity: 61.26% Mismatches: 82
Query Match: 64.34% Indels: 8
DB: Gaps: 4

US-10-069-772-2 (1-377) x US-09-128-602B-9 (1-1155)
QY 1 MetGlyAlaGlyArgMet-----SerAspProSerGluGlyLysAsn 15
DB 1 ATGGGTGCAAGTGGAGATGCAAGATGCTCTCTCCCTCCCAAAAGTGTGAACCGACAC 60
QY 16 ILeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAla 34
DB 61 ATC---AGCGGGTACCCCTGGCAGACACCGCCCTTCACTGTGGAGAACTCAAGAAAGCA 117
QY 35 ILeuProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
DB 118 ATCCACCGCACTGTTTCAACACGCTGATCCCTCGCTTTCCTCAACCTCATCGGAGAC 177
QY 55 LeuIleValAlaTyValPheTyTyTyLeuAlaAsnThrTyTrIleProLeuIleProThr 74
DB 178 ATCATCAATACCTCTGCTTCTTACTAGTCAGTCCACACCACTTACTTCTCTCCCTCAC 237
QY 75 ProLeuAlaTyLeuAlaTrpProValTyTrPheCysGlnAlaSerIleLeuThrGly 94
DB 238 CCTCTCTCTTACTTGGCTCTGCGCTCTCTACTAGGCTGCGACGGAGCTGCTTACCGGCG 297
QY 95 LeuTrpValIleGlyHisGluCysGlyHisIleAlaPheSerAspTyTrGlnLeuIleAsp 114
DB 298 GTCGTGGTCAATGACCAAGTGGCGGCAACAGCCTTCAAGCAGTACCAAGTGGCTGAC 357
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTrPheSerTrpLysTy 134
DB 358 GACACCGTGGCGCTCATCTTCACTCTCTTCTCTCTGCTGCTCTTACTTCTCTGGAATAC 417
QY 135 SerHisArgAsnHisIleAlaSerThrAsnSerLeuAspAsnAspGluValTyTrIlePro 154
DB 418 AGTATTCAGCGCACCATCTTCAACACACTGGCTCCCTTGAAGAGACGAAGTGTGTGCCC 477
QY 155 LysArgLysSerLysValLysIleTySerLysLeuLeuAsnAsnProProGlyArgVal 174
DB 478 AAGAAGAAGTCAAGATCAAGTGTACCGGCAAGTACCTCAACAAACCTTTGGAGCGCAC 537
QY 175 PheThrIleValPheArgLeuThrIleGlyPheProLeuTyTrIleLeuThrAsnIleSer 194
DB 538 GTGAGTGTAAACGTTCACTTCACTTCCGCTGCGCTTGTACTTACCTTCAACGTCG 597

```

QY 195 GlyLysLysTyr---GlyArgPheAlaAenHisPheAspProMetSerProIlePheAsn 213  
Db 598 GGGAGACCTTACGAGCGCGCTTCCTCCATTTCCACCCCAAGCCTCCCATCTACAC 657  
QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233  
Db 658 GACCGTAGCGCTCTCCAGATATACATCTCCAGCGCTGCGCATCTCGCCCTGCTACCGGT 717  
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIlePro 253  
Db 718 CTTACCGCTACGCTGCTGCTCCAGAGATTGCTCGATGCTGCTTACGAGATTCT 777  
QY 254 ValLeuGlyValSerValPhePheValLeuIleTyrLeuHisHisThrHisIleSer 273  
Db 778 CTTTGATTTGTCACGCGGTTCTTAGTTTGTATGATCTTACCTTCAGACACGATCTCTCC 837  
QY 274 LeuProHisTyrAspSerThrGluTyrPheAsnTyrIleLysGlyAlaLeuSerThrIleAsp 293  
Db 838 CTGCTCTCATATGACTCGCTGCTGATGAGGAGTGTGAGGAGCTTTGCGCACCGTTCAC 897  
QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValIleLeuHis 313  
Db 898 AGAGACTACGAGATCTTGACAGAGGTCTTCCAGATATACAGGACACGACGCTGCGCAT 957  
QY 314 HisLeuIleSerTyrIleProHisTyrHisAlaLysGlyAlaArgAspAlaIleLysPro 333  
Db 958 CACCTGTTCTGACACATGCGCATATATCATGCGATGAGTACAGACGATTAAGCGCG 1017  
QY 334 ValLeuGlyLysTyrIleLysIleLeuAspArgThrProIlePheLysAlaMetTyrArgLys 353  
Db 1018 ATACTGGGAGATATTATATCATGAGGAGCGCGGTGTTAAGCGCATGAGAGGAG 1077  
QY 354 AlaLysGlyLysTyrIleLysIleLysProAspGluAspSerGluHisLysGlyValPheTyr 373  
Db 1078 GCGAAGAGATGATCTATGATGACCGGACAGGACAGGACAGGAGAAAGGTGTTCTCG 1137  
QY 374 TyrHis 375  
Db 1138 TACAC 1143

RESULT 11  
US-09-995-297-9  
Sequence 9, Application US/09995297  
Patent No. 6649782  
GENERAL INFORMATION:  
APPLICANT: Kodali, Dharna  
APPLICANT: Pan, Zhegong  
APPLICANT: DeBonte, Lorin R.  
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
FILE REFERENCE: 07148-072002  
CURRENT APPLICATION NUMBER: US/09/995,297  
CURRENT FILING DATE: 2001-11-27  
PRIOR APPLICATION NUMBER: US 09/128,602  
PRIOR FILING DATE: 1998-08-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 1155  
TYPE: DNA  
ORGANISM: Brassica napus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1152)  
US-09-995-297-9

Alignment Scores:  
Pred. No.: 2,716-155 Length: 1155  
Score: 1317.00 Matches: 234  
Percent Similarity: 76.44% Conservative: 58  
Best Local Similarity: 61.25% Mismatches: 82  
Query Match: 64.34% Indels: 8

DB: 4 Gaps: 4  
US-10-069-772-2 (1-377) x US-09-995-297-9 (1-1155)  
QY 1 MetGlyAlaGlyLysArgMet-----SerAspProSerGluGlyLysAsn 15  
Db 1 ATGGGTGAGAGGTGGAGAAATGCAAGTGTCTCTCTCCCAAAAAGTCTGAAACGACAAAC 60  
QY 16 IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 34  
Db 61 ATC---AAGCGCGTACCTCGGAGACACCGCCCTTACCTGTCGAGAACTCAAGAAACCA 117  
QY 35 IleProThrHisCysPheGluArgSerValIleAspSerTyrTyrValValHisAsp 54  
Db 118 ATCCACCGCACGTGTTTAAACGCTGATACCTCGCTCTTCTCTTCTTCTTCTTCTTCTGAGAC 177  
QY 55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAenThrTyrIleProLeuIleProThr 74  
Db 178 ATCATCATAGCTCTGCTGCTTCTACGCTGCGACACTTACTTCTCTCTCTCTCTCTCTCAC 237  
QY 75 ProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGly 94  
Db 238 CTTCTCTCTACTTCTGCTGCTGCT 297  
QY 95 LeuTyrValIleGlyHisGlyCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAsp 114  
Db 298 GTCTGGGTTCATAGCCCAAGAGTGGCGCCACACGCTTACAGACTTACAGTGGCTGAC 357  
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrLysTyr 134  
Db 358 GACACCGTGGCTCTATCTTCT 417  
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIlePro 154  
Db 418 AGTCATCAGCCGACCATTCCTCAACACATGCTCCCTCGAGAGAGAGAAAGTGTGTTCTCCC 477  
QY 155 LysArgLysSerLysValLysIleTyrSerLysLeuLeuAsnProProGlyArgVal 174  
Db 478 AAGAAGAAATGACATAGAGTGAAGGACGCAAGTACTTCAACACCTTTGGAGAGCAC 537  
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSer 194  
Db 538 GTGATGTTAAGCGTTCAATTCATCTCGGCTGCTTGTACTTACCTTCAACGCTCTCG 597  
QY 195 GlyLysLysTyr---GlyArgPheAlaAenHisPheAspProMetSerProIlePheAsn 213  
Db 598 GGGAGACCTTACGAGCGCGCTTCCTGATTTCCACCCCAAGCCTCCCATCTACAC 657  
QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233  
Db 658 GACCGTAGCGCTCTCCAGATATACATCTCCAGCGCTGCGCATCTCGCCCTGCTACCGGT 717  
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIlePro 253  
Db 718 CTTACCGCTACGCTGCTGCTCCAGAGATTGCTCGATGCTGCTTACGAGATTCT 777  
QY 254 ValLeuGlyValSerValPhePheValLeuIleTyrLeuHisHisThrHisIleSer 273  
Db 778 CTTTGATTTGTCACGCGGTTCTTAGTTTGTATGATCTTACCTTACGACACGATCTCTCC 837  
QY 274 LeuProHisTyrAspSerThrGluTyrPheAsnTyrIleLysGlyAlaLeuSerThrIleAsp 293  
Db 838 CTGCTCTCATATGACTCGCTGATGAGGAGTGTGAGGAGGAGCTTTGCGCACCGTTCAC 897  
QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValIleLeuHis 313  
Db 898 AGAGACTACGAGATCTTGACAGAGGTCTTCCAGATATACAGGACACGACGCTGCGCAT 957  
QY 314 HisLeuIleSerTyrIleProHisTyrHisAlaLysGlyAlaArgAspAlaIleLysPro 333  
Db 958 CACCTGTTCTGACACATGCGCATATATCATGCGATGAGGAGTGAAGGATTAAGCGCG 1017  
QY 334 ValLeuGlyLysTyrIleLysIleLeuAspArgThrProIlePheLysAlaMetTyrArgLys 353

```

Db      1018 ATACTGGAGAGTATATCATGTCAGTGGAGCCGCGTGTAAAGCGATGCGAGGAG 1077
Qy      354 AAlaySGuCyvIlEtYrIlEgluPrOaRgluAaRserGluHlEyluGlyValPheTrp 373
Db      1078 GCGAGGAGGTATGTATGTGAGACCGGACGAGGAGGTGAAGAGAGGTGTGTCTGG 1137
Qy      374 TyrHis 375
Db      1138 TACAAC 1143

RESULT 12
US-09-133-962A-3
; Sequence 3, Application US/09133962A
; Patent No. 6372965
; GENERAL INFORMATION:
; APPLICANT: JONATHAN EDWARD LIGHTNER
; JOHN JOSEPH OKULEY
; TITLE OF INVENTION: GENES FOR MICROSOFTAL FATTY ACID
; DELTA-12 DESATURASES AND RELATED
; ENZYMES FROM PLANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/133,962A
; FILING DATE: 14-AUG-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 07/977,339
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNN M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1043-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302)992-5481
; TELEFAX: (302)773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..1284
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-133-962A-3

Alignment Scores:
Pred. No.: 3,84e-155 Length: 1426
Score: 1317.00 Matches: 234
Percent Similarity: 76.44% Conservatave: 58
Best Local Similarity: 61.26% Mismatches: 82
Query Match: 64.34% Indels: 8
DB: 4 Gaps: 4

```

```

US-10-069-772-2 (1-377) x US-09-133-962A-3 (1-1426)
Qy      1 MetGluAlaGluValArgMet-----SerArgProSerGluGlyValAsn 15
Db      130 ATGGGTGAGGAGGAGAGAGATGCAAGTGTCTCTCCCTCCAAAGCTGTGAACSSAAG 189
Qy      16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAla 34
Db      190 ATC---AAGCGGTACCCCTGGAGACACCGCCCTTCACTGTGGAGAACTGAAGAAACA 246
Qy      35 IleProThrHisCyvPheGluArgSerValIleArgSerTrpYrValValHisAsp 54
Db      247 ATCCACCGGCACTGTTCATAACGCTCGATCCCTCTTCTCTCTACTACTCGGAGC 306
Qy      55 LeuIleValAlaYrValPheTrpYrLeuAlaAsnThrYrIleProLeuIleProThr 74
Db      307 ATCAATAGCGCTCTGCTTACTAGCTGCGACACCACTTACTCTCTCTCTCTCTCTCAC 366
Qy      75 ProLeuAlaYrLeuAlaTrpProValYrTrpPheCyGlnAlaSerIleLeuThrGly 94
Db      367 CCGTCTCTCTACTCTGCGCTGCTCTCTACTGCGGCTGCGAGGCTGCGCTCTCAACGGC 426
Qy      95 LeuTrpValIleGlyHisGluCyGlyHisHisAlaPheSerAspYrGlnLeuIleAsp 114
Db      427 GCTGGGTCAATAGCCCAAGAGTGGGCCCAACCGCTTCACTACAGTGGCTGGAC 486
Qy      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProYrPheSerTrpYrTrp 134
Db      487 GACACCGGTGCTCATCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
Qy      135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnArgValYrIlePro 154
Db      547 AGTATGACGCCCAACCAATTCACACAGTCCCTCCGAGAGAGAGAGAGAGTGTCTCC 606
Qy      155 LysArgIleSerTrpValValIleYrSerIleLeuLeuAsnProProGlyArgVal 174
Db      607 AAGAAGAAGTACAGATCAATCAAGTGTACCGCAAGTACCTCAACCAACCTTTGGGAC 666
Qy      175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuYrLeuLeuThrAsnIleSer 194
Db      667 GTGATGTAAAGCTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
Qy      195 GlyIleValYr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsn 213
Db      727 GGAAGACCTTACGACAGCGGCTTCCGCTTCCATTCACCCCAACGCTCCCATCTACAC 786
Qy      214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheYrAla 233
Db      787 GACCGTACGCTCTCCAGATATATACATCCGACGCTGCGATCTCGCGTGTGACGCT 846
Qy      234 IleYsIleLeuValAlaAlaValGlyAlaAlaTrpValIleAsnMetYrAlaIlePro 253
Db      847 CTTCACGCTACGCTGCTGCTCAAGAGGTGCTCGAGGTCTCTCTCTCTCTCTCTCTCT 906
Qy      254 ValIleGlyValSerValPhePheValLeuIleThrYrLeuHisHisIleThrIleLeuSer 273
Db      907 CTTCATATGTCACACGCGTCTTATGTTATATCACTTATGTCACACACACACACCTTCC 966
Qy      274 LeuProHisYrAspSerThrGluTrpAsnTrpIleYsGlyAlaLeuSerThrIleAsp 293
Db      967 CTGCGTCACTATGACTGCTGAGTGGAGATGTGTGAGGAGGAGCTTGGCCACCGTTGAC 1026
Qy      294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313
Db      1027 AGAAGACTAGGAATCTGAAACAGCTCTTCCAAATATCAACGACACGACGACGAGCGCAT 1086
Qy      314 HisIleLeuSerYrIleProHisIleYrHisHisAlaValGluAlaAspAlaIleYsPro 333
Db      1087 CACCTGTCTTCCGACACAGCCGATTAATCATCCAGTGAAGTACGAGGCGATAAAGCG 1146
Qy      334 ValLeuGlyGluYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 353
Db      1147 ATACTGGAGAGTATATCATGTCAGTGGAGCCGCGTGTAAAGCGATGTGAGGAG 1206

```

Qy 354 AlaysgluCyIleTyrIleGluProAspGluAspSerGluHisIleYsgIValPheTrr 373  
Db 1207 GCGAAGAGGTATCTATGTGGAACCGGACGAGCGAAGGTAGAAAGAGTGTCTGG 1266  
Qy 374 TyrHis 375  
Db 1267 TACAAC 1272

RESULT 13  
US-09-354-231B-11  
; Sequence 11, Application US/09354231B  
; Patent No. 6342658  
; GENERAL INFORMATION:  
; APPLICANT: DeBonte, Lorin R.  
; APPLICANT: Shorrosh, Basil S.  
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
; FILE REFERENCE: 07148-063002  
; CURRENT APPLICATION NUMBER: US/09/354,231B  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 08/874,109  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1152)  
US-09-354-231B-11

Alignment Scores:  
Pred. No.: 8,62e-155 Length: 1155  
Score: 1313.00 Matches: 233  
Percent Similarity: 76.44% Conservative: 59  
Best Local Similarity: 60.99% Mismatches: 82  
Query Match: 64.14% Indels: 8  
Gaps: 4

US-10-069-772-2 (1-377) x US-09-354-231B-11 (1-1155)

Qy 1 MetGlyAlaGlyAlaArgMet-----SerAspProSerGluGlyValAsn 15  
Db 1 ATGGGTGACGGTGGAGAAATGCAAGTGTCTCTCCCTCCAAAAGCTGGAACCGACAC 60  
Qy 16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAsn 34  
Db 61 ATC---AAGCGGTAACCTCGGACGACACCGCCCTTCACTGTGGAGAACTCAAGAAAGCA 117  
Qy 35 IleProThrHisCyPheGluArgSerValIleArgSerSerTyrTyrValValHisAsp 54  
Db 118 ATCCACCGCACTGTTTCAAGAGCTCGATCCCTGCTCTTCTCCTACCTACCTGGAGC 177  
Qy 55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74  
Db 178 ATCAACAAAGGCTCTGCTGTCTACTACGTCGACACACTTACTCTCTCTCTCTCTCAC 237  
Qy 75 ProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCyGlnAlaSerIleLeuThrGly 94  
Db 238 CCT 297  
Qy 95 LeuTyrValIleGlyHisIleGluCyAspGlyHisIleAlaPheSerAspTyrGlnLeuIleAsp 114  
Db 298 GTCTGGGTCTATGACCAACAGTGGCGGACCAACGCTTCAAGGACTACCAAGTGGTGGAC 357  
Qy 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTrrPlyTyr 134  
Db 358 GACACCGGTGGCGCTCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417  
Qy 135 SerHisArgAsnHisIleAlaAsnThrAsnSerIleuAspArgAlaGluValTrrIlePro 154

Db 418 AGTCATGACCGCCACATCTCCAAACATGGCTCCCTCCGAGAGACGAAGTGTGTCCCC 477  
Qy 155 LysArgIleSerLeuValIleTyrSerIleLeuLeuAsnProProGlyArgVal 174  
Db 478 AAGAAAGATGACATCAAGTGTACCGCAAGTAACTCAACAACCTTTGGGCGCACCC 537  
Qy 175 PheThrLeuValPheAspGluLeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSer 194  
Db 538 GTGATGTTAAACGGTTCAAGTCACTCGCTGGCTGTGTGACTTACGCTTCAACGCTCG 597  
Qy 195 GlyIleValTyr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213  
Db 598 GGGAGACCTTACGACCGGGGCTTGGCTTGCATTTCCACCCCAACGCTCCCATCTACAC 657  
Qy 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233  
Db 658 GACCGTGAAGCTCTCCAGATATACATCTCCGACCGCTGCATCTCGCTGTGCTACCGGT 717  
Qy 234 IleIleValLeuValAlaIleValGlyAlaIleTrrValIleAsnMetTyrAlaIlePro 253  
Db 718 CTTACCGCTACCGCTGTGTCGAAGAGTTCCTCGATGTCGTGCTTACGAGTTCCT 777  
Qy 254 ValIleGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrIleLeuSer 273  
Db 778 CTCTGATGTCACACGGGTTCTTAGTTTGTATCACTTACTTGCAGACACCATCTTCC 837  
Qy 274 LeuProHisTyrAspSerThrGluTrrAsnTrrIleIleValAlaLeuSerThrIleAsp 293  
Db 838 CTGCCTCACTATGACTCGTGTGAGGAGTGTGTGAGGAGGAGCTTTGGCACCGTGTAC 897  
Qy 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleValLeuHis 313  
Db 898 AGAGACTAGCGAATCTTGAAACAGGCTTCCACATATACAGGACGACACCGAGTGGCGAT 957  
Qy 314 HisLeuIleSerTyrIleProHisIleTyrHisIleAlaValAspAlaIleAspPro 333  
Db 958 CACCTGTTCTGACCATGCCCATTTATATCATGATGAGATGACGAAGCGATAAAGCG 1017  
Qy 334 ValIleGlyGluTyrTyrIleAspArgThrProIlePheValIleMetTyrArgGlu 353  
Db 1018 ATACTGGAGAGTATCTATCATGTCGATGAGACCGCGGTGTTAAGCGATGTGGAGGAG 1077  
Qy 354 AlaysgluCyIleTyrIleGluProAspGluAspSerGluHisIleYsgIValPheTrr 373  
Db 1078 GCGAAGAGGTATCTATGTGGAACCGGACGAGCGAAGGTAGAAAGAGTGTGTCTGG 1137  
Qy 374 TyrHis 375  
Db 1138 TACAAC 1143

RESULT 14  
US-09-128-602B-11  
; Sequence 11, Application US/09128602B  
; Patent No. 6414223  
; GENERAL INFORMATION:  
; APPLICANT: Kodali, Dharma  
; APPLICANT: Fan, Zhongyong  
; APPLICANT: DeBonte, Lorin R.  
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED  
; FILE REFERENCE: 07148-072001  
; CURRENT APPLICATION NUMBER: US/09/128,602B  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1152)  
US-09-128-602B-11

## Alignment Scores:

Pred. No.: 8,62e-155 Length: 1155  
 Score: 1313.00 Matches: 233  
 Percent Similarity: 76.44% Conservative: 59  
 Best Local Similarity: 60.99% Mismatches: 82  
 Query Match: 64.14% Indels: 8  
 Gaps: 4

US-10-069-772-2 (1-377) x US-09-128-602B-11 (1-1155)

```

QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db 1 ATGGGTGACAGGTGGAAGATGCAAGTGTCTCTCCCTCCCAAAAAGTGTGAACCGACAC 60
QY 16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAla 34
Db 61 ATC---AAGCGCGTACCCCTCGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
Db 118 ATCCACCGGACCTTTTCAAGCGTCAATCCCTGCTTTCTCTACCTCATCTGGGAC 177
QY 55 LeuIleValAlaTyValPheTyTyLeuAlaAsnThyTyIleProLeuIleProThr 74
Db 178 ATCATCATAGGCTCTGCTCTTACTACGTCGACCACTTACTTCCCTCTCTCTCAC 237
QY 75 ProLeuAlaTyLeuAlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThyGly 94
Db 238 CCTCTCTCTACTTCCGCTGCGCTCTCTACTGCGGCTGCGGCTGCGCTTAACCGGC 297
QY 95 LeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyTyGlnLeuIleAsp 114
Db 298 GTCTGGGTCAATAGCCCAACATGCGGCCACACCGCTTACGACGATCACTAGCTGAC 357
QY 115 AspIleValGlyPheValIleuHisSerAlaLeuLeuThrProTyPheSerTrpLysTy 134
Db 358 GACACCGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyIlePro 154
Db 418 AGTCATGAGCGCACCAATCCACACCTGCTCCCTCGAGAGACGAAGTGTGTCCTCC 477
QY 155 LysArgLysSerLysValLysIleTySerLysLeuLeuAsnAsnProProGlyArgVal 174
Db 478 AAGAAGAGATGACGACATCAAGTGTACGCGAAGTACCTCAACACCTTTGGAGCACC 537
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSer 194
Db 538 GTGATGTTAAGCGTTCAGTTCACCTCGGCTGCGCTTGTACTTAGCTTCAACGTCG 597
QY 195 GlyLysLysTyTy---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
Db 598 GGGAGACCTTACGACGCGGCTTGTGCTTCCATTTTCCACCCCAACGCTCCCATTTACAC 657
QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAla 233
Db 658 GACCGTAGCGTCTCCGATATACATCTCCGACGCTGACCTCTCGCGTCTGCTACGGT 717
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyAlaIlePro 253
Db 718 CTTCACCGCTACGCTGCTGCTCAAGAGAGTTCCTCGATGCTGCTTACGAGAGTTCCT 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThyTyLeuHisHisThrHisLeuSer 273
Db 778 CTTCATGTTGCAACGGGTCTTGTAGTTTGTATCACTTACGACACACCATCTCTTCC 837
QY 274 LeuProHisTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
Db 838 CTGCTCACTATGACTGCTCTGAGTGGATGTGTGAAGGAGCTTTGGCACCCTTAC 897
QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisHisValLeuHis 313
  
```

```

Db 898 AGAGACTACGGAATCTTGAACCAAGTCTTCCAAATATCAACGACGACGTCGGCAT 957
QY 314 HisLeuLeuSerTyTyIleProHisTyTyHisAlaLysGluAlaAspAlaIleLysPro 333
Db 958 CACCTGTTCTGACCAATGCCGATATATCATGCAAGTACGAAGCGATTAAGCG 1017
QY 334 ValLeuGlyGlyTyTyTyTyLysAlaAspArgThrProIlePheLysAlaMetTyArgGlu 353
Db 1018 ATACTGGAGAGATATATCATGATTCGATGAGCGCGGCTGTGTTAAGCGCATGAGGAG 1077
QY 354 AlaLysGlyCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyValPheTrp 373
Db 1078 GCGAAGAGATATATCATATGTGAACCGACAGCAAGGTGAAGAAAGTGTCTGG 1137
QY 374 TyHis 375
Db 1138 TACAC 1143

RESULT 15
US-09-995-297-11
; Sequence 11, Application US/09995297
; Patent No. 6649782
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharma
; APPLICANT: Fan, Zhongong
; APPLICANT: Desbonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; TITLE OF INVENTION: FATTY ACID CONTENT
; FILE REFERENCE: 07148-072002
; CURRENT FILING DATE: US/09/995,297
; PRIOR APPLICATION NUMBER: 2001-11-27
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ. ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-995-297-11

Alignment Scores:
Pred. No.: 8,62e-155 Length: 1155
Score: 1313.00 Matches: 233
Percent Similarity: 76.44% Conservative: 59
Best Local Similarity: 60.99% Mismatches: 82
Query Match: 64.14% Indels: 8
Gaps: 4

US-10-069-772-2 (1-377) x US-09-995-297-11 (1-1155)
QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db 1 ATGGGTGACAGGTGGAAGATGCAAGTGTCTCTCCCTCCCAAAAAGTGTGAACCGACAC 60
QY 16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAla 34
Db 61 ATC---AAGCGCGTACCCCTCGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
Db 118 ATCCACCGGACCTTTTCAAGCGTCAATCCCTGCTTTCTCTACCTCATCTGGGAC 177
QY 55 LeuIleValAlaTyValPheTyTyLeuAlaAsnThyTyIleProLeuIleProThr 74
Db 178 ATCATCATAGGCTCTGCTCTTACTACGTCGACCACTTACTTCCCTCTCTCTCAC 237
QY 75 ProLeuAlaTyLeuAlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThyGly 94
Db 238 CCTCTCTCTACTTCCGCTGCGCTCTCTACTGCGGCTGCGGCTGCGCTTAACCGGC 297
  
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 16:53:33 ; Search time 402 Seconds  
(without alignments)  
4296.196 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEKNIILERV.....IYEPDESEHKGVFWYHKM 377

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 229054650 residues  
Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xjh  
-Q=/cgn2/1/USFTO.spool/US10069772/rnatc\_18062004\_145514\_5404/app\_query.fasta\_1.519  
-DB=Published\_Applications\_NA -QFW=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOPCB=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANSNUM=40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MTLEN=0  
-MATEL=200000000 -USER=US10069772@cgn\_1\_1\_354@rnatc\_18062004\_145514\_5404  
-NCUG=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSEBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US00\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US00\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries  
Query  
No. Score Match Length DB ID Description

1	1716.5	83.9	1199	9	US-09-981-124-19	Sequence 19, Appli
2	1592	77.8	1309	9	US-09-981-124-3	Sequence 3, Appli
3	1589.5	77.7	1358	9	US-09-981-124-1	Sequence 1, Appli
4	1356.5	66.3	1586	13	US-10-425-114-14778	Sequence 14778, A
5	1356.5	66.3	2931	13	US-10-424-599-123945	Sequence 123945,
6	1356.5	66.3	6220	15	US-10-465-800-3	Sequence 3, Appli
7	1356.5	66.3	6220	15	US-10-176-149-3	Sequence 3, Appli
8	1346.5	65.8	1457	13	US-10-425-114-12782	Sequence 12782, A
9	1332.5	65.1	1422	9	US-09-837-751-5	Sequence 5, Appli
10	1323.5	64.7	1411	9	US-09-852-399-3	Sequence 3, Appli
11	1318	64.4	1155	9	US-09-995-287-13	Sequence 13, Appli
12	1318	64.4	1155	10	US-09-771-904-13	Sequence 13, Appli
13	1318	64.4	1155	17	US-10-715-100-13	Sequence 13, Appli
14	1317	64.3	1155	9	US-09-995-297-9	Sequence 9, Appli
15	1317	64.3	1155	10	US-09-771-904-9	Sequence 9, Appli
16	1317	64.3	1155	17	US-10-715-100-9	Sequence 9, Appli
17	1315	64.2	1156	16	US-10-330-775-3	Sequence 3, Appli
18	1313	64.1	1155	9	US-09-995-287-11	Sequence 11, Appli
19	1313	64.1	1155	10	US-09-771-904-11	Sequence 11, Appli
20	1313	64.1	1155	16	US-10-330-775-5	Sequence 5, Appli
21	1313	64.1	1155	17	US-10-715-100-11	Sequence 11, Appli
22	1312	64.1	1155	9	US-09-995-287-5	Sequence 5, Appli
23	1312	64.1	1155	10	US-09-771-904-5	Sequence 5, Appli
24	1312	64.1	1155	16	US-10-435-521-5	Sequence 5, Appli
25	1312	64.1	1155	17	US-10-715-100-5	Sequence 9, Appli
26	1311	64.0	1155	9	US-09-995-287-15	Sequence 15, Appli
27	1311	64.0	1155	10	US-09-771-904-15	Sequence 15, Appli
28	1311	64.0	1155	17	US-10-715-100-15	Sequence 15, Appli
29	1310	64.0	1155	9	US-09-995-287-17	Sequence 17, Appli
30	1310	64.0	1155	10	US-09-771-904-17	Sequence 17, Appli
31	1310	64.0	1155	17	US-10-715-100-17	Sequence 17, Appli
32	1308	63.9	1155	16	US-10-435-521-3	Sequence 3, Appli
33	1305	63.8	1155	9	US-09-995-287-7	Sequence 7, Appli
34	1305	63.8	1155	10	US-09-771-904-7	Sequence 7, Appli
35	1305	63.8	1155	17	US-10-715-100-7	Sequence 7, Appli
36	1299	63.5	1155	9	US-09-995-287-1	Sequence 1, Appli
37	1299	63.5	1155	10	US-09-771-904-1	Sequence 1, Appli
38	1299	63.5	1155	16	US-10-435-521-1	Sequence 1, Appli
39	1299	63.5	1155	17	US-10-715-100-1	Sequence 1, Appli
40	1296.5	63.3	1411	9	US-09-837-751-3	Sequence 3, Appli
41	1295	63.3	1155	9	US-09-995-287-3	Sequence 3, Appli
42	1295	63.3	1155	10	US-09-771-904-3	Sequence 3, Appli
43	1295	63.3	1155	17	US-10-715-100-3	Sequence 3, Appli
44	1283.5	62.7	1724	13	US-10-425-114-25066	Sequence 25066, A
45	1283.5	62.7	1729	13	US-10-425-114-21414	Sequence 21414, A

ALIGNMENTS

RESULT 1  
US-09-981-124-19  
; Sequence 19, Application US/09981124  
; Patent No. US20020166144A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Lemman, Maric  
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
; FILE REFERENCE: 26-98A  
; CURRENT APPLICATION NUMBER: US/09/981,124  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: US 09/059769  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/043706  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR APPLICATION NUMBER: AU P06223  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR APPLICATION NUMBER: AU P06226  
; PRIOR FILING DATE: 1997-04-15  
; PRIOR APPLICATION NUMBER: US 60/050403

; PRIOR FILING DATE: 1997-06-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 1199  
 ; TYPE: DNA  
 ; ORGANISM: Vernonia galamensis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (44)..(1195)  
 ; OTHER INFORMATION:  
 US-09-981-124-19

## Alignment Scores:

Pred. No.:	5,846-197	Length:	1199
Score:	1716.50	Matches:	312
Percent Similarity:	90.26%	Conservative:	31
Best Local Similarity:	82.11%	Mismatches:	34
Query Match:	83.85%	Indels:	4
DB:	9	Gaps:	3

US-10-069-772-2 (1-377) x US-09-981-124-19 (1-1199)

```

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGly--LysAsnIleLeuGluArg 19
DB 44 ATGGAGAGCTGGTGGCGAATGATACCAACCGATGATGATCAGAGAATCTCTCCACAGCC 103
QY 20 ValProValAsp---ProPheThrLeuSerAspLeuLysAlaIleProThrHis 38
DB 104 GTCACAGCTCCCAACACCACTCTCTGCTGATCTTAAAGAACCTACACCCAC 163
QY 39 CysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAla 58
DB 164 TGTTCACAAAGATCCCTCCGCTTCATCTTACTATGATGCTTCATGATCTCGTACAGCC 223
QY 59 TyrValPheTyrTyrLeuAlaSerThrTyrIleProLeuIleProThrProLeuAlaTyr 78
DB 224 TAGCTCTTACTATCTCGCCACACATACATCCCTCTCTCCCTCTCTCTCTCTCTCTAC 283
QY 79 ---LeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeuTyrVal 97
DB 284 TTATTAGCTGGCCCTTACGTTCTGTCTGAGGATGATCTTACCGGTCTGCGGTC 343
QY 98 IleGlyIleGluCysGlyHisIleAlaPheSerAspTyrGlnLeuIleAspIleVal 117
DB 344 ATCGCTCATGATGATGGCCACCATGCTTCACTGATCATCAATGATAGACACACTGG 403
QY 118 GlyPheValLeuHisSerAlaLeuThrProTyrPheSerTyrIleGlySerHisArg 137
DB 404 GCGTCATCTCTCTGCTGCTGCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 463
QY 138 AsnHisIleAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLys 157
DB 464 ATATCCATGCTCCCAACCAACTCTCTTGTATACGATGATGATGATGATGATGATGATGAT 523
QY 158 SerLysValLysIleTyrSerLysLeuLeuAsnProProGlyArgValPheThrLeu 177
DB 524 TCCAGAGCTTTCCTTATTCCTTCAAAATCCTTACCAACCTCTGCTGCTGCTTTCCTTGC 583
QY 178 ValPheAlaGluThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysLys 197
DB 584 GCTTCAGATTGATGCTGGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 643
QY 198 TyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAspAspArgLysArg 217
DB 644 TACGACAGCTTTCCTTTCCTTATTCCTTATTCCTTATTCCTTATTCCTTATTCCTTATTCCT 703
QY 218 ValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeu 237
DB 704 GTACAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 763
QY 238 ValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValLeuGlyVal 257
  
```

```

DB 764 GTATGCTTAAAGAGGCTTGGGATGATGTCATTTACGAGATTCCTGTGCGCCGTA 823
QY 258 SerValPhePheValLeuIleThrTyrLeuHisIleThrHisIleSerLeuProHisTyr 277
DB 824 AACGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 883
QY 278 AspSerThrGluTyrAsnThrPheLysGlyValAlaLeuSerThrIleAspArgAspPheGly 297
DB 884 GATTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 943
QY 298 PheLeuAsnArgValPheHisAspValThrHisIleThrHisIleValLeuHisIleSer 317
DB 944 TTTCTTGAATAGGCTTTCCTTTCACGACCTGACACACACCTTGTCTTGCATTTGATATCG 1003
QY 318 TyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGluGly 337
DB 1004 TACATTCCTCATTTATCATGACAAAGAGGACAAAGAGCGCATCAACCGGTGTGGCGCA 1063
QY 338 TyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGlyLys 357
DB 1064 TACTATTAAGATGACAGACACACCGATCGTGAAGGCAATGTGAGGGAAGC-AAAGAAATGC 1122
QY 358 IleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLysMet 377
DB 1123 ATATTCATTTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182

RESULT 2
US-09-981-124-3
; Sequence 3, Application US/09981124
; Patent No. US2002016144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Marit
; APPLICANT: Styume, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981,124
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR FILING DATE: 1998-04-14
; PRIOR FILING DATE: 1997-04-16
; PRIOR FILING DATE: 1997-04-16
; PRIOR FILING DATE: 1997-04-15
; PRIOR FILING DATE: 1997-04-15
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1309
; TYPE: DNA
; ORGANISM: Crepis sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (937)..(937)
; OTHER INFORMATION: N is any nucleotide residue
; NAME/KEY: CDS
; LOCATION: (26)..(1147)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (901)..(901)
; OTHER INFORMATION: N is any nucleotide residue
US-09-981-124-3

Alignment Scores:
Pred. No.: 7,73e-182 Length: 1309
Score: 1592.00 Matches: 287
Percent Similarity: 86.51% Conservative: 40
Best Local Similarity: 75.93% Mismatches: 45
  
```



Query Match: 77.77% Indels: 6  
DB: 9 Gaps: 4  
US-10-069-772-2 (1-377) x US-09-981-124-3 (1-1309)

QY 1 MetG1YAlaG1YArgMetSerAspProSerGluGlyValAsn1LeuGluArgVal 20  
DB 26 ATGGGTGCGCGCGCGCT-----GCTCGGTGGA---AAGTCGGTATGGAACGATC 76

QY 21 ProValAspPro---ProPheThrLeuSerAspLeuValAsn1LeuProThrHisGly 39  
DB 77 TCAGTATATCAAGTAACCTTCTCACTAGATATTGAAGCAAGCAATCCCTCACTTGC 136

QY 40 PheGluArgSerVal1LeuArgSerSerTyTyValValHisAspLeu1LeuAlaTy 59  
DB 137 TTCAGGAGATGTCATCCGCTTCTTATACGTTGTCAGATCATATATGCTTAC 196

QY 60 ValPheTyTyLeuAlaAsnThrTyTyrLeuProLeu1LeuProThrProLeuAlaTy 79  
DB 197 ATCTTCTACTTCTCTTGCACACATATATCCCTATCCCTCACTTCTTGCCTACTTA 256

QY 80 AlaTrpProValTyTyTrpPheCysGluAlaSer1LeuThrGlyLeuTrpVal1Leu 99  
DB 257 GCTTGGCCGCTTACTGTTTGTCAAGCTAGCCGCTCCTCAGTGGTATGATCCTCGC 316

QY 100 HisGluCysGlyHis1AlaPheSerAspTyTyGlnLeu1LeuAspAsp1LeuAlaTy 119  
DB 317 CATGAATGTGTCACATCCCTATAGCACTACATGCGTTCAGACACTGTGGCTTC 376

QY 120 ValLeuHisSerAlaLeuLeuThrProTyTyPheSerTyTySerHisArgAsnHis 139  
DB 377 ATCATCATTCATCTTCTCTCACCCCGTATCTTCTGGAATATACGTACCGGAATCAC 436

QY 140 HisAlaAsnThrAsnSerLeuAspAspGluValTyTyrLeuProValArgTySerHis 159  
DB 437 CATTCACACAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 496

QY 160 ValTyTySerTyTySerTyTyLeuAsnAsnProProGlyArgValPheThrLeuValPhe 179  
DB 497 CTCAGAGGATCTATAAATCTTATACACACCTGCTGCTGCTGCTGCTGCTGCTGCT 556

QY 180 ArgLeuThrLeuGlyPheProLeuTyTyrLeuThrAsn1LeuSerGlyValTyTy 199  
DB 557 ATGTTCACCCCTAGGATTTCTTATCTTCTTGAACAATATTTCCGGCAAGAAATAGCAT 616

QY 200 ArgPheAlaAsnHisPheAspProMetSerPro1LeuPheAsnAspArgGluArgValGln 219  
DB 617 AGGTTTGCACCAACCTTGCACCCCATGATGATGATGATGATGATGATGATGATGATGAT 676

QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAla1LeuValLeuValAla 239  
DB 677 GTCCTCTTCTGATCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 736

QY 240 AlaTyTyAlaAlaAlaTyTyVal1LeuAsnMetTyTyAla1LeuProValLeuGlyValSerVal 259  
DB 737 AATTAAGAGAGCTGCTGGGTGGCGATGATGATGATGATGATGATGATGATGATGATGAT 796

QY 260 PhePheValLeu1LeuTy 279  
DB 797 TTTTTCATGTGATCAGATCTTCTTACCCACACCATCATGCTGCTGCTCATTAATGATTTCA 856

QY 280 ThrGluTrpAsnTrp1LeuGlyAlaLeuSerThr1LeuAspArgAspPheGlyPheLeu 299  
DB 857 ACTGAAATGAACTGATCAGAGGAGCTTGTGACCAATGATGATGATGATGATGATGATGAT 916

QY 300 AsnArgValPheHisAspValThrHisValLeuHis1LeuLeuSerTyTyTyr 319  
DB 917 AATGATGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 976

QY 320 ProHisTyTyHisAlaTyTyGluAlaArgAspAla1LeuProValLeuGlyGluTyTy 339  
DB 977 CCACACTATCATGCAAGAGAGCAAGGATGATCAATCAACCGATCTTGGGCGACTTTTAT 1036

QY 340 Lys1LeuAspArgThrPro1LeuPheLysAlaMetTyTyArgGluAlaGlyCys1LeuTy 359  
DB 1037 ATGATCATATGAGATCCCAATTTTAAAGCAATGAGAGGCGCAATGATGATGATGAT 1096

QY 360 IleGluProAspGluAspSerGluHisGlyValPheTyTyTyTyTyTyTyTyTyTyTy 377  
DB 1097 ATCAGAGCT-----GATAGCAAGCTCAAGGTTTATGATGATCAATTAATTTG 1144

RESULT 3  
US-09-981-124-1  
Sequence 1, Application US/09981124  
Patent No. US20020165144A1  
GENERAL INFORMATION:  
APPLICANT: Green, Allan  
APPLICANT: Singh, Surinder  
APPLICANT: Lemman, Marie  
APPLICANT: Skymee, Sten  
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD  
FILE REFERENCE: 26-98A  
CURRENT APPLICATION NUMBER: US/09/981,124  
PRIOR APPLICATION NUMBER: US 09/059769  
PRIOR FILING DATE: 1998-04-14  
PRIOR FILING DATE: 1997-04-16  
PRIOR APPLICATION NUMBER: AU P06223  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: AU P06226  
PRIOR FILING DATE: 1997-04-15  
PRIOR APPLICATION NUMBER: US 60/050403  
PRIOR FILING DATE: 1997-06-20  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1358  
TYPE: DNA  
ORGANISM: Crepis palaestina  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1151)  
OTHER INFORMATION:  
US-09-981-124-1

Alignment Scores:  
Pred. No.: 1,65e-181 Length: 1358  
Score: 1589.50 Matches: 285  
Percent Similarity: 85.98% Conservative: 40  
Best Local Similarity: 75.40% Mismatches: 48  
Query Match: 97.65% Indels: 5  
DB: 9 Gaps: 3

US-10-069-772-2 (1-377) x US-09-981-124-1 (1-1358)

QY 1 MetG1YAlaG1YArgMetSerAspProSerGluGlyValAsn1LeuGluArgVal 20  
DB 30 ATGGGTGCGCGCGCT-----GTCGACATCGGAAAAATGCGTATGGAACGATC 83

QY 21 ProValAspPro---ProPheThrLeuSerAspLeuValAsn1LeuProThrHisGly 39  
DB 84 TCAGTATATCAAGTAACCTTCTCACTAGATATTGAAGCAAGCAATCCCTCCCATTGC 143

QY 40 PheGluArgSerVal1LeuArgSerSerTyTyValValHisAspLeu1LeuAlaTy 59  
DB 144 TTCAGAGATCTGTAACCCGCTCATCTTACTATGTTTCAAGATCTCATTAATGCTTAC 203

QY 60 ValPheTy 79  
DB 204 ATCTTCTACTTCTTGCACACATATATCCCTACTTCTTCTACTAGTATGCTTACTTA 263

QY 80 AlaTrpProValTyTyTrpPheCysGluAlaSer1LeuThrGlyLeuTrpVal1Leu 99  
DB 264 GCTTGGCCGCTTACTGTTTGTCAAGCTAGCGTCTCCTCATGATGATGATGATGATGAT 323

```

QY      100 Hisglucysglyhisalapheseraptryglnleuileaspaspilevalglyphe 119
DB      324 CACGATGTGGTACCATGCGCTTTAGCAACTACATGATGTTGACGACATGTGGGCTTC 383
QY      120 ValleunisseralaleuenthProtyrPheSerTrpIySerHisArgAsnHis 139
DB      384 ATCCCTCCACTATTTCTCTCCACCCCGATATTTCTTGGAATTTAGTACCCGGATATAC 443
QY      140 HisAlaAntThrAsnSerleuaspasnapgluValTyrIleProIyArgIySerIys 159
DB      444 CATTCACACAGAGTTCATGATGATACATGATGATGATGATGATGATGATGATGATGAT 503
QY      160 ValIySileTySerIySerleuaspasnapProIyArgIyValPheThrIleuValPhe 179
DB      504 CTCGGCGGTATCTAATAACTCTTATACACACCACTGGCGGCTGTGGTTGATATAC 563
QY      180 ArgIeuthrIleuGlyPheProleuTyIleuenthThrAsnIleSerGlyLysIyTyGly 199
DB      564 ATGTTCACCTTAGATTTCTTTATACCTTTGACAAATATTTCCGGCAAGAAATACGAC 623
QY      200 ArpPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgIyArgValGln 219
DB      624 AGGTTTGGCAACCACTTGCACCCCATGATGATGATGATGATGATGATGATGATGATGAT 683
QY      220 ValIleuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysIleuValAla 239
DB      684 GTCTTCCTTGGGATCTTGCTCTTCTGCGGTTTATGAAATTAAGATTCCTGATACA 743
QY      240 AlalysglyAlaIleTyrValIleAsnMetTyrAlaIleProValIleuGlyValSerVal 259
DB      744 AATAAGAGAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 803
QY      260 PhePheValIleuIleThrTyIleuHisIleThrHisIleuSerIleuProHisTyrAspSer 279
DB      804 TTTTCGATGTGATACCTTCTTGCACACACCACTGATGATGATGATGATGATGATGATGAT 863
QY      280 ThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299
DB      864 ACTGAATGGAATGTGATCAGAGGGGCTTGTGCAAGATCAGATGAGGACTTGGATTCCTG 923
QY      300 AsnArgValPheHisAspValThrHisIleValIleuHisIleuIleSerTyIle 319
DB      924 AATAGTGTTCCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983
QY      320 ProHisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValIleuGlyValTyrTyr 339
DB      984 CCACATTCATGCAAGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1043
QY      340 LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr 359
DB      1044 ATGATCGACAGGACTCCATTTTAAAGCAATGTAAGAGGAGGAGGAGGAGGATGATGAT 1103
QY      360 IleGluTrpAspGluAspSerGluHisIySileGlyValPheTyrTyrHisIyMet 377
DB      1104 ATCGAGCTT-----GATAGCAAGCTCAAGGTGTTTATGTGATCATTAATG 1151

```

## RESULT 4

```

US-10-425-114-14778
; Sequence 14778, Application US/10425114.
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28

```

```

; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14778
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-001-B9_FLI
US-10-425-114-14778

Alignment Scores:
Pred. No.: 3,24e-153 Length: 1586
Score: 1356.50 Matches: 237
Percent Similarity: 78.42% Conservative: 61
Best Local Similarity: 62.37% Mismatches: 77
Query Match: 66.27% Indels: 5
DB: 13 Gaps: 2

US-10-069-772-2 (1-377) x US-10-425-114-14778 (1-1586)
QY      1 MetGlyAlaGlyIyArgMetSerAspProSerGluGlyLys-----AsnIle 16
DB      74 ATGGGGGGGGGTGGCGCAAGTGAATGTTCTCTGCCAAGAGAGTCAAGGTTGACCT 133
QY      17 LeuGluArgValProValAsp---ProPheThrIleuSerAspLeuValAlaIle 35
DB      134 TTGAAGCGGGTCCATTGGAACCTTCATTTAGTCTCAGCCAAATCAAGAGGTCAAT 193
QY      36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValAlaHisAspLeu 55
DB      194 CCACCTCACTGTTTCCAGCGCTTCTGTTCCGCTCATCTCTCATGTTGTTAGACCTC 253
QY      56 IleValAlaTyrValPheTyrTyIleuAlaAsnThrTyIleProleuIleProThrPro 75
DB      254 ACCAATAGCTTCTGCGCTTATTAATGTTCCACCACTTATCTTCCACCTTCCAGCCCT 313
QY      76 LeuAlaTyrIleuAlaIleTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95
DB      314 CTCTTCTTCTTGGATGCGCAATCTACCTGCGCTGCTCCAGGTTGCATCTTACGAGATT 373
QY      96 TrpValIleGlyHisGluCysGlyHisIleAlaPheSerAspTyrGlnIleAspAsp 115
DB      374 TGGGCTATGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433
QY      116 IleValGlyPheValIleuHisSerAlaLeuLeuThrProTyPheSerTrpIyTySer 135
DB      434 ATGTGTCCTTGTGCTTCCATCCGCTGCTTCCATGATGATGATGATGATGATGATGATGAT 493
QY      136 HisArgAsnHisIleAlaAsnThrAsnSerIleuaspasnapgluValTyrIleProLys 155
DB      494 CATGCCCTGCACCACTCCAACTGCTTCTTGAAGCGGAGTGAAGATTTGTGCAAG 553
QY      156 ArgIySerIyLysValIySileTySerIySerleuaspasnapProIyArgValPhe 175
DB      554 CAGAAATCTGTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
QY      176 ThrIleuValPheArgLeuThrIleuGlyPheProleuTyIleuLeuThrAsnIleSerGly 195
DB      614 ACTCTTGTCTGCACCTCACACTGTGTTGGCCCTGTGATGCTTGAATGTTCTGGA 673
QY      196 LysIySileTyGlyIyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
DB      674 AGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733
QY      216 GluArgValGlnIleuLeuSerAspPheGlyLeuAlaValPheTyrAlaIleLys 235
DB      734 GATGACTTCAAAATATATATATATATATATATATATATATATATATATATATATATATAT 793
QY      236 LeuLeuValAlaAlaLysGlyAlaAlaIleTyrValIleAsnMetTyrAlaIleProValLeu 255
DB      794 CGCTTGGCATGCGAAAGAGCTTGGCGGAGTGTGTTTATGAGGTTCCATGCTGA 853
QY      256 GlyValSerValPhePheValIleuIleThrTyIleuHisIleThrHisIleuSerIleuPro 275

```

Db 854 GTGCTAATGATTTTGGTGTGATTAATCATTTGACAGCATCTACCTGCAATTTGCCA 913  
 Qy 276 HistyrAspSerThrGluTrpAsnTrpIleuysGlyAlaLeuSerThrIleAspArgAsp 295  
 Db 914 CATTAACCTTCTCTGAGTGGGACGCTGTGAGAGAGCTTTAGCAACAGTGTAGATGAAAT 973  
 Qy 296 PheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisIleu 315  
 Db 974 TATGGAATCTGAAACAAGAGCTCTTCATATAATTAACAGACACTGATGACATCATCTTG 1033  
 Qy 316 IleSerTrpIleProHisIleThrHisAlaIleuGlyAlaIleAspAlaIleLeuProValIleu 335  
 Db 1034 TTCTCCACAATGCCCATTTATCATGCAATGAGGCTACAAAGGCATATAAACCCTTTTGG 1093  
 Qy 336 GlyGluTrpTrpLysIleAspArgThrProIlePheIleuAlaMetTrpArgGluAlaLys 355  
 Db 1094 GGAAGATTATTCGTTGATGAGACTCATTTGTCAAAGGCATGTGAGAGAGCAAGA 1153  
 Qy 356 GluCyAlieTrpIleGluProAspGluAspSerGluHisIleGlyValPheTrpTrpHis 375  
 Db 1154 GAGGTATTATTATGTGAGCAGATCAAGTACCGAGCAAAAGGTGATTGTTGTGACAAAC 1213

## RESULT 5

US-10-424-599-123945/c  
 ; Sequence 123945, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424.599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 123945  
 ; LENGTH: 2931  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_8292C.1  
 US-10-424-599-123945

## Alignment Scores:

Pred. No.: 8,86e-153 Length: 2931  
 Score: 1356.50 Matches: 237  
 Percent Similarity: 78.42% Conservative: 61  
 Best Local Similarity: 62.37% Mismatches: 77  
 Query Match: 66.27% Indels: 5  
 Gaps: 2

US-10-069-772-2 (1-377) x US-10-424-599-123945 (1-2931)

Qy 1 MetGlyAlaGlyLysArgMetSerAspProSerGluGlyLys-----AsnIle 16  
 Db 1713 ATGGGGGGGGGTGGCCCACTGATGTTCTCTCTGCCAACAGGAAGTCAAGAGTTGACCT 1654  
 Qy 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysIle 35  
 Db 1653 TTGAAGGGGGGTGCAATTTGAAAAACCTTCATTTAGTCTCAGCAAAATCAAGAAGTCAATT 1594  
 Qy 36 ProThrHisCysPheGluArgSerValIleArgSerSerTrpTrpValValHisAspLeu 55  
 Db 1593 CCACCTCACTGTTTCCAGCGTTCGTGTTTCCGCTCATTTCTCTATGTTGTTTACGACCTC 1534  
 Qy 56 IleValAlaTrpValPheTrpTrpLeuAlaAsnThrTrpIleProLeuIleProThrPro 75  
 Db 1533 ACCTATGCTTCTGCTCTATATATATGTCACACCACTTATCTTCACCTCTTCCAGCCCT 1474  
 Qy 76 LeuAlaTrpLeuAlaTrpProValTrpTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95

Db 1473 CTCCTTTCTTGGCATGGCCCAATCTACTGGCTGTCCAAAGGTGCATCTTAATGAGATT 1414  
 Qy 96 TrpValIleGlyHisGluCysGlyHisHisIleAspSerAspTrpGluLeuIleAspAsp 115  
 Db 1413 TGGGTCAATGGCCATGATGTGGCCCAATCATTAATGATGATCTACAGCTTGTGATGAT 1354  
 Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTrpPheSerTrpLysTrpSer 135  
 Db 1353 ATGTGGCTTGTGTCCTTCATCTCCGGTCTCTAATGCCATCTTTTCATGAAATATACAGC 1294  
 Qy 136 HistArgAsnHisHisAlaAsnThrAsnSerLeuAsnAspAspGluValTrpIleProLys 155  
 Db 1293 CATGGCGCTGCACCTCCAAACACTGTTCTCTTGAAGCGGATGAAATTTGTGCCAAG 1234  
 Qy 156 ArgLysSerLysValLysIleTrpSerLysLeuLeuAsnAspProGlyArgValPhe 175  
 Db 1233 CAGAAGTCTGTATCAAGTGTACTTAAATACCTTAACAATCTCCAGGAGAGTCTTC 1174  
 Qy 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTrpLeuLeuThrAsnIleSerGly 195  
 Db 1173 ACTCTGTGTGCACCTTCACACTGTGTGGCTTGTACTGGCTTTAAATGTTTCTGGA 1114  
 Qy 196 LysLysTrpGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215  
 Db 1113 AGGCGTTATGATTAATTTGCTTGCACACTATACCCATATGCGTCCATTTACTGTATGCT 1054  
 Qy 216 GluArgValGluValLeuLeuSerAspPheGlyLeuLeuAlaValPheTrpAlaIleLys 235  
 Db 1053 GACGACTTCCAAATATATATATATCAAGTCAGAGAGTACTTGCAGTATGCTATGGCTTTC 994  
 Qy 236 LeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTrpAlaIleProValLeu 255  
 Db 993 CGTCTGTCATGGCAAAAGACTTGCCTGGGTGGTGTGTTATGAGGTTCCATGCTCA 934  
 Qy 256 GlyValSerValPhePheValLeuIleThrTrpLeuHisHisThrHisLeuSerLeuPro 275  
 Db 933 GTGGTCATGATGATTTTGGTGTGATTAATCATTTGACGACATATCTACCCCTGATGGCA 874  
 Qy 276 HistyrAspSerThrGluTrpAsnTrpIleuysGlyAlaLeuSerThrIleAspArgAsp 295  
 Db 873 CATTAACCTTCTCTGAGTGGGACGCTGTGAGAGAGCTTTAGCAACGATGATGAAAT 814  
 Qy 296 PheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisIleu 315  
 Db 813 TATGGAATCTGAAACAAGGCTTCCATATAATTAACAGACACTCATGTAGCATCATCTTG 754  
 Qy 316 IleSerTrpIleProHisIleThrHisAlaIleuGlyAlaIleAspAlaIleLeuProValIleu 335  
 Db 753 TTCTCCACAATGCCCATTTATCATGCAATGAGGCTACAAAGGCATATAAACCCTTTTGG 694  
 Qy 336 GlyGluTrpTrpLysIleAspArgThrProIlePheIleuAlaMetTrpArgGluAlaLys 355  
 Db 693 GGAAGATTATTCGTTGATGAGACTTCATTTGTCAAAGGCATATGAGAGAGCAAGA 634  
 Qy 356 GluCyAlieTrpIleGluProAspGluAspSerGluHisIleGlyValPheTrpTrpHis 375  
 Db 633 GAGGTATTATTATGTGAGCAGATCAAGTACCGAGCAAAAGGTGATTGTTGTGACAAAC 574

## RESULT 6

US-10-465-800-3  
 ; Sequence 3, Application US/10465800  
 ; Publication No. US20040029283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fillicetti, JoAnne  
 ; TITLE OF INVENTION: Intron Double Stranded RNA Constructs and Uses Thereof  
 ; FILE REFERENCE: 16517.266  
 ; CURRENT APPLICATION NUMBER: US/10/465.800  
 ; CURRENT FILING DATE: 2003-06-20  
 ; PRIOR APPLICATION NUMBER: US 60/390,186  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3

```

; LENGTH: 6220
; TYPE: DNA
; ORGANISM: Glycine max
US-10-465-800-3

Alignment Scores:
Pred. No.: 3,036-152 Length: 6220
Score: 1356.50 Matches: 237
Percent Similarity: 78.42% Conservative: 61
Best Local Similarity: 62.37% Mismatches: 77
Query Match: 66.27% Indels: 5
DB: 13 Gaps: 2

US-10-069-772-2 (1-377) x US-10-465-800-3 (1-6220)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
DB 4734 ATGGGGGGGGGGTGGCCGAACGTATGTTCTCTGCGCAACAGAGAGTCAAGGTGACCT 4793

QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAlaIle 35
DB 4794 TTGAAGCGGGTCCATTGCAAAACCTTCATTAGTTCAGCCAAATCAAGAGGTCAAT 4853

QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAspLeu 55
DB 4854 CCACTCTCACTGTTTCCAGCGTTCTGTTCCCTCATTTCTCTATGTTGTTTACACCTC 4913

QY 56 IleValAlaTyValPheTyTyTyLeuAlaAsnThrTyTyrIleProLeuIleProThrPro 75
DB 4914 ACCATAGCTCTGCTGCTCATATATATGTGCAACCCATTACTTCACCTCTCCAGCCCT 4973

QY 76 LeuAlaTyLeuAlaTrpProValTyTyTyPheCysGlnAlaSerIleLeuThrGlyLeu 95
DB 4974 CTCTCTTTCTTGGCAGTGGCAATCTACGCGTGTCCAGGTTGCACTTACTGAGAT 5033

QY 96 TrpValIleGlyHisGlyCysGlyHisHisAlaPheSerAspTyGlnLeuIleAspAsp 115
DB 5034 TGGGCATTTGCCAGAGGTGGCCACCATTCAGTACGATTCAGTGGCTTATGAT 5093

QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTyPheSerTyTySer 135
DB 5094 ATTGTTGGCTGTGCTCTCCACTCCGAGTCTCTAGTCCCATCTTTCAATGAAATACAGC 5153

QY 136 HisAlaGlnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyTyrIleProLys 155
DB 5154 CATGCCCGCTCACCTCCAAACCTGTTCTCTTGAGCGGAGAAATTTTGGCCAAAG 5213

QY 156 ArgLysSerTyValLysIleTyTySerLysLeuAsnAsnProProGlyArgValPhe 175
DB 5214 CAGAACTCTGTATCAAGTGTACTTAAATACCTTAACATCTCCAGGCGAGATCTTC 5273

QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSerGly 195
DB 5274 ACTTTGGCTGTACACCTCACCTGTTGGCCCTTGACTGCTTAAATGTTTCTGGA 5333

QY 196 LysLysTyTyGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
DB 5334 AGGCTTATGATGATGTTGCTTGGCCCATATGACCATATGATGTCATTAATCTGATCGT 5393

QY 216 GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyrAlaIleLys 235
DB 5394 GAAACACTTCAATATATATATATCAATGAGAGATCTTGCATGCTATGAGCTTTTC 5453

QY 236 LeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyTyrAlleProValLeu 255
DB 5454 CGTCTTGCATGCAAAAGAGCTTGCCTGGGGTGGTGGTGTATTAAGAGTTCAATGGCA 5513

QY 256 GlyValSerValPhePheValLeuIleThrTyTyLeuHisHisHisLeuSerLeuPro 275
DB 5514 GTGGATCATGATGATTTTGGTGTGATTAATCTTGGCAGCATACCTCCAGCTTGGCA 5573

QY 276 HisTyArgSerThrGluTrpAsnThrIleLysGlyAlaLeuSerThrIleAspArgAsp 295

```

```

DB 5574 CATTACCTCTCTGAGTGGAGACTGTGTGAGAGAGCTTTAGCAACAGTGATAGAGAT 5633
QY 296 PheGlyPheLeuAsnArgValPheHisAspValThrIleThrHisValLeuHisIleLeu 315
DB 5634 TATGAAATCTGAACAAAGCTCTTCCATATATATTAACAAGACTAGTGCACATCACTTG 5693
QY 316 IleSerTyTyrIleProHisIleTyHisAlaLysGluAlaAspAlaIleLysProValLeu 335
DB 5694 TTCTCCAAATGCCCATTTATCATGCAATGAGAGGTACAAAGGCATTAATAAACCTTTTG 5753
QY 336 GlyLysTyTyTyLysIleAspArgThrProIlePheLysAlaMetTyTyArgGluAlaLys 355
DB 5754 GGAGAGTATTAATCGGTTTGAATGAGACTCAATTTGCAAGGCATATGTGAGAGAGCAAGA 5813
QY 356 GluCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyValPheTyTyHis 375
DB 5814 GAGTGTATTTATGTGGAGCCAGATCAAAATGACCGAGCAAAAGGTATTTTGTATCAAC 5873

RESULT 7
US-10-176-149-3
; Sequence 3, Application US/10176149
; Publication No. US20030172399A1
; GENERAL INFORMATION:
; APPLICANT: Filiaati, Joanne, J.
; TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of P
; FIDE REFERENCE: 16518.056
; CURRENT APPLICATION NUMBER: US/10/176.149
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/151,224
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/172,128
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: US 09/638,508
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6220
; TYPE: DNA
; ORGANISM: Glycine max
US-10-176-149-3

Alignment Scores:
Pred. No.: 3,036-152 Length: 6220
Score: 1356.50 Matches: 237
Percent Similarity: 78.42% Conservative: 61
Best Local Similarity: 62.37% Mismatches: 77
Query Match: 66.27% Indels: 5
DB: 15 Gaps: 2

US-10-069-772-2 (1-377) x US-10-176-149-3 (1-6220)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
DB 4734 ATGGGGGGGGGGTGGCCGAACGTATGTTCTCTGCGCAACAGAGAGTCAAGGTGACCT 4793

QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysAlaIle 35
DB 4794 TTGAAGCGGGTCCATTGCAAAACCTTCATTAGTTCAGCCAAATCAAGAGGTCAAT 4853

QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAspLeu 55
DB 4854 CCACTCTCACTGTTTCCAGCGTTCTGTTCCCTCATTTCTCTATGTTGTTTACACCTC 4913

QY 56 IleValAlaTyValPheTyTyTyLeuAlaAsnThrTyTyrIleProLeuIleProThrPro 75
DB 4914 ACCATAGCTCTGCTGCTCATATATATGTGCAACCCATTACTTCACCTCTCCAGCCCT 4973

QY 76 LeuAlaTyLeuAlaTrpProValTyTyTyPheCysGlnAlaSerIleLeuThrGlyLeu 95
DB 4974 CTCTCTTTCTTGGCAGTGGCAATCTACGCGTGTCCAGGTTGCACTTACTGAGAT 5033

```

```

Qy      96  TrpValIleGlyHisGluCysGlyHisIleAspSerArgLysIleLeuIleAspArg 115
Db      5034 TGGGTCAATTGGCCATGAGTGTGGCCACCATCATTCAGTACAGTACAGTCTTGAT 5093
Qy      116  IleValGlyPheValIleHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer 135
Db      5094 ATTGTGGCTTGTGCTCCATCCGCTCCGCTCTTCTAGTCCATCTTTTCATGAAATACAGC 5153
Qy      136  HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgIleValTyrIleProLys 155
Db      5154 CATGCCGCTCACCACTCCACACATGCTTCTTTAGCGCGGATGAGATTTGTGCGCAAG 5213
Qy      156  ArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProProGlyArgValPhe 175
Db      5214 CAGAAAGCTCTGTACAGTGTACTCTTAATACCTTAACTTCAATCCCGACGAGAGCTCTC 5273
Qy      176  ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db      5274 ACTCTTGCTGTACCCCTCACACTTGTTGGCTTGTGCTTGTAAATGTTTCTGGA 5333
Qy      196  LysLeuTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
Db      5334 AGGCGCTTATGATATATATTTGCTTCCCATATACACCATATGCTCCCATTTACTGTAGTCT 5393
Qy      216  GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235
Db      5394 GAACGACTTCAAAATATATATATCATGATGACAGTACTTGCAGTATGCTAGGCTTTC 5453
Qy      236  LeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValIleu 255
Db      5454 CGCTTGCCATGAGCAAAAGAGCTTGCCTGGGTGTGTGTATGAGAGTTCATTTGCTA 5513
Qy      256  GlyAlaSerValPhePheValLeuIleThrTyrLeuHisIleSerHisLeuSerIlePro 275
Db      5514 GTGGTCATAGGATTTTGGTGTGATATATCTTGTGACGATACCTCACCTGATGCA 5573
Qy      276  HisTyrAspSerThrGluTyrAsnTyrIleLysGlyAlaLeuSerThrIleAspArgAsp 295
Db      5574 CATTAACCTTCTCTGAGTGGAGCTGTGTGAGAGAGCTTTAGCAACAGTGTATGAT 5633
Qy      296  PheGlyPheLeuAsnArgValPheHisAspValThrHisIleValIleHisIleu 315
Db      5634 TATGGAATCCGAAACAAGCTCTCCATATATTAACAACACTGATGACATCATCTTG 5693
Qy      316  IleSerTyrIleProHisIleTyrHisIleAlaLysGlyAlaAspAlaIleLysProValIleu 335
Db      5694 TTCTCCCAATGACCAATATATCATGCAATGAGGCTCAAAAGGCATTAATCCCATTTTG 5753
Qy      336  GlyLysTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGlyAlaLys 355
Db      5754 GGAAGATTTATCCGTTTGTATGAGATCTCATTTGTCAAGGCAATGTGAGAGAGCAAGA 5813
Qy      356  GluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyrTyrHis 375
Db      5814 GAGGTGATTTATGTGAGAGCAGATCAAGGTACCGAGACAAAGGTATTTTGTGACAC 5873

```

## RESULT 8

```

US-10-425-114-12782
; Sequence 12782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

```

```

; SEQ ID NO 12782
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701211444_F11
US-10-425-114-12782

Alignment Scores:
Pred. No.: 4,58e-152 Length: 1457
Score: 1346.50 Matches: 236
Percent Similarity: 78.16% Conservative: 61
Best Local Similarity: 62.11% Mismatches: 78
Query Match: 65.78% Indels: 5
DB: 13 Gaps: 2

US-10-069-772-2 (1-377) x US-10-425-114-12782 (1-1457)
Qy      1  MetGlyAlaGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
Db      30  ATGGGGGGGGGTGGCCGACAGTATGCTCTCCCAACAGGAGTCAAGAGTTCGACCT 89
Qy      17  LeuGluArgValProValAsp--ProProPheThrLeuSerAspLeuLysValAlaIle 35
Db      90  TTGAAGCGGGTGCATTTGAAAACTCCATTTAGTCTCAGCCAAATCAAGAGTCAAT 149
Qy      36  ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValAlaHisAspLeu 55
Db      150  CCACCTCACTGTTCACAGCGTTGTTTCCGCTCATCTTCCTTAAGTTGTTAGACCTC 209
Qy      56  IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75
Db      210  ACCATAGCTTCTGCTCTATATATGTTGCAACCATTAATCTCCACCTCTCCAGCCCT 269
Qy      76  LeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95
Db      270  CTCTCTTCTTGGATGGATGCCAATCTAGTGGCTGTCCAGAGTTCATCTTACGAGTT 329
Qy      96  TrpValIleGlyHisGluCysGlyHisIleAspSerArgLysIleLeuIleAspArg 115
Db      330  TGGGTCAATTGGCCATGAGTGTGGCCACCATCATTCAGTACAGTACAGTCTTGATAT 389
Qy      116  IleValGlyPheValIleHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer 135
Db      390  ATTGTGGCTTGTGCTCCATCCGCTCTCTTCTTATCCATCTTTTCATGAAATACAGC 449
Qy      136  HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgIleValTyrIleProLys 155
Db      450  CATGCCGCTCACCACTCCATACATGCTTCTTGAAGGAGTGAAGTATTTGTGCGCAAG 509
Qy      156  ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPhe 175
Db      510  CAGAAAGCTCTGTATCAAGTGTACTTAAATACCTTAAATCTTCCAGGAGAGTCTC 569
Qy      176  ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db      570  ACTCTTGCTGTACCCCTCACACTTGTTGGCTTGTGCTTGTAAATGTTTCTGGA 629
Qy      196  LysLeuTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
Db      630  AGGCGCTTATGATATATTTGCTTCCCATATACCATATGCTCCATTTACTGTAGTCTG 689
Qy      216  GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235
Db      690  GAACGACTTCAAAATATATATATCATGATGACAGTACTTGCAGTATGCTAGGCTTTC 749
Qy      236  LeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValIle 255
Db      750  CGTCTTGCCATGAGCAAAAGAGCTTGGTGTGTGTATTTAGAGTTCCATTTGCTA 809
Qy      256  GlyAlaSerValPhePheValLeuIleThrTyrLeuHisIleSerHisLeuSerIlePro 275
Db      810  GTGGTCATAGGATTTTGGTGTATTAATCTTGCAGCATACCTGCACTGCAATTTGCA 869

```

Qy 276 HistyAapSerThgIuTTPasntRplelysgIyAlaLeuSerThrIleAspArg 295  
Db 870 CATTAACCTCTCGAGTGGAGCTGTGAGAGAGAGCTTTAGCAACAGTGAATGAGAT 929  
Qy 296 PheGlyPheLeuAsnArgValPheHisAspValThrIleSThrHisValLeuHisIleu 315  
Db 930 TATGGAATCCGAACAGTCTCCATATATTTACAGACACTGATGACATCACTTG 989  
Qy 316 IleSerTyRleProHisTyRHisAlaIygsIuaIaArgAspAlaIleAspProValIleu 335  
Db 990 TTCTCCAAATGCCCATTTATATCATGAGAGCTTACAAAGGCATATAAACCCATTG 1049  
Qy 336 GlyIuTyRlyValIleAspArgThrProIlePheIyAlaMetTyRArgIuaIyAs 355  
Db 1050 GGAGAGTATATCCGTTGATGAGACTCATTTGTCAAGGCATGTGAGAGAGCAAGA 1109  
Qy 356 GluCyIleTyRleGluProAspGluAspSerGluHisIyGlyValPheTrpThrHis 375  
Db 1110 GAGGTATTTATGTGAGCCAGATCAAGATCCGAGCAAGAGTGTATTTGTGACAC 1169

RESULT 9  
US-09-837-751-5  
; Sequence 5, Application US/09837751  
; Patent No. US20020104124A1  
; GENERAL INFORMATION:  
; APPLICANT: Green, Allan  
; APPLICANT: Singh, Surinder  
; APPLICANT: Liu, Qing  
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil  
; FILE REFERENCE: 45-00  
; CURRENT APPLICATION NUMBER: US/09/837,751  
; CURRENT FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: US 60/198,124  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 1422  
; TYPE: DNA  
; ORGANISM: Gossypium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98)..(1246)  
US-09-837-751-5

Alignment Scores:  
Pred. No.: 2,176-150 length: 1422  
Score: 1332.50 Matches: 220  
Percent Similarity: 79.16% Conservative: 70  
Best Local Similarity: 60.69% Mismatches: 74  
Query Match: 65.10% Indels: 5  
Gaps: 2

US-10-069-772-2 (1-377) x US-09-837-751-5 (1-1422)

Qy 1 MetGlyAlaGlyIyArgMetSerAspProSerGluGlyIyS-----AsnIle 16  
Db 98 ATGGGTGCTGAGGAGGAGATGTCCGTTCCAAAGTCCAAAACCCGAATTGCAATCA 157  
Qy 17 LeuGluArgValProValAsp---ProProPheThrIleuSerAspLeuIyValAlaIle 35  
Db 158 CTGAAGCGAGTTCCTACTCAAGCCACCTTCACTGTGAGTAATCAAGAAACCCATC 217  
Qy 36 ProThrHisCySPheGluAspSerValIleArgSerSerTyRlyValValHisAspLeu 55  
Db 218 CCACCACTGTTTCAAGGCTCCGTTTACGCTCATTTCTCATCTCTCTTACACATTT 277  
Qy 56 IleValAlaTyRValPheTyRlyLeuAlaAsnThrTyRleProLeuIleProThrPro 75  
Db 278 ATATTGGCTCTCTTTTACATGATGGCCACCAATTAATCTCTTACACTTCTCAGGCT 337  
Qy 76 LeuAlaTyRLeuAlaTrpProValTyRTrpPheCySGlnAlaSerIleLeuThrGlyLeu 95

Db 338 CTCTCCAAAGTGGCTTGGCTCTTTATTTATGAGCCATGCAAGGTGATTTTACCGGCTT 397  
Qy 96 TrpValIleGlyHisIyGlyCyGlyHisIleAlaPheSerAspTyRGlLeuIleAspArg 115  
Db 398 TGGGTCAATAGCCCATGATGATGGCCACCATCTTTCAGTATATATCAATGAGCTTGACAGC 457  
Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyRPheserTrpIyTyrSer 135  
Db 458 ACCGGGGCTTATCTTCCACTCTCTCTCTTATGCTCATATTTCTTGGAAATATAGC 517  
Qy 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgIuaIyTrleProIyS 155  
Db 518 CACGGGCTCACTTCTTCAACCGGTTCCCTCCAAAGGATGAGAGTGTGTTCCCAAG 577  
Qy 156 ArgIySerIySValIyIleTyRserIyLeuLeuAsnAsnProProGlyArgValPhe 175  
Db 578 AAAAATCTGTTTAAATGATGGTGGCCAAACATTCACCAATCCACCGGTCGGTTCTG 637  
Qy 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyRLeuLeuThrAsnIleSerGly 195  
Db 638 TCAATCACCATTCACATTAACCTTGTGGTGGCCGCTTATGCTTCAACGTTGCCGCG 697  
Qy 196 LysIyTyRglYArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215  
Db 698 CGGCTTACGACAGGTGCTTGCCTGCACTATAGACCTTACGCCCCATATTTTCCAGCGG 757  
Qy 216 GluArgValAlaIyLeuLeuSerAspPheGlyLeuLeuAlaValPheTyRAlaIleIyS 235  
Db 758 GAAAGATCCCAATCTATATCTGAGCGCGCGCTCGCTGCTGCTATGCGGCTTAC 817  
Qy 236 LeuLeuValAlaAlaIyGlyAlaAlaTrpValIleAsnMetTyRAlaIleProValLeu 255  
Db 818 CGTCCGTTGGGCGCAAGGGGTAGTGGTGTGTATACGTTTATGGGGTCCATTAATG 877  
Qy 256 GlyValSerValPhePheValLeuIleThrTyRLeuHisIleSThrHisLeuSerLeuPro 275  
Db 878 GTGGTTAAGCCTTCTTATGATGATACGATTTTGCACACACTCACTCATCTTGGCG 937  
Qy 276 HistyAapSerThgIuTTPasntRplelysgIyAlaLeuSerThrIleAspArg 295  
Db 938 CACTATGATTCCTCGAGTGGAGACTGATGAGAGAGGACTTATCACTGTGACAGAGAT 997  
Qy 296 PheGlyPheLeuAsnArgValPheHisAspValThrIleSThrHisValLeuHisIleu 315  
Db 998 TATGGATTTTAAACAGGTTTCCATTAACATAACCGACCTCATGTGCTCATCATTTG 1057  
Qy 316 IleSerTyRleProHisTyRHisAlaIygsIuaIaArgAspAlaIleAspProValIleu 335  
Db 1058 TTTTGCACATAGCTCTCATATCATGCCATGTGGCCACCAAGGCATATAAGCCATATTG 1117  
Qy 336 GlyIuTyRlyValIleAspArgThrProIlePheIyAlaMetTyRArgIuaIyAs 355  
Db 1118 GGGGAATCTATCACTTGTGATGGAGTGGCTGTCTATAAGCGAATATGAGAGGAGCGAAG 1177  
Qy 356 GluCyIleTyRleGluProAspGluAspSerGluHisIyGlyValPheTrpThrHis 374  
Db 1178 GAGGTCTCTTACGTTGAACAGATGAGGCGCAAGATAAAGTGTGTTTGTGTTT 1234

RESULT 10  
US-09-852-399-3  
; Sequence 3, Application US/09852399  
; Patent No. US2002045232A1  
; GENERAL INFORMATION:  
; APPLICANT: Olu, Xiao  
; TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND  
; TITLE OF INVENTION: LINOLENIC ACIDS IN PLANTS  
; FILE REFERENCE: BNZ-002  
; CURRENT APPLICATION NUMBER: US/09/852,399  
; CURRENT FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: USN 60/203,027  
; PRIOR FILING DATE: 2000-05-09  
; NUMBER OF SEQ ID NOS: 4

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Calendula officinalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89) ... (1237)
US-09-852-399-3

Alignment Scores:
Pred. No.: 2,63e-149 Length: 1411
Score: 1323.50 Matches: 233
Percent Similarity: 76.32% Conservative: 57
Best Local Similarity: 61.32% Mismatches: 83
Query Match: 64.66% Indels: 7
DB: Gaps: 2

US-10-069-772-2 (1-377) x US-09-852-399-3 (1-1411)
QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyAsnIleLeuGluArgVal 20
DB 89 ATGGGTGAGCGCGGTGCAATGCAAGATCCCAACGAGTGGAACAAACGAGCCGAA 148
QY 21 ProValAsp-----ProProPheThrLeuSerAspLeuLysVal 34
DB 149 CCAATCCAAACGGGTCCCAATGAAACACCCCATTCACAGTTGAGACATGAGAAACG 208
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyTyValValHisAsp 54
DB 209 ATCCCACTCATGTTTTCACACGATCGGTAAATCGTATATTTTCACTAGCTTTTACGAC 268
QY 55 LeuIleValAlaTyTyValPheTyTyLeuAlaAsnThrTyTyIleProLeuIleProThr 74
DB 269 CTCACATCGGTGCAATCTTGTACTGACATGCCAACATTCATCTACCTCCCTACG 328
QY 75 ProLeuAlaTyTyLeuAlaATPProValTyTyTyPheCysGlnAlaSerIleLeuThrGly 94
DB 329 CCGCTCGCTACGATGCGATGCGCCGTTCATGCGCCGTCCAAAGGCGCTTAAACCGG 388
QY 95 LeuThrValIleGlyHisGluCysGlyHisIleAlaPheSerAspTyTyGlnLeuIleAsp 114
DB 389 GTGTGGGTCATAGCCACGAAATGCGCATCATGTTTTCACGACACCAATGGCTCGAT 448
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTyPheSerTyTyTyTy 134
DB 449 GACACCGTGGGTCTCGTCTTGCATCTGTTCTACTCGGCCCTTACTTTTCTGAAAAAT 508
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyTyIlePro 154
DB 509 AGCCACCGTAGGACACCACTCGAACACGCGGTCTGATCGACGACGATGAGTTTTCGTC 568
QY 155 LysArgLysSerLysValLysIleTyTySerLysLeuAsnAsnProProGlyArgVal 174
DB 569 AAGTTGAATAGGCGGTCCGTCGACCGCCGGAACCTTAAACCAACCCGCGCGCATC 628
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSer 194
DB 629 TTGACCTCACTCGTAACCTTAACCTCGGTGGCTCTATACCTCAAGTTCAAGCTTTCG 688
QY 195 GlyLysLysTyTyGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
DB 689 GAGCGGTACTACGACCGGTTCGCGTTCGATTCGACCGGATGACCGCATCTACGAAAG 748
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAlaIle 234
DB 749 CGCAACGCGGTCAAAATCTTCATATCCGACCGCGGATCTTACGCGGATCTTGTGATC 808
QY 235 LysLeuLeuValAlaAlaLysGlyValAlaAlaIleAsnMetTyTyTyValValHisAspLeu 254
DB 809 TTCGCACTCGCAAGACCAAGGCGTCAAGTGGTCTTCAACATGATGAGGCGCCGTTA 868
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyTyLeuHisHisThrHisLeuSerLeu 274

```

```

DB 869 CTCGTGTCACGCGTTCCTAGTCTTATGATCATTCCTACACACACTCACCCTTCGCTC 928
QY 275 ProHisTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
DB 929 CCGCACTTAGCTACACCGAATGAGATGGATTGGTGGGCGCTTCACCAATGACACCT 988
QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValIleHisHis 314
DB 989 GATTACGGGATCTTAACCAAGTGTTCATTAACCAACGACACTCAGTGGCCACCAT 1048
QY 315 LeuIleSerTyTyIleProHisTyTyHisAlaLysGluAlaArgAspAlaIleLysProVal 334
DB 1049 TTGTCTCTTACAAAGCCCTCATTCACATGACATGAGACGAAAGGTGATCAACCGATT 1108
QY 335 LeuGluGlyTyTyTyTyLysIleAspArgThrProIlePheLysAlaMetTyTyArgGluAla 354
DB 1109 TTGGCGCATTTATATCACTTTGACGGAGCTCGATTTTAAAGCGATGTATCGGAAACA 1168
QY 355 LysGluCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyValPheTyTy 374
DB 1169 AAGAGTGCAATTTATGTTGATGAAGATGAGAGGTGAAA---GATGGTGTATTGTTAT 1225

RESULT 11
US-09-995-297-13
; Sequence 13, Application US/09995297
; Patent No. US20020092038A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharma
; APPLICANT: Fan, Zhongong
; APPLICANT: Debono, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; TITLE OF INVENTION: FATY ACID CONTENT
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/09/995,297
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1152)
US-09-995-297-13

Alignment Scores:
Pred. No.: 8,77e-149 Length: 1155
Score: 1318.00 Matches: 233
Percent Similarity: 77.17% Conservative: 61
Best Local Similarity: 61.15% Mismatches: 81
Query Match: 64.39% Indels: 6
DB: Gaps: 4

US-10-069-772-2 (1-377) x US-09-995-297-13 (1-1155)
QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
DB 1 ATGGGTGACAGGTGGAAGAATGCAAGTGTCTCCCTCCCAAGAGTGTGAACGACACC 60
QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAlaIle 35
DB 61 ATCAAGCGGTACCTTCGACACCGCCCTTCACTGTGGAATCTCAAGAAAGCAATC 120
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTyTyValValHisAspLeu 55
DB 121 CCACCGCACTGTTTCAACACGCTGATCCCTGCTCTTCTTCATCTCATCTGGAGATC 180
QY 56 IleValAlaTyTyValPheTyTyTyLeuAlaAsnThrTyTyIleProLeuIleProThrPro 75

```



Db 181 ATCATAGCCTCTGCTTCTACTACGTGGCCACCACTTACTTCCCTCTCTCCCTACCCCT 240  
Qy 76 LeuAlaTyLeuAlaTrpProValTyTrpPheCysGlnAlaSerIleLeuThiGlyLeu 95  
Db 241 CTCCTCTACTCTCGCTGGCTCTCTCACTGGGCTGCCAAGGGTGGCTCTTACACGGGCTC 300  
Qy 96 TrpValIleGlyHisGlyCysGlyHisIleAlaPheSerArgTyTrpGlnLeuIleAspArg 115  
Db 301 TGGGTCATAGGCCACAGATGGGGCCACCAAGCTTACAGCTACCACTGAGCTTGTACAC 360  
Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThiProTyTrpPheSerTrpIleTySer 135  
Db 361 ACCGTGGCTCATCTTCCACT 420  
Qy 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAspGlyValTyTrpIleProIys 155  
Db 421 CATGACGCCACCATTCACACACTGGCTCCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
Qy 156 ArgIysSerIysValIleValIleTySerIysLeuLeuAsnAsnProGlyArgValPhe 175  
Db 481 AAGAAGTCAGACATCAGTGGTACCGCAAGTACCTCAACACCTTGGAGCGACCGTG 540  
Qy 176 ThrLeuValPheArgLeuThiLeuGlyPheProLeuTyTrpLeuThiAsnIleSerGly 195  
Db 541 ATGTTAACGGTTCATCTCTCGCTGGCCGCTTGTACTTACCTTCAAGCTCTCGGGA 600  
Qy 196 LysIlyTyTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214  
Db 601 AGACCTTACGACGGGGCTTGGCTTGCATTTCCACCCCAACGGCTCCATCTACACAGC 660  
Qy 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAlaIle 234  
Db 661 CGCGAGCGCTCTCCAGATATACATCTCCACAGCTGGACATCTCGCGTCTGACAGCTGC 720  
Qy 235 LysLeuLeuValAlaIleGlyValAlaTrpValIleAsnMetTyAlaIleProVal 254  
Db 721 TTCCTTACGCCCGCGCGAGGAGTGGCTTGCATGTGTCTTCTTACAGAGTCCGCTT 780  
Qy 255 LeuGlyValSerValPhePheValLeuIleThiTyLeuHisIleThiIleSerLeu 274  
Db 781 CTGATGTTCATAGCTTCTCTCTGTGTGTATCACTTCTTGCAGCACACGATCTTCCGCT 840  
Qy 275 ProHisTyArgPheSerThiGlyTrpAsnTrpIleGlyAlaLeuSerThiIleAspArg 294  
Db 841 CCTCACTACGATTCCTCCGAGTGGAGTGGTGTGAGGGAGGAGCTTGTGCTTACACGA 900  
Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValIleThiIleThiIleHis 314  
Db 901 GACTACGAGATCTTACACAGGCTTCCACATATTACCGACACCGACGCTGGCGCATCT 960  
Qy 315 LeuIleSerTyTrpIleProHisTyTrpHisAlaGlyGlnAlaArgAspAlaIleTySer 334  
Db 961 CTGTTCTCAGATCCGCTTATTCACCGGATGAGAGTACCAAGCGCATTAAGCGGATA 1020  
Qy 335 LeuGlyGlyTyTrpIleAspArgThrProIlePheIleHisAlaMetTyArgGlyAla 354  
Db 1021 CTGGAGAGGATATACATTCATGATGGAGCGCGGTGTAAAGCGCATGTGGAGGAGCG 1080  
Qy 355 LysGlyCysValIleTyTrpIleGluProAspGlyAspSerGlyHisGlyValPheTrpTy 374  
Db 1081 AAGGAGTGTATGTAGTGGACCGGACAGGAGTGAAGAAAGTGTGTCTGGTAC 1140  
Qy 375 His 375  
Db 1141 AAC 1143

RESULT 12  
US-09-771-904-13

; Sequence 13, Application US/09771904  
; Publication No. US2003013179A1  
; GENERAL INFORMATION:  
; APPLICANT: DeBonte, Lorin R.  
; APPLICANT: Fan, Zhongong

; APPLICANT: Miao, Guo-Hua  
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
; FILE REFERENCE: 07148-063003  
; CURRENT APPLICATION NUMBER: US/09/771,904  
; CURRENT FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: US 08/874,109  
; PRIOR FILING DATE: 1997-06-12  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Brassica napus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ... (1152)  
US-09-771-904-13  
Alignment Scores:  
Pred. No.: 8,77e-149 Length: 1155  
Score: 1318.00 Matches: 233  
Percent Similarity: 77.17% Conservative: 61  
Best Local Similarity: 61.15% Mismatches: 81  
Query Match: 64.39% Indels: 6  
Gaps: 4  
US-10-069-772-2 (1-377) x US-09-771-904-13 (1-1155)  
Qy 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGlyGlyS-----AsnIle 16  
Db 1 ATGGGTGAGAGTGGAGAGATCAAGTGTCTCTCTCTCCCAAGAGTCTGAACAGCACGCC 60  
Qy 17 LeuGluArgValProValAsp--ProProPheThiLeuSerAspPheLeuIleValAlaIle 35  
Db 61 ATCAAGCGCGTACCTCGAGACACACCGCCCTTCACTGCGAGAACTCAAGAAAGCAATC 120  
Qy 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTrpValValHisAspLeu 55  
Db 121 CCACCGACCTGTTCACACGCTGATCCCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
Qy 56 IleValAlaTyValPheTyTrpLeuAlaAsnThiTyTrpLeuIleProThiPro 75  
Db 181 ATCATAGCCTCTGCTTCTTACTACGTGCCACCACTTACTTCCCTCTCTCCCTCACCT 240  
Qy 76 LeuAlaTyLeuAlaTrpProValTyTrpPheCysGlnAlaSerIleLeuThiGlyLeu 95  
Db 241 CTCCTCTACTCTCGCTGGCTCTCTCACTGGGCTGCCAAGGGTGGCTCTTACACGGGCTC 300  
Qy 96 TrpValIleGlyHisGlyCysGlyHisIleAlaPheSerArgTyTrpGlnLeuIleAspArg 115  
Db 301 TGGGTCATAGGCCACAGATGGGGCCACCAAGCTTACAGCTACCACTGAGCTTGTACAC 360  
Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThiProTyTrpPheSerTrpIleTySer 135  
Db 361 ACCGTGGCTCATCTTCCACT 420  
Qy 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAspGlyValTyTrpIleProIys 155  
Db 421 CATGACGCCACCATTCACACACTGGCTCCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
Qy 156 ArgIysSerIysValIleValIleTySerIysLeuLeuAsnAsnProGlyArgValPhe 175  
Db 481 AAGAAGTCAGACATCAGTGGTACCGCAAGTACCTCAACACCTTGGAGCGACCGTG 540  
Qy 176 ThrLeuValPheArgLeuThiLeuGlyPheProLeuTyTrpLeuThiAsnIleSerGly 195  
Db 541 ATGTTAACGGTTCATCTCTCGCTGGCCGCTTGTACTTACCTTCAAGCTCTCGGGA 600  
Qy 196 LysIlyTyTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214  
Db 601 AGACCTTACGACGGGGCTTGGCTTGCATTTCCACCCCAACGGCTCCATCTACACAGC 660  
Qy 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAlaIle 234



[illegible]

```

Db      1081 AAGAGGTATCTATGTGGAACCGGACGAGGTGGAAGAAAGGTGTCTGTGATC 1140
Qy      375 His 375
Db      1141 AAC 1143

RESULT 14
US-09-995-297-9
; Sequence 9, Application US/09995297
; Patent No. US20020092038A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharm
; APPLICANT: Fan, Zhegong
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/09/995,297
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-995-297-9

Alignment Scores:
Pred. No.:      1,166-148      Length:      1,155
Score:          1,317.00      Matches:      234
Percent Similarity: 76.44%      Conservative: 58
Best Local Similarity: 61.26%      Mismatches: 82
Query Match:      64.34%      Indels:      8
DB:               9          Gaps:      4

US-10-069-772-2 (1-377) x US-09-995-297-9 (1-1155)

Qy      1 MetGlyAlaGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db      1 ATGGGTGACGGTGGAGAAATGCAAGTGTCTCTCCCTCCCAAAAGTCTGMAAACGACAAAC 60
Qy      16 IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysVala 34
Db      61 ATC--AAGCGGTAACCTCGGAGACACCGCCCTTCACTGTGAGAACTCAAGAAAGCA 117
Qy      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
Db      118 ATCCACCGGCACTGTTTCAAGCGTCGATCCCTGCTCTTCTCTACTATCATCGGAGAC 177
Qy      55 LeuIleValAlaTyValPheTyTyTyLeuAlaAsnThrTyTyrIleProLeuIleProThr 74
Db      178 ATCATCATAGGCTCTGCTTCTACTACGTCGACACACTTACTTCCCTCTCTCTCTCAC 237
Qy      75 ProLeuAlaTyTyLeuAlaTrpProValTyTyTyPheCysGlnAlaSerIleLeuThrGly 94
Db      238 CCTCTCTCTACTTGGCTGCTGCTTCTACTACGCTGAGGCTCTCCAGGCTGCTCAACCGGC 297
Qy      95 LeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyGlnLeuIleAsp 114
Db      298 GTCTGGGTGATAGCCCAAGAGGCGGCAACACGCTTCAAGGACTACAGAGGCTGAGAC 357
Qy      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTyPheSerTrpLysTy 134
Db      358 GACACCGTGGGCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
Qy      135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspArgGlnValTyTyrIlePro 154

```

```

Db      418 AGTCATGACGCCACCATTCACACACTGGCTCTCCGAGAGACGAAGTGTGTGCCCC 477
Qy      155 LysArgLysSerLysValLysIleTySerLysLeuLeuAsnProProGlyArgVal 174
Db      478 AAGAAGAGTCAACATCAAGTGTACCGCAAGTACTCAACAAACCTTTGGAGCGCACCC 537
Qy      175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSer 194
Db      538 GTGATGTAAACGTTCAAGTTCACTCTCGGCTGGCTTTGTATCTTAAGCTTCAAGTCTCG 597
Qy      195 GlyLysLysTyTy---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsn 213
Db      598 GGGAGACCTTACGACGCGGCTTGGCTTGCATTTCCACCCCAACGCTCCCATCTACAGAC 657
Qy      214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAla 233
Db      658 GACCGTAGCGCTCCAGATATACATCTCCGACCGTGCATCTCCGCGTGTGCTACCGGT 717
Qy      234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyTyAlaIlePro 253
Db      718 CTTCACCGCTACCGCTGCTGTCCAAGAGTTGCTTCGATGTCTGCTCTTACGAGTTCT 777
Qy      254 ValLeuGlyValSerValPhePheValLeuIleThrTyTyLeuHisHisThrHisLeuSer 273
Db      778 CTCTGATGTGCAACGCGTTCTTGTATGATCACTTACCTTGACAGCACACCATCTTCC 837
Qy      274 LeuProHisTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
Db      838 CTGCTCATCTATGACTGCTGATGAGGATTTGTTGAGAGGAGCTTTGGCACCGTTGAC 897
Qy      294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisAspValLeuHis 313
Db      898 AGAGACTACGGAATCTTGACACAGTCTTCCAAATATCAACGACGACGACGACGTCGAT 957
Qy      314 HisLeuIleSerTyTyIleProHisTyHisAlaLysGluAlaAspAlaIleLysPro 333
Db      958 CACTGTCTTGCACCATGCCCATTTATCATTCATGAGAGTCAAGAGCGATTAAGCGG 1017
Qy      334 ValLeuGlyGluTyTyTyTyLysIleAspArgThrProIlePheLysAlaMetTyTyArgGlu 353
Db      1018 ATACTGGAGAGTATATCATGTTGATGAGAGCGCGGCTTAAGCGCATGTGAGGGAG 1077
Qy      354 AlaLysGluCysIleTyTyIleGlnProAspGluAspSerGlnHisLysGlyValPheTrp 373
Db      1078 GCGAAGAGTGTATCTATGTGGAACCGGACGAGGAGGTGGAAGAAAGTGTCTTGG 1137
Qy      374 TyrHis 375
Db      1138 TACAAAC 1143

RESULT 15
US-09-771-904-9
; Sequence 9, Application US/09771904
; Publication No. US20030133799A1
; GENERAL INFORMATION:
; APPLICANT: Debonte, Lorin R.
; APPLICANT: Fan, Zhegong
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)

```

US-09-771-904-9

## Alignment Scores:

Pred. No.:	1.16e-148	Length:	1155
Score:	1317.00	Matches:	234
Percent Similarity:	76.44%	Conservative:	58
Best Local Similarity:	61.26%	Mismatches:	82
Query Match:	64.34%	Indels:	8
DB:	10	Gaps:	4

US-10-069-772-2 (1-377) x US-09-771-904-9 (1-1155)

```

QY 1 MetGAlaGlyGlyArgMet-----SerAspProSerGluGlyAsn 15
Db 1 ATGGGTGACGGTGAAGATGCAGTGTCTCTCCCTCCAAAAGTCTGAAACGACAC 60
QY 16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuVal 34
Db 61 ATC--AAGCGGTACCTCGGAGACACCGCCCTTCACGTGCGAAGCTCAAGAAACA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTrValValHisAsp 54
Db 118 ATCCACCGCGACGTGTTCAAGCGTCGATCCCTGCTCTTCTCTACTCATCTGGAGAC 177
QY 55 LeuIleValAlaTyTrValPheTyTrLeuAlaAsnThrTyTrIleProLeuIleProThr 74
Db 178 ATCATCATAGCGCTCTGCTCTACTAGCGCCACCATTACTTCTCTCTCTCTCTC 237
QY 75 ProLeuAlaTyTrLeuAlaITrProValTyTrPheCysGlnAlaSerIleLeuThrGly 94
Db 238 CCTCTCTCTACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297
QY 95 LeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyTrGlnLeuIleAsp 114
Db 298 GTCTGGGTCAATAGCCACGAGCGGCGGCAACAGCCTTCAAGGACTACAGGCGTGAC 357
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTrPheSerTrpIleTyTr 134
Db 358 GACACCGTGGGCTCATCTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspGluValTyTrIlePro 154
Db 418 AGTATTCAGCCGCCACATTCACACCTGCTCCCTCGAGAGAGAGAGAGAGAGAG 477
QY 155 LysArgLysSerLysValLysIleTyTrSerLysLeuLeuAsnAspProGlyArgVal 174
Db 478 AAGAAAGATCAAGACATCAAGGTACGCGCAAGTACTTCAACACCTTGGGAGCAC 537
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTrLeuLeuThrAsnIleSer 194
Db 538 GTGATGTTAAGGGTCAAGTCACTCGGCTGGCTTGTACTTACCTTCAAGCTCTCG 597
QY 195 GlyLysLysTyTr--GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
Db 598 GGGAGACCTTACGACGGGCGCTTCGCTTCCATTTCCACCCCAAGCTCCCATCAAC 657
QY 214 AsparGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTrAla 233
Db 658 GACCGTGAGCGCTTCAGATATACATCTCCGAGCTGGCATCTCGCGCTGCTACG 717
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaITrValIleAsnMetTyTrAlaIlePro 253
Db 718 CTCTACCGCTACGCTGCTGCTCAAGAGAGTGTCTCGATGCTGTCTTACGAGTCTCT 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThrTyTrLeuHisHisThrHisLeuSer 273
Db 778 CTCTGATGTCAAGGGGTCTTACTTGTGATCACTTACCTGACACACGATCTCTCC 837
QY 274 LeuProHisTyTrAspSerThrGluTrpAsnITrIleLysGlyAlaLeuSerThrIleAsp 293
Db 838 CTGCTCTCATAGACTCTGTGAGGGAGTGTGAGGGAGCTTGTGGCCACCGTTGAC 897
QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313

```

```

Db 898 AGAGCTACGGAAATCTGAAACAGGTCTTCCACATATCACAGACACCGACGTGGCAT 957
QY 314 HisLeuIleSerTyTrIleProHisTyTrHisAlaLysGluAlaArgAspAlaIleLysPro 333
Db 958 CACCTGTTCTGACCATGCGCATATATCATGATGAGGTACGAGCGCATTAAGCGG 1017
QY 334 ValLeuGlyGluTyTrTyTrIleAspArgThrProIlePheLysAlaMetTyTrArgGlu 353
Db 1018 ATACTGGAGAGATATTATCACTTGCATGCGAGCGCGTGTAAAGCGATGTGAGGAG 1077
QY 354 AlaLysGluCysIleTyTrIleGluProAspGluAspSerGluHisLysGlyValPheTrp 373
Db 1078 GCGAAGAGATGATCTATGTGAAACCGGACAGGCAAGGTGAGAAAGAGTGTCTCG 1137
QY 374 TyrHis 375
Db 1138 TACAAAC 1143

```

Search completed: June 23, 2004, 18:36:31  
 Job time : 428 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 15:39:21 ; Search time 2371 Seconds  
(without alignments)  
4748.225 Million cell updates/sec

Title: US-10-069-772-2  
Perfect score: 2047  
Sequence: 1 MGAGGRMSDSEKQILERV.....IYBPDESEKGVFWYHKM 377

Scoring table: BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n model -DEV=x1h  
-Q=/cgm2\_1/USPTO.spool/US10069772/runat\_18062004\_145512\_5295/app\_query.fasta\_1.519  
-DB=EST -QFMT=fastlap -SUFPR=1 -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blowum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pcc -THR MAX=100 -ALIGN=15 -MODB=LOCAL  
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USRR=US10069772 @CGN 1.1 2607 @runat\_18062004\_145512\_5295 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEOUTRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1283.5	62.7	1856	11 AY104050	AY104050 Zea mays
2	1195	58.4	1807	11 B1683572	B1683572 RocheFord
3	1117	54.6	691	13 BQ994479	BQ994479 OGF7F12.Y
4	1102.5	53.9	989	14 CK269848	CK269848 EST715926
5	1087.5	53.1	973	14 CK262936	CK262936 EST709014
6	1078.5	52.7	725	13 BQ866257	BQ866257 OGC7H15.Y
7	1049.5	51.3	1794	12 B1683576	B1683576 EST 01 B7
8	1048	51.2	918	14 CK269030	CK269030 EST715108
9	1010	49.3	900	29 CG442730	CG442730 OGVH509TV
10	977	47.7	613	14 CF098768	CF098768 OHNF08.Y
11	964.5	47.1	869	28 CC332198	CC332198 OGBIC43TV
12	960	46.9	876	14 CD760583	CD760583 11nFAD2.L
13	959	46.8	1084	14 CK210592	CK210592 FGAS02241
14	955	46.7	963	14 CK270183	CK270183 EST716261
15	950	46.4	1080	13 BU238570	BU238570 D801.13f0
16	941	46.0	948	14 CK278983	CK278983 EST725061
17	937	45.8	763	13 BQ853589	BQ853589 OGB20018
18	937	45.8	784	12 B1925058	B1925058 EST544947
19	929.5	45.4	891	14 CK250323	CK250323 EST733960
20	928	45.3	924	28 CC338891	CC338891 OGPBC69TV
21	924.5	45.2	809	10 BE998745	BE998745 EST430532
22	924.5	45.2	975	29 CG304699	CG304699 OGB263TV
23	923.5	45.1	901	14 CK263172	CK263172 EST709250
24	918.5	44.9	831	14 CF511517	CF511517 CABud0002
25	916	44.7	916	29 CG249959	CG249959 OGG044TV
26	910	44.5	756	13 BQ857435	BQ857435 TO84F10.P
27	906	44.0	753	13 BQ857435	BQ857435 OGB7104.Y
28	900.5	44.0	911	14 CF215372	CF215372 CABT0001
29	899	43.9	772	12 B1933814	B1933814 EST553703
30	897	43.8	624	14 CF096571	CF096571 QNR23719
31	884.5	43.2	811	14 CF444900	CF444900 EST681245
32	884.5	43.2	865	12 CK262670	CK262670 EST708748
33	876	42.8	755	12 BM109924	BM109924 EST557460
34	876	42.8	764	10 AM201738	AM201738 sf06f08.Y
35	874	42.7	905	14 CB349164	CB349164 CAB2SG000
36	870	42.5	856	14 CK278793	CK278793 EST724871
37	864.5	42.2	810	13 BQ505963	BQ505963 EST613378
38	863.5	42.2	771	29 CC731290	CC731290 OGBS36TV
39	862.5	42.1	837	14 CK276272	CK276272 EST722350
40	862	42.1	901	14 CB978093	CB978093 CAB40005
41	857.5	41.9	889	14 CK277512	CK277512 EST723590
42	855	41.8	798	13 BQ858101	BQ858101 QGB9F12.Y
43	842.5	41.2	840	14 CF437157	CF437157 EST673502
44	840.5	41.1	724	13 BQ868052	BQ868052 QGD12009
45	840.5	41.1	775	12 BM407951	BM407951 EST582278

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
AY104050	AY104050	Zea mays PC0088038 mRNA sequence.	AY104050	AY104050.1	GI:21207128	Zea mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	1 (bases 1 to 1856)



```

Email: trocheff@uinc.edu
Seq primer: M13 reverse.
Location/Qualifiers
1. .1807
FEATURES
source

```

```

/organism="Zea mays"
/mol_type="mRNA"
/db_xref="caxon:4577"
/clone="cdbf85"
/tissue_type="Embryo"
/dev_stage="developmental stage"
/clone_1b="B3 LIBRARY"
/note="vector: pSORT1; Site_1: SalI; Site_2: NotI;"

```

## ORIGIN

Alignment Scores:	
Pred. No.:	2,48e-134
Score:	1195.00
Percent Similarity:	77.05%
Best Local Similarity:	56.92%
Query Match:	56.38%
DB:	12
	Gaps: 3

US-10-069-772-2 (1-377) x BI683572 (1-1807)

[illegible]

Dd	918	GGCGTCCGCGCGCGGCGGCTTCGGGCTGTACAAAGTGGCGGCGGCTTCGGGCTCGGTG	977
Dy	246	VaIIleasmetYrAlaIleProValIleuGIyValSerValPhePheValIleuIleThr	265
Dd	978	GTGGTGGCGCGGTATACGCGCGTCCGCTGTATGTCAACGCGGTGGTGTCTCATCAG	1037
Dy	266	TyIleuIleShIeThrIleSleuSerIleuProIleSIyIleAspSerThrGIuTPAsnThrIle	285
Dd	1038	TACCTGCAGCACACCCACCGCGCGCTGCCACATCAACATCTCGGCGAGGTGGAGTGGCTG	1097
Dy	286	LysGIyAlaIleuSerThrIleAspAspAspPheGIyPheIleuAnaIyValPheIleAsp	305
Dd	1098	CGCGGCGCGCTGCACCGCTGCACCGAGCTACGAGCGCTCTCAACCGGCTTCCACAC	1157
Dy	306	ValThrIeThrIeSValIleuIleShIeIleuIleSerTyIleProIleSIyIleAlaIleS	325
Dd	1158	ATCAACGAGACACGACGCTGGCGACACACTCTTCTCCACAGCGCGCATACGAGCGCTG	1217
Dy	326	GIuIlaIarGAspAlaIleIySProValIleuGIyGIuTyTyIyIleAspArgThrPro	345
Dd	1218	GAGGCCACACAGGGCGATCAAGGCGCGCTCGGCGAGTACATCAAGTTCCAGCCGACCCCT	1277
Dy	346	IlePheIySalameTyIleArgGIuAlaIySGIuCySIleTyIleGIuProAspGIuAsp	365
Dd	1278	GTCCGCCAAGGCGCACTGGCGGAGAGCCAGGAGGTGCACTTACGTGAGCCCTGAAGAAC--	1335
Dy	366	SerGIuIleIySGIyValPheThrTyIleHis	375
Dd	1336	CGCAACCGCAAGGCGGTCTTCTGTATACAC	1365

RESULT 3	BO994479	691 bp	mRNA	linear	EST 21-AUG-2002
LOCUS	BO994479				
DEFINITION	BO994479				
	CGE7F12.79.ab1				
	CGE7F12.79				
	CGE7F12.79				
ACCESSION	BO994479				
VERSION	BO994479.1				
KEYWORDS	EST.				
SOURCE	<i>Lactuca sativa</i>				
ORGANISM	<i>Lactuca sativa</i>				

```

Location/Qualifiers
1. 691
/organism="Dactyca sativa"
/mol_type="mRNA"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGFP12"
/lab_host="E. coli"
/clone_lib="QG_EFGHJ lettuce serriola"
note="Vector: pBacDNASTAB; The library was constructed

```

from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at [http://cpdb.ucdavis.edu/TAG\\_TISUB-seg/germinating\\_seeds](http://cpdb.ucdavis.edu/TAG_TISUB-seg/germinating_seeds)  
TAG\_Lib=Q5\_EFGH lettuce *sepiola*  
TAG\_SEQ=TCGTGCGCG



Oy		36	Prothrhiasysphglsalgservallleasgerserytyryvalvahlshapleu	55
Db		145	CCACCTCACTGCTTTCMAAGSTCTCTCATCCGCCTATTTCTTAATTGTGTATGATCACTC	204
Oy		56	IleValAlaTyRvaIpheTyTYrDeuAlaenThTYrIleProLeuIleProThPro	75
Db		205	ATACTGCTCCATCATGACTAAGTAGCGAAACACTTACTTCACACTCCCTTCATCCCCA	264
Oy		76	LeuAlaTYrLeuAlaTrIProValTYrTrPheCyGlnAlaSerIlleLeuthrglyLeu	95
Db		265	TATGGCTCATTTGCCGTGACCTTAATTACAGGAATTCACAGGGTGTGGTTCACCTGGT	324
Oy		96	TrPVAlIIlegLYHISGLUCysglYHISHIALApheSerAspTYrGlIleuIleasp	115
Db		325	TGGGTAAATGCCCAAGAAATGTGGCATACAGCTTTCAGTGATTCACAATGGGTATAGC	384
Oy		116	IleValGIypheValIleuHisSerAlaLeuLeuthrProTYrPheSerTrIpsTYrSer	135
Db		385	ACCCTTGACCTTAATCTTCACCTGCTGCTGTGGTGGCGGTAATCTCTCTTGGAAATATAGT	444
Oy		136	HIsatgaamHISHIALaanthrxanserleuabpaanbpGlValITyrIleProlys	155
Db		445	CATGCTCCGACCACTCCAAACACTGCTCCCTCCGACGCGTGAAGAAGTCTTGTGCCAAG	504
Oy		156	ArgLysSerLySValIylsIetyrSerLySleuLeuaAnspProGlyVArGValPhe	175
Db		505	CCAAATCTCACCTCGATGGATGTATTCAGATCTTGAACAATCACTCAAGGAGGGTCTC	564
Oy		176	ThrIleuValPheaXrLeuThrlengIYPheProLeuTYrLeuLeuthrAsnIleSerGly	195
Db		565	TCACCTTAACAATCACTCCATCTTGGTGGCGGCTGTACTGGCTCAATGTTCCTGAC	624
Oy		196	LysIlystYrGYlAngPhelAlaamHISHephaPPrometSerProIlePheaaasparg	215
Db		625	AGACCATACGACCGGATTTGCATGTACATAGACCTTATGGCCCAATGTACAAACAACGC	684
Oy		216	GUATrGVAlGInValIleuLeuSeraspPheGlyLeuLeuAlaValPheTYrAlaIlelys	235
Db		685	GAGAGGCTACACAGATCTTGTCTATGCTGAGATTTCTCGAAGTTGTATTCGTCTAAC	744
Oy		236	LeuLeuValAlaAlaLYsglyAlaAlaTrPVAlIleamMetYrAlaIleProValIleu	255
Db		745	CGTGTGCTTACGTAAAGTCTTACCTTGGCTAGTGGATCTCAAGGTGATCCCTCCTT	804
Oy		256	GLYAlaSerValPhePheValIleuIleThrTYrLeuHISHISTHSHIleuSerIleuro	275
Db		805	GTCGTGAACGGCTTCCTTGTCTGTATCACTCACTTGCAGCACACACTCACCCATCATTTGCT	864
Oy		276	HISrYAASerTHrGlUTrPAANTrIleuYrSGlyAlaLeuSerThrIlleaspargasp	295
Db		865	CACrACGATTCACACGAGTGGATTTGCTTACGGAGACCTTTGGGACCTGTGACAGAAAC	924
Oy		296	PheGlyPheLeuAanrValPheHISHAspValTrHISHIHleValIleuHISHIleu	315
Db		925	TATGGGCTTCTTAAACAGAGTCTTCCCAACATCAACGACACTCACTGATGATGACCATCTG	984
RESULT 5				
CK62936		973 bp	mRNA	EST 12-DEC-2003
LOCUS		EST770914	pocato abiotic stress cDNA library Solanum tuberosum CDNNuc	
DEFINITION		clone POABJ3 5' end, mRNA sequence.		
ACCESSION		CK62936		
VERSION		CK62936.1		
KEYWORDS		EST.		
SOURCE		Solanum tuberosum (potato)		
ORGANISM		Solanum tuberosum		
REFERENCE		Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS		Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
TITLE		asteroids; lamids; Solanales; Solanales; Solanales; Solanum.		
		1 (bases 1 to 973)		
		Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.		
		Generation of ESTs from abiotic stressed potato tissue		

**JOURNAL**      Unpublished (2003)  
**COMMENT**      Other ESTs: EST09015  
                     Contact: Robin Buell  
                     The Institute for Genomic Research  
                     9712 Medical Center Dr., Rockville, MD 20850, USA  
                     Email: potato-array@tigr.org  
                     Clones can be requested from TIGR via potato@tigr.org  
                     Seq primer: ATT TAG GTG ACA CTA TAG.  
                     Location/Qualifiers

/labus type="abiotic stress treated leaf and root tissue  
 /file host="DH108-TONA"  
 /clone lib="potato abiotic stress cDNA library"  
 /note=Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;  
 supplier: Solanum tuberosum var. Kennebec plants were  
 grown from cuttings on a 16hr 14hr/8 hr dark cycle at 25  
 C for 3-4 weeks. Abiotic stress conditions were applied to  
 four separate sets of plants. Set 1 involved saturation of  
 the soil with 150 mM NaCl and tissues were harvested at  
 following application of the salt stress (leaves: 2hr,  
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
 Set 2 were grown under the standard conditions and then  
 were water stressed by withdrawal of further watering  
 applications. Drought stressed plants were harvested after  
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
 and 5d). Set 3 were grown under the standard conditions  
 and then were cold stressed by placement at 4 C. Cold  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d. Set 4 were grown under the standard conditions and  
 then were heat stressed by placement at 35 C. Heat  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d and 4d and heat-stressed roots were harvested at 6 hr,  
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
 equal RNA from each tissue and stress was pooled to  
 construct the cDNA library. RNA sample."

ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
		1.33e-121	Length: 973				
		1087.50	Matches: 194				
		77.22%	Conservative: 50				
		61.39%	Mismatches: 67				
		53.13%	Indels: 6				
			Gaps: 2				
US-10-069-772-2 (1-377) x CK262936 (1-973)							
QY 1 MetGlyAlaGlyGlyArgMetSerAspProSer-----GluGlyLysAsnIle 16							
Db 25 ATGGAGAGCTGGTGGTGGTATGTCCTGCTCCAAATGSCGAGACTGAAGTAAAGAAATCCT 84							
QY 17 LeuGluArgValProValAsp---ProProPheThrIleuSerAspLeuLysValAlaIle 35							
Db 85 CTTCGAAAGGTGACCAACTCGAAGCCCTTCCTTCACAGTGGTGATATCAAGAAAGGCTATC 144							
QY 36 ProThrHisGlyPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55							
Db 145 CCACCTCATCTGCTTCAA-AGGCTCTCATCCGGCTATCTCTCATGTTGTGTAGACCTC 203							
QY 56 IleValAlaIleValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75							
Db 204 ATACTGCTGCATCATGTAAGTACTACCTGCAAACTTCACTTCCACCTCTTCATCCCA 263							
QY 76 LeuAlaIleLeuAlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95							
Db 264 TATGTCTACATTCGCGGCTATTTACAGCAATTGGCCAGGGTTGTGTTGCACGTGTAAT 323							

OY			96	TTPVALLIEGLYHISHLGUCAGSLYHISHLSALAPHESESASPTRYGLILEULLEASPPR	115
Dd			324	TGGTTAATGCCACGAATTGTGCACATCAGCTTTCAGTAATCCAAATCGGATTAGCATC	383
OY			116	ILeValIGlyPheValIleuHisSerAlaleuLeuThrProTYrPheSerTrpLYSTySer	135
Dd			384	ACC GTTGAGCTTAATCTCACTCTGCTGTTGGTGAGCGGTACTTCTCTTGGAATAATAGT	443
OY			136	HISATGAENHSIHIALAsnThraSnSerLeuAspaSnaArgGIUVALTyrlLerPolys	155
Dd			444	CATCGTCGCCAACACTCCAAACCTGAGCTCCCCTCCGAGCGGTGAAGAAGTCTTGTGCCAAG	503
OY			156	ArGYLSerSYValIylletyrISerYSileuLeuAsanProProGLyARVALPhe	175
Dd			504	CCAAATCTCACGTCGGATGGATTTCANGTACTTGGAACAATCCACGAGCGGGTCTTC	563
OY			176	ThrlEuValPheaArgLeuThrIeuGLYPheProLeuTYrLeuLeuThrAsnILesergLy	195
Dd			564	TCAC TTAC AAT CAC ACC TCA CTCT G TG GG CGG GTT GA CT TG GC CT TA AT CA TTA TC TG CC	623
OY			196	LysLIstYrYGlyARGPheAlaasnHSIPheaSPPrometSerProIIepHeasnsApArg	215
Dd			624	AGACCATACGACCGGATTGCATGTCACATGACCCCTTACGGCCCAATCAACAACACCGT	683
OY			216	GluARGValIGlnValIleuLeuSeraspPhegLYLeuLeuAlaValPheTYrAlalLeys	235
Dd			684	GAGAGGCTPACAGATCTTCGTTCTGATGCTGAGTTCGTGCAGGTTGTATTCGTATAC	743
OY			236	LeuLeuValAlalaalyeGlYAlaAlatRPValIlleaMetYrAlaIleProValIleu	255
Dd			744	CGTATGTCCTTAGTGAAGAAGCTCTACTTGCGTCAAGTGCATGTACGGTGTACCCCTCTC	803
OY			256	GIYALServalPhePheValIleuIleThrTYrLeuHIshISThrHisLeuSerLeuPro	275
Dd			804	GTCGGGAACGGGCTTCCTTGCTTGTAATCACTACTTGACAGACATCAACCCATCATTTGCCA	863
OY			276	HIS TRYASP Ser Thr Glut Trp Asn Trp Ile Lys GL Y Al a le u Ser Th r I l e a s p R g S P	295
Dd			864	CAC TAC GAT TCA AC C G AG G G G A T T G G C T T T AA G G A G C T T T G G C AAC C T G T G A C A G A G A C	923
OY			296	PheglYPhelEuaSnArgvalPhehisAspValIThrhisESThisVal 311	
Dd			924	TATGGGCTTCTPAACAAGTCTTCCAACAATCACCGACCTCACTCAAGTG 971	
RESULT 6					
BQ866257			BO866257	725 bp mRNA linear EST 14-AUG-2002	
LOCUS			OGCH15.Y5.abl OG ABCDI lettuce salinas lactuca sativa cDNA clone		
DEFINITION			OGCH15.mRNA sequence.		
ACCESSION			BQ866257		
VERSION			BO866257.1 GI:22251722		
SOURCE			EST.		
ORGANISM			Lactuca sativa		
			Lactuca sativa		
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
			Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
			Asterids; campanulids; Asterales; Asteraceae; Cicorioideae;		
			Cichoriaceae; Lactuca.		
			1 (bases 1 to 725)		
REFERENCE			Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesenberg,L.,		
AUTHORS			Liu,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J.,		
			Ellison,P., Kolman,J., Slabaugh,M.S., Livingstone,K., Zhou,Y.,		
			Lai,Z., Church,S., Jackson,L. and Bradford,K.		
			Lettuce and Sunflower ESTs from the Compositae Genome Project		
			http://compgenomics.ucdavis.edu/unpublished (2002)		
JOURNAL COMMENT			Contact: Alexander Kozik [R.W.Michelmore]		
			Department of Vegetable Crops, R.W.Michelmore lab		
			University of California at Davis (UCD)		
			Agriculture Hall, UCD, Davis, CA 95616, USA		
			Tel.: 1-(530)-742-1742		
			Fax: 1-(530)-752-9659		
			Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]		

belongs to config QG\_CA\_Config2502, see <http://csgpdb.ucdavis.edu/> for details.  
 Plate: QGC7 row: H column: 15.  
 Location/Qualifiers  
 1. .725

```

/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGCTH15"
/lab_host="E.coli"
/clone_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRCDNA511AB. The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpb.ucdavis.edu/
TAG_TISSUE=ABCDI lettuce salinas
TAG_LIB=QG_ABCDI
TAG_SEQ=TG1AGCCGCG"

```

**Alignment Scores:**

Pred. No.:	1,066-120	Length:	725
Score:	1078.50	Matches:	200
Percent Similarity:	94.62%	Conservative:	11
Best Local Similarity:	89.69%	Mismatches:	11
Query Match:	52.69%	Indels:	2
DB:	13	Gaps:	1

1 MetG1ValAG1yG1yArgMet---SerAspProSerGluG1yLysAsn11LeuGluArg 19  
Db ATGGGAGCAGGGTGGTGGATGTCAGAGCGATCCATTGATGGTAAAAAGATCCTGGAAAGT 11.5  
Qy 20 ValProValAspProProPheThrLeuSerAspLeuLysValAla11LeuProThrHisCys 39  
Db 116 GTGCCACGT-GATGCCACCGTTCATTAAGATGATTTAAAGAAAGGAGATCCCTGCCCAATGCG 174  
Qy 40 PheGluArgSerVal11LeuArgSerSerTyrrTyrrValValHisAspLeu11LeuAla11Arg 59  
Db 175 TTCAACGAGATCCGTCATCCGTTCACTTAAGTGTGTTCACGATCGATGTTGGCTTAC 234  
Qy 60 ValPheTyrrTyrrLeuAlaAsnThrTyrr11LeuProLeu11LeuProThrProLeuAlaTyrrLeu 79  
Db 235 GTTTTCTACTTCCTTGCAAAATCATATATATTCCTTTTCTTCACGCTCCTTGGCCTACTTA 294  
Qy 80 AlaTrpProValTyrrTrpPheCysGln11Aser11LeuThrArg11LeuTrpVal11LeuGly 99  
Db 295 GCTTGGCCGGTATATGTTGTTGTGTAACCAAGCATCTTCACAGGCTTAAGGTCATCGC 354  
Qy 100 HisGluCysGluYH1His11AlaPheSerAspTyrrGluLeu11LeuAspAsp11LeuAlaGlyPhe 119  
Db 355 CAGGAATGGCGGTACCAATGCCCTTTAGCGAAATACCAATGATGTATGACATCGTCGGCTTC 414  
Qy 120 ValLeuHisSerAlaLeuLeuThrProTyrrPheSerTyrrTyrrSerHis11ArgAsnHis 139  
Db 415 ATCTCCATCATCGCTCTCATGACACCTTATTTCTCATGGAATATTAAGCCATCGAAATCAC 474  
Qy 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrr11LeuProLysArgLysSerLys 159  
Db 475 CAGGCCAACAACAATTCCTCGATATATATGATGAAGTTTACATTCCTTAACCGAAGCTCAAA 534  
Qy 160 ValIle11LeuSerLysLeuLeuAsnAsnProGluArgValPheThrLeuValPhe 179  
Db 535 GTGAGGTGATCATCAAAACTCTTAACAACCACTGGTCAGAGTTCACATTGGTTTT 594  
Qy 180 ArgLeuThrLeuGlyPheProLeuTyrrLeuLeuThrAsn11SerGlyLysLysTyrrGly 199

```

Db      595 AGGTTCACTCAGAGATTCCTTTATACCTCTTAATAATTTCTGGCAGAGAAATACCGA 654
Qy      200 ArphealaaenhiaphaspromerSerProillepneanaaspargluarValin 219
Db      655 AGGTTGCAACCACTTGATCCATGATGATCAATTTTACCCAGCGGAGGAAATTCAG 714
Qy      220 Valleuenu 222
Db      715 GTTCTGTTA 723

RESULT 7
Bi683576/c 1794 bp mRNA linear EST 31-DEC-2001
LOCUS      Bi683576 LIBRARY Zea mays cDNA clone cmaa92 5', mRNA sequence.
DEFINITION Bi683576
ACCESSION  Bi683576.1 GI:18021477
VERSION    EST.
KEYWORDS   Zea mays
SOURCE     Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 1794)
            Mikkilineni, V. and Rocheford, T.
            Genomic Organization of Fatty Acid-Desaturase-2 ESTs in Maize
            Unpublished (2001)
            Contact: Dr. Torbert Rocheford
            Torbert Rocheford
            University of Illinois
            1102, S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: (217) 333-9643
            Fax: (217) 333-9817
            Email: troche@uiuc.edu
            Seq primer: M13 reverse.
            Location/Qualifiers
            source          1..1794
                           /organism="Zea mays"
                           /mol_type="mRNA"
                           /db_xref="taxon:4577"
                           /clone="cmaa92"
                           /tissue_type="Embryo"
                           /dev_stage="Developmental stage"
                           /clone_id="B73 LIBRARY"
                           /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI"

ORIGIN
Alignment Scores:
Pred. No.: 1.52e-116 Length: 1794
Score: 1049.50 Matches: 209
Percent Similarity: 63.53% Conservative: 61
Best Local Similarity: 49.18% Mismatches: 88
Query Match: 51.27% Indels: 67
Gaps: 9

US-10-069-772-2 (1-377) x Bi683576 (1-1794)
Qy      13 GtlyysaaniileuGluaArgValProValasp---ProProPhethrleuSeraspLeu 31
Db      161 GGTGGCGCGGATCGACCGGTCGGCGGTGAGAAAGCTCCGTTACTCTGGGTCAATC 1702
Qy      32 LyslysaalailleProThrhieCyphhegluaArgSerValilleArgSerSerTyTyVal 51
Db      1701 AAGAAAGGCATCCGCCACACCTGCTTCAGAGCCCTCGGTGCTCAAGTCTCTCCGACGTG 1642
Qy      52 ValhisaspLeuileValaialaTyValaPheTyTyTyLeuailaasnThrTyrlleProleu 71
Db      1641 GTCCACGACCTGTGATGCGCGCGGCTCCTCTGCTCGCGTCGATACATACCGGCG 1582
Qy      72 IleProthrrProleuAlaTyrlleuAlaTrProValTyTyTrpPheCyglAlaSerlle 91
Db      1581 CTCACAGCCGCTCGCTACGCCGCTGCGCTGTACTGTGATCGCAGGGGTGCGTG 1522

```

```

Qy      92 LeuthrGlyLeuTrpValilleGlyHisGluCygluYHisHisAlaIapheserAspTyrgln 111
Db      1521 TGACACCGCGGTGGTGCATCGCCACAGAGCGCGCCACACCGCTTCTCCGACCTACGCG 1462
Qy      112 LeuileaspapriileValilGlyPheValLeuHisSerAlaLeuLeuThr-ProTyRPhese 131
Db      1461 CTCCTGACGACGAGGTGCGCTGTGTGTGACATCGTGTGCTCAATGATGTCCTTACTTC 1402
Qy      131 rTrpLyserTySerHisArgaenHisAlaIasnThr---AsnSerleuAspAspG1 150
Db      1401 GTGGAAGTACAGCCACCGCGCCACACCAATCCAAACAGCGGGTTCCTTGAACGAAACA 1342
Qy      150 uValTyrlle---ProlysaArglySer----- 158
Db      1341 GTTTTCCTTCCTCCCAAAAAAAGAAAGCTGCGCGGTATACCCCTTAACCTTTTAA 1282
Qy      159 -----LysVallysiIeTyserLyble 166
Db      1281 AACCCGCTCGCGCGGTAGGGGCGCTATTTGTGAAGTAAAGCCACGCGCGGCTA 1222
Qy      166 uLeuAsnaAnpProPro-----GlyArgValPheThrleuValaPb 179
Db      1221 TTCACACAGGGGTCTTGTAGCGAAACAAGGTGTGGGGGCGGCTTACCC----- 1170
Qy      179 eArgLeuThrleuGly----- 184
Db      1169 -CGGTTCCCTTGCAATTTCAACCCCAAGGCGCCCTTTTAAAAAAGCGGAAA 1111
Qy      185 -----PheProleuTyrlleuLeuThrAniIleSerGlyly 196
Db      1110 CCCCCCAATTTTCTTTTTCGAAGCGCTGTACTGTGCGACCAACGCGTGGCGG 1051
Qy      196 slyTyrglyArgPheAlaenHisphe---AspPromerSerProillepneanaaspAr 215
Db      1050 GCCGTACCGCGCTTCCGCTCGGACGACCTTCGGGACCCCTACGCGCCCACTCAACAGACG 991
Qy      215 ggluaArgValaIaValleuLeuSeraspPheGlyLeuLeuAlaValaPheTyrlaIailely 235
Db      990 GGAGCGCGCCAGATCTTCGCTCGACGCGCGGTGCGCGGTGCGGTGCGGTGTA 931
Qy      235 sleuLeuValaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 255
Db      930 CAACTGCGCGCGCTTCGCGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Qy      255 uGlyValaserValaPhePheValleuIleThrTyrlleuHisHisThrHisleuSerleuPr 275
Db      870 GATGTGAACCGGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
Qy      275 oHisTyRaspserThrgluTrpAenTrpIleTyrlleGlyAlaIaIaIaIaIaIaIaIaIaIaIaIa 295
Db      810 CCACCTAGACCTCGAGCGAGTGTGAGCTGTGCGCGCGCTGTGCGCCACATGACCGCG 751
Qy      295 sPheGlyPheLeu-AsnaArgValaPheHisaspValaThrHisThrHisValaIaIaIaHis 314
Db      750 ACTACGGCATCTTCAACCGCGGTGTTCACAAATCAACAGACAGCAGCAGTGTGCGGACAC 691
Qy      315 leuIleSerTyrllePro-HisTyRHisAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 334
Db      690 CTCTTCTCACCAAGCGCGGCTACACCAACGATGAGGCCACCAAGGAGATAGGCCAT 631
Qy      334 lleuGlyIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 354
Db      630 CCGTGGGAGACTACACCACTTGCAGCCGAGCCCGCTGTGCAAGGAGACTGTGCGGAGAGC 571
Qy      354 alysgluCyserIleTyrlleGluProaspGluaspSerGluHislysglyValaIaIaIaIaIa 374
Db      570 CAGGAGTGCATCAACGTGAGCCGAG-----GACCGCAAGGCGGTCTTGTGTA 520
Qy      374 rHisLyb 376
Db      519 CAACAG 513

```

RESULT 8

CK269030  
 LOCUS CK269030 918 bp mRNA linear EST 12-DEC-2003  
 DEFINITION EST15108 potato abiotic stress cDNA library Solanum tuberosum cDNA  
 clone POACK42 5' end, mRNA sequence.  
 ACCESSION CK269030  
 VERSION CK269030.1 GI:39826008  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 918)  
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  
 TITLE Generation of ESTs from abiotic stressed potato tissue  
 JOURNAL Unpublished (2003)  
 COMMENT Other ESTs: EST15109  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 Clones can be requested from TIGR via potatoc@tigr.org  
 Seq primer: ATT TAG GTG ACA CTA TAG.  
 FEATURES  
 source location/Qualifiers  
 1..918  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="POACK42"  
 /tissue\_type="abiotic stress treated leaf and root tissue"  
 /lab\_host="DH10B-TonA"  
 /clone\_1ib="potato abiotic stress cDNA library"  
 /note="Vector: pCMVSPORTC.1; Site 1: EcoRI; Site 2: NotI;  
 supplier: Solanum tuberosum var. Kennebec plants were  
 grown from cuttings on a 16hr light/8 hr dark cycle at 25  
 C for 3-4 weeks. Abiotic stress conditions were applied to  
 four separate sets of plants. Set 1 involved saturation of  
 the soil with 150 mM NaCl and tissues were harvested at  
 following application of the salt stress (leaves: 2hr,  
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d,  
 2d). Set 2 were grown under the standard conditions and then  
 were water stressed by withdrawal of further watering  
 applications. Drought stressed plants were harvested after  
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
 and 5d). Set 3 were grown under the standard conditions  
 and then were cold stressed by placement at 4 C. Cold  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d. Set 4 were grown under the standard conditions and  
 then were heat stressed by placement at 35 C. Heat  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d and 4d and heat-stressed roots were harvested at 6 hr,  
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
 equal RNA from each tissue and stress was pooled to  
 construct the cDNA library. RNA sample."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8.2e-117 Length: 918  
 Score: 1048.00 Matches: 185  
 Percent Similarity: 76.72% Conservative: 49  
 Best Local Similarity: 60.66% Mismatches: 66  
 Query Match: 51.20% Indels: 6  
 DB: 14 Gaps: 2  
 US-10-069-772-2 (1-377) x CK269030 (1-918)  
 QY 2 gjyalaglygylarimetserasppro-----Sergluglilylsanlleu 17  
 DB 3 GGAGCTGGGGTGGTATGCTCTCAATGGGAGAGTGAAGTA-AAAGAGATCTCTT 61  
 QY 18 GUAAGVALProValAsp---ProProPheThrLeuSerAspLeuLysAlaIlePro 36

Db 62 CAAAGGATCCACCACTCGAGACCCCTTTCACAGTGTGTATATCAGAGGCTATCCCA 121  
 QY 37 ThrHisCysPhegluArgSerValIleArgSerSerTyrrValValHisAspLeuIle 56  
 Db 122 CCTGACTGCTTTCAAGGTCCTCATCGGCTCATCTTCCTATGTTGTATGACTCATTA 181  
 QY 57 ValAlaTyrrValPheTyrrTyrrLeuAlaAsnThrTyrrIleProLeuIleProTh 76  
 Db 182 CTCGCTTCACAGTATCTTACGTTGCAAACTTATCTTCCACCTTCCTCCATCCCAAT 241  
 QY 77 AlaTyrrLeuAlaTrrProValTyrrTyrrPheCysGlnAlaSerIleLeuThGlyLeuTrp 96  
 Db 242 TGTCTACATGGGTGGGCTTATTTACTGATTTGCCAGGTTGTGTGACTGGATTTGG 301  
 QY 97 ValIleGlyHisGluCysGlyValHisAlaPheSerAspTyrrGlnLeuIleAspAspIle 116  
 Db 302 GTTATGGCCCAAGATGGGCAATGAGCATCAGCTTTCAGTATACCAATGGGATGATGACACC 361  
 QY 117 ValGlyPheValLeuHisSerAlaLeuLeuThrProTyrrPheSerTyrrSerHis 136  
 Db 362 GTTGACTTATTCCTTCACTCTGCTCTGTGTGGCCGTACTTCTTGGAAATATATGTCAT 421  
 QY 137 ArgAsnHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrrIleProLysArg 156  
 Db 422 GTGGCCCACTCCACACACTGGCTCCTTCAGCGTATGAGTCTTGTGCCAAGCCA 481  
 QY 157 LysSerLysValLysIleTyrrSerLysLeuLeuAsnAsnProProGlyArgValPheThr 176  
 Db 482 AATCTCAGTCGGATGTATTCAGATGTAATGGAACATCCACAGGAGGTCCTCTCA 541  
 QY 177 LeuValPheValGluThrLeuGlyPheProLeuTyrrLeuThrAsnIleSerGlyLys 196  
 Db 542 CTTCACATCACCTCACCTCTGGTGGCGCTGTGAATCTTGAGCTTCAATGATATGGCAGA 601  
 QY 197 LysTyrrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAspAspArgGlu 216  
 Db 602 CCATACGACCAATTTGATGATGATATACCTTATACGCGCCAACTTACACACCGTATAG 661  
 QY 217 ArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrrAlaIleLysLeu 236  
 Db 662 AGGCTACAGATCTTCTTGTGATGCTGAGATTCGAGATTGTTGTTATCTCTATACCGT 721  
 QY 237 LeuValAlaAlaLysGlyAlaAlaTrrPValIleAsnMetTyrrAlaIleProValLeuGly 256  
 Db 722 ATGGCTTATGGAAGGCTTATGCTGTGATGTCATCTGATGTCAGTACCGTCTCTGTC 781  
 QY 257 ValSerValPhePheValLeuIleThrTyrrLeuHisIleThrHisLeuSerLeuProHis 276  
 Db 782 GTGACGGCTTCTTGTCTTATCATCTTATGACGACACATCCATCATTTGCCACAC 841  
 QY 277 TyrrAspSerThrGluTrrAsnTrrPheLysGlyAlaLeuSerThrIleAspArgAspPhe 296  
 Db 842 TACGATTCACCGATGGATGAGTGGTATGGGAGAGTTGGCAACCTTGACAGACAGACTAT 901  
 QY 297 GlyPheLeuAsnArg 301  
 Db 902 GGGGTTCTTAACAG 916  
 RESULT 9  
 CG442730/C CG442730 900 bp DNA linear GSS 17-SEP-2003  
 LOCUS OGVS09TV ZM.0.7.1.5\_KB Zea mays genomic clone ZM86M4046A17,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG442730  
 VERSION CG442730.1 GI:34822716  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 900)

## AUTHORS

Whitejaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Reenick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nundberg, A., Robbins, D. and Lakey, N.

## TITLE

Consortium for Maize Genomics

## JOURNAL

Unpublished (2002)

## COMMENT

Other\_GSSs: OGVH509TH  
Contact: Cathy Whitejaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitejaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..900

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBMA0486A17"

/clone\_lib="ZM 0.7 1.5\_KB"

/note="Vector: pBCSK-7 Site 1: HincII, 0.7-1.5 kb

methylation filtered genomic DNA library"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.52e-112 Length: 900  
Score: 1010.00 Matches: 170  
Percent Similarity: 78.72% Conservative: 63  
Best Local Similarity: 57.43% Mismatches: 59  
Query Match: 49.34% Indels: 4  
DB: 29 Gaps: 2

US-10-069-772-2 (1-377) x CG442730 (1-900)

QY 82 ProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrrValIleGlyHisGln 101  
Db 900 CCGCTCTAGTGGATCGACAGGCTGCGTGCACCGGCTGTGATCGATCGGACGAG 841  
QY 102 CysGlyHisAlaPheSerAspTyrGlnLeuIleAspPheValGlyPheValLeu 121  
Db 840 TGTGGCCACAGCGCTTCTCGAGAGTACCGCTCTCGACGATGTGGCTGTGTGCTG 781  
QY 122 HisSerAlaLeuLeuThrProTyrPheSerTrrPylsTyrSerHisArgAsnHisAla 141  
Db 780 CACTGTGCTGATGTGCTCCGACTTCTGTGAAAGTACAGCCAGCGGACCACTCC 721  
QY 142 AsnThrAsnSerLeuAspAsnAspGlnValTyrIleProLysArgLysSerLysValLys 161  
Db 720 AACATTGGCTCCCTCGACGCGGACGAGGTGTGTGCGCCAGAGAGAGAGAGAGCGCTCCG 661  
QY 162 IleTyrSerLys--LeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180  
Db 660 TGGTACAGCGGTACGTGTGCAACAGCCCGGCGGCGCTGTCTGCAATGCTGTGAG 601  
QY 181 LeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysLysTyrGlyArg 200  
Db 600 CTAAACCTCGGAGTGGCACTGACTGTGGCCACCAAGTGTGGAGTGGCCCGTACCCGCGC 541  
QY 201 PheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGlnArgValGlnVal 220  
Db 540 TTCGCTGCCCACTAGACCCCTTACCGCCGATCTACAGCAGCGGAGCGGCCCGCCGTC 481  
QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAlaAla 240  
Db 480 TTCGCTCGGACGCGCGGTGTGGCCCGGCTGTGCGGCTGTACAAAGCTGGCGCGGACG 421  
QY 241 LysGlyAlaAlaTrrPvalIleAsnMetTyrAlaIleProValLeuGlyValSerAlaPhe 260  
Db 420 TTCGGGTTCGTGGT 361  
QY 261 PheValLeuIleThrTyrLeuHisIleThrHisLeuSerLeuProIleTyrAspSerThr 280

## Db

360 CTGGATCGTACCTTCTCTCAGACACACCGCGGTCTCCCGGCTAGACATCCAGC 301

## QY

281 GluTrrPantTrrIleLysGlyAlaLeuSerThrIleAspAspPheGlyPheLeuAsn 300

## Db

300 GAGTGGAGCTGCGCGCGGCTGACCAAGCGGATGAGCGGATGAGCGGCGCTTCAAC 241

## QY

301 ArgValPheHisAspValThrHisIleThrHisValLeuHisIleLeuSerTrrIlePro 320

## Db

240 CGCGTGTTCACACATACACGACACACAGCGTGTGACCATCTCTTCCACCGTGC 181

## QY

321 HisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValLeuGlyGluTyrTrrLys 340

## Db

180 CACTACCAAGCGCGTGCAGCTTACCAAGCGGATGAGCGGATGAGCGGATGAGCTATCAG 121

## QY

341 IleAspArgThrProIlePheLysAlaMetTyrTrpGlyAlaLysGlyCysAlleTrrIle 360

## Db

120 TTGACCCCGACCCCGATGCGCAAGCGGATGAGCGGAGCTGAGGATGATCTTACGTC 61

## QY

361 GluProAspGluAspSerGluHisLysGlyValPheTrrTrrHisLys 376

## Db

60 GAGCCCGAGAACGCGC-----AGGGCATCTTATGTATCAACAG 22

## RESULT 10

## CF098768/c

## LOCUS

## DEFINITION

OHN8F08.y3.ab1 OH N sunflower H. argophyllus (drought stress)

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Alexander Kozik [R.W.Michelmores]  
Department of Vegetable Crops, R.W.Michelmores Lab  
University of California at Davis (UCD)  
Asmudson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.org [michelmores@vegmail.ucdavis.edu]  
belongs to contig OH\_Ca\_Content96400, see http://cgpdb.ucdavis.edu/  
for details.  
Plate: OHN8 row: F column: 08.

## FEATURES

## source

## Location/Qualifiers

## 1..613

## /organism="Helianthus argophyllus"

## /mol\_type="mRNA"

## /db\_xref="taxon:73275"

## /clone="OHN8F08"

## /lab\_host="E.coli"

## /clone\_lib="OH N sunflower H. argophyllus (drought stress)"

## /note="Vector: pGBM-1; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and cloned into a high-copy vector pGBM-1. Details of library construction can be obtained at http://cgpdb.ucdavis.edu/"

## ORIGIN

## Alignment Scores:

Pred. No.: 2.1e-108 Length: 613

Score: 977.00 Matches: 176

Percent Similarity: 97.85%  
 Best Local Similarity: 94.62%  
 Query Match: 47.73%  
 DB: 14  
 Gaps: 0

US-10-069-772-2 (1-377) x CF098768 (1-613)

QY 1 MetGlyAlaGlyValGlyMetSerAspProSerGluGlyValAsnIleLeuGluArgVal 20  
 DB 560 ATGGGTGAGGATGGCCGATGTCAGACCATCTGAGGCGAAAGATCCCTCGAAGCTGC 501  
 QY 21 ProValAspProPheThrLeuSerAspLeuValAlaIleProThrHisGlyPhe 40  
 DB 500 CCCATTGATCCACCATCTCACTTAAGCATTAAGAAAGACATCCCTCGCTCATGCTTC 441  
 QY 41 GluArgSerValIleArgSerSerTyrrValValHisAspLeuIleValAlaTyrrVal 60  
 DB 440 GAACATCTGTATCTCGTTCACTTACTATGTGTTCATGACTGATGTCCTATGTC 381  
 QY 61 PheTyrrTyrrLeuAlaAsnThrTyrrIleProLeuIleProThrProLeuAlaTyrrLeuAla 80  
 DB 380 TTTTACTCTCTGCGAAGCATATACCTCTTCTTCTTCCCTACCCCATGGGCTTACTAGCA 321  
 QY 81 TTPProValTyrrTTPPheCysGlnAlaSerIleLeuThrGlyLeuTTPValIleGlyHis 100  
 DB 320 TGGCGGTTTACTGTTTGTTCAGCTGATCCATCCCTGAGGCTTATGGCTCATCGCTAC 261  
 QY 101 GluCysGlyHisHisAlaPheSerAspTyrrGlnLeuIleAspAspIleValAlaTyrrVal 120  
 DB 260 GAATCGGTCACCAAGCCATATGATGATCAATGATGATGATGATGATGATGATGATGATG 201  
 QY 121 LeuHisSerAlaLeuLeuThrProTyrrPheSerTTPlySerHisArgAsnHis 140  
 DB 200 CTCCTTACAGCTCTCTATACCCCTTATTTCTCTGGAATACAGCCATCGAAGCACACAC 141  
 QY 141 AlaAsnThrAsnSerLeuAspAsnAspGluValTyrrIleProValArgIleSerVal 160  
 DB 140 GCAACAGCAATTCCTTGATACAGTGAAGTTTCAATTCCTTAAGCGAAGCGCAAGT 81  
 QY 161 LysIleTyrrSerLeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180  
 DB 80 GCAAGTTTACTCAAACTCTTACATCCCTGATGAGTTCATCTTGTGTTTGG 21  
 QY 181 LeuThrLeuGlyPhePro 186  
 DB 20 TTAACCTTAGGGTTTCCC 3

RESULT 11  
 CC332198 869 bp DNA linear GSS 16-MAY-2003  
 LOCUS OG1BC43TV ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0362G13,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC332198  
 VERSION CC332198.1 GI:30801369  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 869)  
 Whitealaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 CONTACT: Cathy Whitealaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitealaw@tigr.org  
 Seq primer: TP

FEATURES  
 source  
 Class: sheared ends.  
 Location/Qualifiers  
 1..869  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0362G13"  
 /clone\_id="ZM 0.7.1.5 KB"  
 /note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

ALIGNMENT Scores:  
 Pred. No.: 1,22e-106 Length: 869  
 Score: 964.50 Matches: 163  
 Percent Similarity: 77.16% Conservative: 60  
 Best Local Similarity: 56.40% Mismatches: 65  
 Query Match: 47.12% Indels: 1  
 DB: 28 Gaps: 1

US-10-069-772-2 (1-377) x CC332198 (1-869)

QY 39 CysPheGluArgSerValIleArgSerSerTyrrValValHisAspLeuIleValAla 58  
 DB 1 TGTTCAGCGCTCGGTGCTCAAGTCTTCTCTTCAAGTCTCGTACCTGATCCGCGC 60  
 QY 59 TyrrValPheTyrrTyrrLeuAlaAsnThrTyrrIleProLeuIleProThrProLeuAlaTyrr 78  
 DB 61 GCGGCGCTCGTACTTGGCCCTGTACCATCCCGGCGCTCCGAGCCGCTTCAGATAC 120  
 QY 79 LeuAlaTTPProValTyrrTTPPheCysGlnAlaSerIleLeuThrGlyLeuTTPValIle 98  
 DB 121 GCCGCTGCGCTCTCTATGATGCGCACAGCTGCGTGCACCGCGCTGTGGCTATC 180  
 QY 99 GlyHisGluCysGlyHisHisAlaPheSerAspTyrrGlnLeuIleAspAspIleValAla 118  
 DB 181 GGGCAGGATGGCGACACAGCCCTTCTGGAATACCCGCTCTCGAGCATCTTGGC 240  
 QY 119 PheValLeuHisSerAlaLeuLeuThrProTyrrPheSerTTPlySerHisArgAsn 138  
 DB 241 CTGGTGTGCACTGTGCTGATGTCCTCGTATCTCTGTGAAGTACAGCACCGGCGC 300  
 QY 139 HisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrrIleProValArgIleSer 158  
 DB 301 CACCATCTCAACATTTGCTCTGAGCGCACAGGAGTGTGCTCCCAAGAAAGAGAA 360  
 QY 159 LysValLysIleTyrrSerLys--LeuLeuAsnAsnProProGlyArgValPheThrLeu 177  
 DB 361 GCGTGGCGGTATCACCGCGTACGTGTGCAACAGCCCGTGGGCGGTCTGTCAGATC 420  
 QY 178 ValPheArgLeuThrLeuGlyPheProLeuTyrrLeuLeuThrAsnIleSerGlyLysVal 197  
 DB 421 GTTCGACAGCTAACCTCGGTGCGCACTGATCTGCGCACCAACGTCTCGGTGCGCGC 480  
 QY 198 TyrrGlyArgPheAlaAsnHisPheAspProLysSerProIlePheAsnAspArgGluArg 217  
 DB 481 TACCGCGCTTGGCTGCTGACGACCCCTTAAGCGCCGATCTACAGGACCGGAGCGC 540  
 QY 218 ValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrrAlaIleLysLeuLeu 237  
 DB 541 GCCAGGCTTCTGCTCGACGCGCGCTGTGCGCGGTGCTGCGGCTGTACAGCTG 600  
 QY 238 ValAlaAlaLysGlyAlaAlaAlaTTPValIleAsnMetTyrrAlaIleProValLeuGlyVal 257  
 DB 601 GCGGAGAGCTTGGGTCTGTTGGTGTGCGCGCTACAGCGCGCTGTGATGTG 660  
 QY 258 SerValPhePheValLeuIleThrTyrrLeuHisHisThrHisLeuSerLeuProHisTyrr 277  
 DB 661 AACCGTGGCTGTGATGTACATCTCTCCAGACACCCAGCGGCTCTCCCGCTAC 720  
 QY 278 AspSerThrGluTTPAsnThrIleLysGlyAlaLeuSerThrIleAspArgAspPheGly 297

Db 721 GACTCCAGGAGTGGCTGGCGCGGCTAGCCACCAGTACCGGACTACGCG 780  
 Qy 298 PheleusnargValPhehisaspValThrhisValleuHisleuleser 317  
 Db 781 GCCCTCAACCGCGTTCACACATCCACACACACGTCGTGCACATCTCTTTC 840  
 Qy 318 TyrileproHisTyrhisAlalyeGlu 326  
 Db 841 ACCGTCCGCACTACCAACCGCGTGGAG 867  
 RESULT 12  
 LOCUS CD760583 876 bp mRNA linear EST 01-JUL-2003  
 DEFINITION LinFAD2 lin Linum usitatissimum cDNA, mRNA sequence.  
 ACCESSION CD760583 GI:32372153  
 VERSION CD760583.1 GI:32372153  
 KEYWORDS EST.  
 SOURCE Linum usitatissimum (flax)  
 ORGANISM Linum usitatissimum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosids; eurosids I; Malpighiales; Linaceae; Linum.  
 1 (bases 1 to 876)  
 Cloutier,S. and Fofana,B.  
 One Step RT-PCR on total RNA isolated from 12 after anthesis flax  
 boll  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dr. Sylvie Cloutier  
 Cereals Research Centre, Agriculture and Agri-food Canada  
 195 Dufour Rd, Winnipeg, MB, Canada R3T 2M5  
 Tel: (204) 983-2340  
 Fax: (204) 983-4604  
 Email: secloutier@agr.gc.ca  
 The 'lin' sequences are derived from cloning of fragments obtained  
 by One Step RT-PCR on total RNA isolated from 12 days after  
 anthesis flax boll  
 Seq primer: M13 forward.  
 FEATURES  
 source Location/Qualifiers  
 1..876  
 /organism="Linum usitatissimum"  
 /mol\_type="mRNA"  
 /cultiivar="AC McDuff"  
 /db\_xref="taxon:4006"  
 /tissue\_type="Bolls"  
 /dev\_stage="12 days after flowering"  
 /lab\_host="EMDH10B-TONA"  
 /clone\_lib="Lin"  
 /note="Vector: pBluescript KS+ (Stratagene); Site 1: NotI;  
 Site 2: MuiI; mRNA obtained from bolls 12 days after  
 flowering"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,39e-106 Length: 876  
 Score: 960.00 Matches: 171  
 Percent Similarity: 77.06% Conservative: 44  
 Best Local Similarity: 61.29% Mismatches: 62  
 Query Match: 46.90% Indels: 2  
 DB: 14 Gaps: 2  
 US-10-069-772-2 (1-377) x CD760583 (1-876)  
 Qy 35 IlleprothrhHisCysPhegluArgSerValleArgSer---SerTyrTyrValValHis 53  
 Db 2 ATCCACCGCGACGTCTTCACAGCTCAATCCCGGATCGTTCGTGTACGTGGGATC 61  
 Qy 54 AspleuileValAlaTyrValPheTyrTyrleuAlaSerThrTyrleProleuilePro 73  
 Db 62 GACCTCAACATGACGACATCTTACTACATGCGACACCACTTATCCACTCTCCCT 121  
 Qy 74 ThrProleuAlaTyrleuAlaTyrProValTyrTyrPheCysGlnAlaSerleuThr 93  
 Db 122 AGCCCTCAACTACTCTGCGCTGGCGGTCTACTGCGCTGCAGGCGCTGATCTCTACT 181

Qy 94 GlyleuTyrValleuGlyHisGluCysGlyHisAlaPheSerAspTyrGlnleuile 113  
 Db 182 GGAATATGCGGTGTGGCTGACAGATGGCGGTGACCATGCTTCAAGACTTACAGAGGCTC 241  
 Qy 114 AspleuileValGlyPheValleuHisSerAlaLeuLeuThrProTyrPheSerTyrlys 133  
 Db 242 GACCAATGATGGCTTCTGCTTCATTCGCTCCCTCTTGTCTTCTTCTCTCCGGAAG 301  
 Qy 134 TyrSerHisArgAsnHisAlaSerThrAspSerleuAspAsnAspGluValTyrTle 153  
 Db 302 CACAGCCACCGCGCCACCATTCACACGCGGATCGCTTGATCGTGAAGAGTGTGTC 361  
 Qy 154 ProlyAsArglySerSerlyValleuileTyrSerlyleuLeuAsnAsnProGlyArg 173  
 Db 362 CCNAGAGAGAGGCGGAATGCGGTGATCTCCNAGATCTTACACACCCACCTGCGCT 421  
 Qy 174 ValPheThrleuValPheArgleuThrleuGlyPheProleuTyrleuThrAsnle 193  
 Db 422 GTGATCACTATGGCGCGTCACTTAACCTCGGTGCTGTGATCTTGCGATCAACGTC 481  
 Qy 194 SerGlylyslsTyrGlyArgPheAlaAsnHisPheAspPrometSerProilePheAsn 213  
 Db 482 TCCGGAGACCAATGACCGGTTGCAATGCCATTTCACCTTCACGCTCGATTTACAT 541  
 Qy 214 AspargluArgValAlaValleuLeuSerAspPheGlyleuLeuAlaValPheTyrAla 233  
 Db 542 GATGCGAGCGTATGAGATATCTTATCCAGCAGGAGATATTCACCGTGTCTATC 601  
 Qy 234 IlelyleuLeuValAlaAlaAlaGlyAlaAlaTyrValleuAsnMetTyrAlailePro 253  
 Db 602 CTATACAGACTCGTCTCCACGAAAGACTCGTTGGCGTGCATATACGAGAGTCCA 661  
 Qy 254 ValleuGlyValSerValPhePheValleuLeuThrTyrleuHisThrHisleuSer 273  
 Db 662 CTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721  
 Qy 274 LeuProHisTyrAspSerThrGluTyrAsnTyr---IlelyGlyAlaLeuSerThrle 292  
 Db 722 TTTCGCACTACAAAGTCTCTCGAATGGGAGCTGATGCGAGGCGCTTCCAGCTG 781  
 Qy 293 AspargluArgPheGlyPheleuAsnArgValPheHisaspValThrhisVal 311  
 Db 782 GATGAGACCTACGCGTATCTCAACACCGTGTTCACAAACATCACGATACACATGTC 838  
 RESULT 13  
 CK210592 1084 bp mRNA linear EST 08-DEC-2003  
 LOCUS FGS022415 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
 DEFINITION aestivum cDNA, mRNA sequence.  
 ACCESSION CK210592  
 VERSION CK210592.1 GI:39572982  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Triticeae; Triticum.  
 1 (bases 1 to 1084)  
 Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,  
 Genswein,B., Graf,R., Grylls,P., Hryca,L.D., Laroche,A.,  
 Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,  
 Peniket,C., Roach,J.L. and Sarhan,P.  
 Functional Genomics of Abiotic Stresses in Wheat and Canola Crops  
 Unpublished (2003)  
 CONTACT: Wm L Crosby  
 Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C01 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada  
 Tel: 306 966 1769  
 Fax: 306 966 2033  
 Email: fgas\_este@ce.usask.ca

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [23,806].

Plate: L58023 row: F column: 21.

## FEATURES

source

1..1084  
Location/Qualifiers  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: library 5 GATE 7"  
/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NciI."

## ORIGIN

## Alignment Scores:

Pred. No.: 8.1e-106 Length: 1084  
Score: 959.00 Matches: 174  
Percent Similarity: 77.08% Conservative: 48  
Best Local Similarity: 60.42% Mismatches: 62  
Query Match: 46.85% Indels: 6  
DB: 14 Gaps: 2

US-10-069-772-2 (1-377) x CK210592 (1-1084)

QY 88 GlnAlaSerIleLeuThgYLeuTrpValIleGlyHisGluCyseGlyHisHisAlaPhe 107  
DB 37 CAGGGCTGCTGATGACCGGGCTGCGGTCATCGGACGAGTGGGGCATGACCCCTTC 96  
QY 108 SerApYrYrGlnLeuIleAspAspIleValGlyPheValLeuHisSerAlaLeuLeuThr 127  
DB 97 TCCGACTCTCTGCTGATGACCGCGGCTGCGGCTCTCCACTCGGCTGCTCTTC 156  
QY 128 ProTYrPheSerTrpLYrSerHisArgAsnHisAlaAspThrAsnSerLeuAsp 147  
DB 157 CCTACTTCTCTGGAGTACAGCCACCGTCCCACTCACTTACACCGGGTGGCTGGAG 216  
QY 148 AsnAspGluValTYrIleProLYrAspYrSerLYrValLYrTYrSerLYr--Leu 166  
DB 217 CGCGATGAGGTCTTGTCCCAAGACGAGAGGGCGCTGGCTGTACACCCCTTACATC 276  
QY 167 LeuAsnAspProGlyArgValPheThrLeuValPheArgLeuThrLeuGlyPhePro 186  
DB 277 TACAAACAACCCCGTGGCGCTCTGTCGACACCTGTCGAGCTCACCCCTCGGGTGGCG 336  
QY 187 LeuTYrLeuLeuThrAsnIleSerGlyLYrLYrTYrArgYrPheAlaAsnHisPheAsp 206  
DB 337 CTGACTGGGGCTCAAGCCCTCAGGCGCGCGTACCCCGGGTGTGCTGCCACTTCAC 396  
QY 207 PrometSerProIlePheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGly 226  
DB 337 CCTTACGGCCGATTTACACGACCGGAGGAGCCAGATTTCATCTCAGACCTCGGA 456  
QY 227 LeuLeuAlaValPheTYrAlaIleLYrLeuLeuValAlaAlaLYrGlyAlaAlaTrpVal 246  
DB 457 GTGCTGGCGGTGTCACTTGTCTGTAAGCTCGTGTGGTGGGTTCGGGGTGG 516  
QY 247 IleAsnMetTYrAlaIleProValLeuGlyValSerValPhePheValLeuIleThrTYr 266

DB 517 GTGCGGCTCTACGGCGTCCCTGTACTGTGAACGTTGGCTGCTCATCCTAC 576  
QY 267 LeuHisIleThrHisLeuSerLeuProHisTYrAspSerThrGluTrpAsnTrpIleLYs 286  
DB 577 CTGACGACACCCACCCCGCTGCGGCTGACACTGACGAGTGGAGTGGCTGGCG 636  
QY 287 GlyAlaLeuSerThrIleAspArgAspPheLYrPheLeuAsnArgValPheHisAspVal 306  
DB 637 GGGGGCTGGCCACCATGACCGGACATCGCATCTCCAACCGCGGTTCACAAATC 696  
QY 307 ThrHisThrHisValLeuHisIleLeuIleSerTYrIleProHisTYrHisAlaLYsGlu 326  
DB 637 ACGACACGACACGTGGCCACCACTATCTTCACACCGGCACTACACGATGAG 756  
QY 327 AlaArgAspAlaIleLYrAspProValLeuGlyGluTYrTYrLYrIleAspArgThrProIle 346  
DB 757 GCCACCAAGGAGATCAACCCATCTCGGCGAGTACTACAGTTGACCCACCCCGCTC 816  
QY 347 PheLYrAlaMetTYrArgGluAlaLYrGluCYrIleTYrIleGluProAspGluAspSer 366  
DB 817 GCCAAGGACATGCGCGGAGGCCAG-GAGTGCATCTACGTGAGCCGAG----- 866  
QY 367 GluHisLYrGlyValPheTrpTYr 374  
DB 867 GACCG-CAGGGGCTTCTGTGATC 889

## RESULT 14

CK270183

LOCUS

DEFINITION

EST716261 potato abiotic stress cDNA library Solanum tuberosum cDNA

clone POACR59 5' end, mRNA sequence.

ACCESSION

CK270183

VERSION

CK270183.1 GI:39827161

KEYWORDS

EST.

SOURCE

Solanum tuberosum

ORGANISM

Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterid; Lamiales; Solanales; Solanaceae; Solanum.

1 (bases 1 to 963)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

Unpublished (2003)

Other ESTs: EST716262

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..963

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="POACR59"

/tissue\_type="abiotic stress treated leaf and root tissue"

/lab\_host="DH10B-TonA"

/clone\_lib="potato abiotic stress cDNA library"

/note="Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;

supplier: Solanum tuberosum var. Kennebec plants were

grown from cuttings on a 16hr light/8 hr dark cycle at 25

C for 3-4 weeks. Abiotic stress conditions were applied to

four separate sets of plants. Set 1 involved saturation of

the soil with 150 mM NaCl and tissues were harvested at

following application of the salt stress (leaves: 2hr,

6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).

Set 2 were grown under the standard conditions and then

were water stressed by withdrawal of further watering

applications. Drought stressed plants were harvested after

cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d

and 5d). Set 3 were grown under the standard conditions



and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

## ORIGIN

## Alignment Scores:

Pred. No.:	2.08e-105	Length:	963
Score:	955.00	Matches:	164
Percent Similarity:	80.15%	Conservative:	46
Best Local Similarity:	62.60%	Mismatches:	52
Query Match:	46.65%	Indels:	0
DB:	14	Gaps:	0

US-10-069-772-2 (1-377) x CK270183 (1-963)

```

Oy 113 llaaspplllevalglyphevalleuhsersalaleuethrprotyrphesertp 132
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 6 gttgatgacacccgttgaccttcttccatctgctgttggtgacccgtacttcttgg 65

Oy 133 lyeTyserrHsArGAsnHsHsAlasnthrsasrserleuapAsnAsnGlyValTyr 152
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 AAATATAGTATCGTCGCCACACTCCCAACACTGCTCCCTCGAGCGGATGAGGCTTTT 125

Oy 153 lIleProlyArGlySerSeryVallylleTyserySleuLeuAsnProProGly 172
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 126 GTGCCCAAGCAAAATCTCGACTCGAGTATTCAGATCTTGAACATCCACAGGC 185

Oy 173 ArGyAlPheThrLeuValPheArGleuThrleuGlyPheProLeuTyrLeuLeuThra 192
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 186 AGGGTCTCTCACTTACATCACCTCTTGGCTGGCGGTGTACTTGCGCTTCAT 245

Oy 193 lIleSerGlylylyrGlyArGpHeAlasnthrsPheAsnProMetSerProIlePhe 212
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 246 GTATCTGGACACCATACGACCGATTCAGTCACTAGTCACTTACGCGCCAAATCAC 305

Oy 213 AsnAsnArGAlArGValGlnValleuSerAsnProGlyLeuAlaValPheTyr 232
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 306 AACAAACGTGAGAGGCTACAGATCTCTTCTGATCTGAGTTCGAGTTTGTAT 365

Oy 233 AlaIlelyleuLeuValAlaAlaLyGlyAlaAlaTyrValIleAsnMetTyrAlaIle 252
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 366 CTGCTATACCGTATGCTTACGAAAGTCTAGCTGCTAGTGCATCTACCGTATA 425

Oy 253 ProValleuGlyValSerValPhePheValleuThrTyrLeuHsHsThrHsleu 272
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 426 CCCCTCTCTGTCGTAACGGCTCTTGTCTGTGACACTTCTGACAGACATCACCA 485

Oy 273 SerleuProHsTyrAsnSerThrGlyTyrPheAsnTyrIlelySgLyAlaLeuSerThrIle 292
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 486 TCATTGCCACACTACGATTCACCGAGGAGATGGCTTACGGAGACTTGGCAACCTGT 545

Oy 293 AspArGAsnProGlyPheLeuAsnArGValPheHsAsnValThrHsThrHsleu 312
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 546 GACAGAGACTATGGGGTCTTAAACAGGCTTCCACACATCACCGACATCACGTGTG 605

Oy 313 HsHsleuIleSerTyrIleProHsTyrHsAlaLySgLyAlaAsnAsnAlaIlelyS 332
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 606 CACCATCTGTTCTAACCATGCACTACACCGAGTGGAGGCAACCAAGAGTCAAG 665

Oy 333 ProValleuGlyLylyrTyrTyrLeuIleAsnProIlePheIlePheValIleMetTyrArG 352
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 666 CCACTACTCGAGACTACTACCAATTCATGGAACCCGATTTTCAAGGCAATGGAGG 725

Oy 353 GluAlaLySgLyValTyrIleGlyProAsnProGlyAsnSerGlyHsAlaLySgLyValPhe 372
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 726 GAAGCTAAAGAGTCTCTACGTCGAGAAAGACGAAATCATCTCAAGGCAAGGTCTTC 785
  
```

Oy 373 TrpTyr 374  
 |||  
 Db 786 TGTATC 791

## RESULT 15

BU238570

## DEFINITION

Des01.13f05 A Des01 AAFC ECORC cold stressed Flkweed seedlings  
 LOCUS Descurainia sophia cDNA clone Des01\_13f05, mRNA sequence.

## ACCESSION

BU238570.1 GI:22750395

## VERSION

EST.

## KEYWORDS

EST.

## SOURCE

Descurainia sophia

## ORGANISM

Descurainia sophia

## REFERENCE

1 (bases 1 to 1080)

## AUTHORS

Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,

## TITLE

Expressed Sequence Tags from Cold-Stressed Descurainia sophia

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Singh, J.A.

Agriculture and Agri-Food Canada

Kw Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A

0C6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@em.agr.ca.

## FEATURES

Source

1..1080

/organism="Descurainia sophia"

/mol\_type="mRNA"

/db\_xref="taxon:89411"

/clone="Des01.13f05"

/tissue\_type="leaf, stem"

/dev\_stage="1-month seedlings - 1 cm tall - 8 leaf"

/clone\_id="Des01 AAFC\_ECORC\_cold\_stressed\_Flkweed\_seedling"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 20°C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20°C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."

## ORIGIN

## Alignment Scores:

Pred. No.:	1.02e-104	Length:	1080
Score:	950.00	Matches:	164
Percent Similarity:	78.81%	Conservative:	48
Best Local Similarity:	60.97%	Mismatches:	57
Query Match:	46.41%	Indels:	0
DB:	13	Gaps:	0

US-10-069-772-2 (1-377) x BU238570 (1-1080)

```

Oy 107 PheSerAspTyrGlnLeuIleAsnAspIlleValGlyPheValleuHsSersalaleu 126
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 152 TTCAGCACTACCGAGGCTTGAAGACACAGTCCGCTTATCTTCCATCTCTTCTCTC 211

Oy 127 ThrProTyrPheSerTyrPlyrSeryHsArGAsnHsHsAlasnthrsasrserleu 146
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 212 GTCCCTACTCTCTCTGGAATATACATGATCGCGGTACCATTCACACACGAGTTCCCTC 271

Oy 147 AsnAsnArGAlArGValTyrIleProlyArGlySerSeryVallylleTyserySleu 166
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 272 GAAGAGATGAAGCTTGTGCCCAAGCAGAAATCTCATCAAGTGTGAGGCAAAATAC 331

Oy 167 LeuAsnAsnProProGlyArGValPheThrLeuValPheArGleuThrleuGlyPhePro 186
  
```

